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Docket No.: 797

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
PATENT APPLICATION TRANSMITTAL UNDER 37 CFR 1.53

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): Y. Tom Tang, Ping Zhou, Ryle Goodrich, Chenghua Liu, Vinod Asundi, Feiyan Ren, Jie Zhang, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman, Radoje T. Drmanac

Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. Type of application

x This is a new application for a

- x Utility patent.
- ☐ Design patent.

x Applicants claim small entity status (See 37 CFR 1.27)

2. Application Papers Enclosed

1	Title Page
142	Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)
4	Page(s) of Claims
1	Page(s) of Abstract
0	Sheet(s) of Drawings (Figs. X-X) ☐ Formal ☐ Informal
723	Page(s) of Sequence Listing

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on **November 17, 2000,** in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No EK415382545US

Sandy Fong

3. Oath or Declaration

☐ Enclosed

- ☐ Executed by (check all applicable boxes)
- ☐ Inventor(s)
- ☐ Legal representative of inventors(s) (37 CFR 1.42 or 1.43)
- ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
- ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.

x Unexecuted – the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

4. Additional Papers Enclosed

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- x Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence
- x Statement Under 37 CFR § 1.821
- x Paper copy of sequence listing identical to computer copy (723 pages)
- ☐ Microfiche computer program
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- x Return receipt postcard
- ☐ Other ______________

5. Priority Applications Under 35 USC 119

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below and

- ☐ are attached.
- ☐ will follow.

6. Filing Fee Calculation (37 CFR 1.16)

A. x **Utility Application**

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		**OTHER THAN A SMALL ENTITY**	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				$355.00		$710.00
TOTAL	30-20	= 10	X 9 =	$90.00	X 18=	$0.00
INDEP.	3-3	= 0	X 40 =	$00.00	X 80 =	$0.00
Γ First Presentation of Multiple Dependent Claim			+ 135 =	$135.00	+ 270 =	$0.00
FILING FEE:				**$580.00**	**OR**	$0.00

B. ☐ **Design Application ($160.00/$320.00)** Filing Fee: $______________

C. ☐ **Plant Application ($245.00/$490.00)** Filing Fee: $______________

D. **Other fees**

☐ Recording Assignment [Fee -- **$40.00** per assignment] $____________

☐ Petition fee for filing by other than all the inventors or person on behalf of the inventor where inventor refused to sign or cannot be reached [Fee -- **$130.00**] $____________

☐ Other $____________

TOTAL FEES ENCLOSED $ **580.00**

7. **Method of Payments of Fees**

☐ Enclosed check

x Charge Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed

☐ Not enclosed

8. **Deposit Account and Refund Authorization**

The Commissioner is hereby authorized to charge payment of any additional fees due or credit any overpayment to Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed.

Please refund any overpayment to Hyseq, Inc. at the address below.

Please direct all future correspondence to Leslie A. Mooi at the address below.

Respectfully submitted,

Date: November 17, 2000

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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

Express Mail Label No.: EF415382545US

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. BACKGROUND OF THE INVENTION

1.1 TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

1.2 BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

2. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 – 362 and are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1 – 362 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1 – 362. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1 – 362 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1 – 362. The sequence

information can be a segment of any one of SEQ ID NO: 1 – 362 that uniquely identifies or represents the sequence information of SEQ ID NO: 1 – 362.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-362 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-362 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1–362; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1–362; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1–362. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under

stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1–362; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-362; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and “substantial equivalents” thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These

techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g., in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form

the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products.

Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 1); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

3. DETAILED DESCRIPTION OF THE INVENTION

3.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms “a”, “an” and “the” include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms “biologically active” or “biological activity” refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise “immunologically active” or “immunological activity” refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells” as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms “complementary” or “complementarity” refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5’-AGT-3’ binds to the complementary sequence 3’-TCA-5’. Complementarity between two single-stranded molecules may be “partial” such that only some of the nucleic acids bind or it may be “complete” such that total complementarity exists between the single stranded molecules.

The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of

oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or “probe” or “primer” are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-362.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOs: 1-362. The sequence information can be a segment of any one of SEQ ID NOs: 1-362 that uniquely identifies

or represents the sequence information of that sequence of SEQ ID NO: 1-362. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms “operably linked” or “operably associated” refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term “pluripotent” refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms “polypeptide” or “peptide” or “amino acid sequence” refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term “translated protein coding portion” means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term “mature protein coding sequence” means a sequence which encodes a peptide or protein without a signal or leader sequence. The “mature protein portion” means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol)

and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or “analog”) refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e g*., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. “Conservative” amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions,

deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or “substantially purified” as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli*, will be free of

glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted"

proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M $NaHPO_4$, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no

more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term “totipotent” refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and

the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

3.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1 – 362; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1 – 362; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEQ ID NO: 1 - 362. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1 – 362; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1- 362. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known

methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1 – 362 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1 - 362 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1 - 362 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1 - 362, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can

differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1 - 362, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NOs: 1 - 362 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NOs: 1 - 362, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably

constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by

the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-362, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and

the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 362 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 362 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the

protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived

from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

3.3 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous

promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7

lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5′ flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the

invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this

purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

3.4 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 1-362 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NOs: 1 - 362 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NOs: 1 – 362 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 1-362 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 1-362 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 1-362.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for

example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments

of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: *A Laboratory Manual*; Ausubel et al., *Current Protocols in*

Molecular Biology. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 1-362.

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.,* U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in

the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin

(TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

3.4.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

3.5 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient

expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired

protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.,* inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting

sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

3.6 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased

protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

3.7 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

3.7.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when

labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology:

Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

3.7.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

3.7.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19;

Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter

6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

3.7.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of

mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a

specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

3.7.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation

of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I.

Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

3.7.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue.

De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising

such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

3.7.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes

viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent.

Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected

cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

3.7.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

3.7.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

3.7.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

3.7.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases,

blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl,

Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

3.7.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of

such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of

colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

3.7.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or “leads” via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

3.7.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind

polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.,* increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

3.7.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or

promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

3.7.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

3.7.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases

or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple

sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;
(ii) increased sprouting of neurons in culture or in vivo;
(iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
(iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive

bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

3.7.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

3.7.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving

inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

3.7.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963,

Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

3.8 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

3.8.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically,

the amount of polypeptide administered per dose will be in the range of about 0.01μg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1μg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

3.9 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF),

platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti- inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

3.9.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome

coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

3.9.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol,

propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose,

hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or

aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without

destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T

cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are

useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering

agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final

composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

3.9.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical

procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50}. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

3.9.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

3.10 ANTIBODIES

Another aspect of the invention is an antibody that specifically binds the polypeptide of the invention. Such antibodies include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, including compounds which include CDR and/or antigen-binding sequences, which specifically recognize a polypeptide of the invention. Preferred antibodies of the invention are human antibodies which are produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments, including Fab, Fab′, F(ab′)$_2$, and F$_v$, are also provided by the invention. The term “specific for” indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow et al. (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor , NY (1988),

Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the invention, antibodies of the invention that recognize fragments are those which can distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

Polypeptides of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J. L. Krstenansky, et al., FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions

associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein. In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., J. Immunol. 35:1-21 (1990); Kohler and Milstein, Nature 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72 (1983); Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with a peptide or polypeptide of the invention. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection. The protein that is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to, coupling the antigen with a heterologous protein (such as globulin or β-galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, Western blot analysis, or radioimmunoassay (Lutz et al., Exp. Cell Research. 175:109-124 (1988)). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell,

A.M., Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)). Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody-containing antiserum is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The present invention further provides the above- described antibodies in delectably labeled form. Antibodies can be delectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labeling are well-known in the art, for example, see (Sternberger, L.A. et al., J. Histochem. Cytochem. 18:315 (1970); Bayer, E.A. et al., Meth. Enzym. 62:308 (1979); Engval, E. et al., Immunol. 109:129 (1972); Goding, J.W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of interest is expressed. The antibodies may also be used directly in therapies or other diagnostics. The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the proteins of the present invention.

3.11 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NOs: 1 - 362 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NOs: 1 - 362 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence

information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based

systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

3.12 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

3.13 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays:

Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

3.14 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

3.15 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NOs: 1 - 362, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives

expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a

skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

3.16 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOs: 1 - 362. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NOs: 1 - 362 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

3.17 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.,* 1985; Dahlen *et al.,* 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.,* 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.,* (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond

joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm$_7$), is then added to a final concentration of 10 mM 1-MeIm$_7$. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm$_7$, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of

Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.,* (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

3.18 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to

the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

3.19 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the

density of the wells is achieved. One to 25 dots may be accommodated in 1 mm^2, depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm^2 and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

4.0 EXAMPLES

4.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

4.2 EXAMPLE 2

Novel Nucleic Acids

The novel nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genepet release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide and amino acid sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1- 362.

Table 1 shows the various tissue sources of SEQ ID NO: 1-362.

The homology for SEQ ID NO: 1-362 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1-362 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1-362 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren

Brunak, and Gunnar von Heijne in the publication " Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

TABLE 1

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	AB3001	4 18 39-40 83 88 98 110 112-113 136 168-169 201-203
adult brain	GIBCO	ABD003	7 15-16 31-32 39-41 45 54 58 63 70 73-75 82-84 92 98 106 110 114 116-117 126 128 130 139 144 155 164 168-169 191-192 195 198 204-215 239-240 249 252 258 272-274
adult brain	Clontech	ABR001	10-11 15 19 39-40 88 106 120 144 168 215-216 258
adult brain	Clontech	ABR006	13 17 20 23 33 39-40 50 58 62 75 82 84 88 100 104 121-122 129 149 168 208 216 223 232-233 239 256 269 277 287-288 353 360
adult brain	Clontech	ABR008	4 10-11 13 17 20 23 25 28-30 32 34-35 39-41 48 50 53-54 58 61 63 68-69 74 76 78 80 84-89 91 98 104 107 112-114 118 121-122 130 134-136 143 153-155 158-160 163-166 168 172-173 184-188 199-200 203 212-213 215-216 219-220 226-227 234 239 242 244 251-252 255-257 263 268 271-272 277-280 287 291 300-301 305-306 316 322 338 346-347 360
adult brain	Clontech	ABR011	157 306
adult brain	BioChain	ABR012	36 247
adult brain	Invitrogen	ABR013	176
adult brain	Invitrogen	ABR014	50 53 100 269
adult brain	Invitrogen	ABR015	19 38 74 161-162
brain	Invitrogen	ABR016	53 74 137 139 239
adult brain	Invitrogen	ABT004	8 15 19-20 28 30 35 75 78 100 106-107 113 134 160 179 181 184 198-199 210 216 224 227 252 254-255 288 340
adipocytes	Stratagene	ADP001	9 13 19 45 74 98 121-122 131 164 187 189-190 217 239
adrenal gland	Clontech	ADR002	9 15 18-19 24-25 31-32 46 56 77-78 112 114-115 117-119 121-122 124 139 170 182 192 209 213 218 220 225 249 276 306
adult heart	GIBCO	AHR001	2 4 7 17 19-22 26-27 34 38 45-46 50 53-54 58 60-61 63 74 76-77 86-87 91 96 98 108 112 114 121-122 131 133 136-140 144 155 160 165-168 184 188 217 226 239 241-242 251 259 265 277-278 290 306
adult kidney	GIBCO	AKD001	4 6-11 13 15-17 19-20 24 30-32

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			34 36-38 47 53-54 60-63 66 69 73-75 78 82-85 87 89-92 96 98 100 103 106 108 110 112-113 116 121-123 126 129 131 134 136 139-142 144 153 155 158-159 169-170 176 181 207 237 239 266-267 271-272 306
adult kidney	Invitrogen	AKT002	7-8 10-11 13 15 19 25-27 32 37-38 53 55-56 66 75 86 90 92 108 123 144 165-166 172 182 199 218 225 233 236 238 260 266-267 332
adult lung	GIBCO	ALG001	8 22 26-28 38-40 47 54 78 91 98 104 110 112 117 139 148 168 189 196 225 239 248 351-352
lymph node	Clontech	ALN001	7 26-27 32 35 38-40 79 82 120 127 152 158-159 169 171 219 239 244
young liver	GIBCO	ALV001	7 14 16-17 19 33 37 53 72 77 107 113 116 118 134 152 168 212 249
adult liver	Invitrogen	ALV002	12 14 17 24 28 32-33 36 58 73 75-76 84 101 116 131 138 140 158-160 182 194 212 238 275 284 323 342-343
adult liver	Clontech	ALV003	271 284 358
ovary	Invitrogen	AOV001	4 6-11 13 15-16 18-21 25-27 31-32 34 36 38-40 46 48 50 53-54 56 58 60 65 70 73-78 80 83-84 86 91-92 95 98 100-101 103-106 108 110-112 115 117-118 124 126-127 129-131 136 139-142 144 148 155 157-161 163-167 169 173-174 178 180-186 188-189 191-193 196 199-200 204-208 210-211 220-223 233 236 239 249-252 260-263 266-270 287-288 306 315 351-352
placenta	Clontech	APL001	30 50 74 82 230
placenta	Invitrogen	APL002	45 50 59 70 75 103 163 223
adult spleen	GIBCO	ASP001	7 19 30 38 45 54 58 62 74 81 83 91 106 110 112-113 116 131 144 151 155 162 165-166 172 176 189 191 215 230 236 239 249 329
testis	GIBCO	ATS001	4 15 19-20 30 48 53 74 89 94 110 126 140 158-159 173 214-215 220 239 245 306
bladder	Invitrogen	BLD001	30 35 59 61 74-75 123 164 221 241 318
bone marrow	Clontech	BMD001	3 6-7 9 13 17 20 26-27 30-31 34 38-40 42 46 53-54 63-79 82-83 85 91 93-98 101 105 110 115 121-122 126 128-129 133-134

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			143 145 154 161-162 176 192 205-206 234 236 239 243 264 289 306 322
bone marrow	Clontech	BMD002	3-4 7 9 13 16-17 19-20 23 30 32 34 36 38-40 47-48 54-56 58 61 68-69 74-75 79 84 108 118-119 121-122 125 128-129 131 133 140 144 147 149 153-154 158-159 161 163 167 171 174 176 185-187 200 211 218 232 239 241 247 252 277-278 285 296 303 310 320 324 329 339 341 353 356 359
bone marrow	Clontech	BMD004	64
colon	Invitrogen	CLN001	18 32 100 106 110 143 153 163-164 178 213 247 266-267 284
cervix	BioChain	CVX001	4 6 8-9 19 22 24-25 28 32 45-46 53 55-56 63 74-75 77-78 83 87 91-92 95 102 105 108 110 123 127 136-137 140 169 172 182 184-186 189-191 199 211 238 249 266-267 274 283 306-308 317 354
endothelial cells	Stratagene	EDT001	2 4 6-7 9 15 17-21 25-28 30 32 36 39-40 45 47-48 53 55-57 60 62-63 69-70 74-76 78 83 85-87 98 101-104 106 108 112-113 119 121-123 130-131 136-137 139-142 155-156 158-159 161 174 189-192 204 208 218 220 223 230 239 251 280 306
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM001	223
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM003	223
Genomic clones from short arm of chromosome 8	Genomic Data from Genetic Research	EPM004	223
fetal brain	Clontech	FBR001	32 227
fetal brain	Clontech	FBR004	319
fetal brain	Clontech	FBR006	7 10-11 13 17 20 23-25 28-29 32 35 41-42 48 50 53 63 75 80 89 91 104 112 121-122 125 130 154 163 165-166 168 171 173 191 199 210 215-216 218 226 232 239 256 272 277 290 300 306 309 319-320 333 353 360
fetal brain	Invitrogen	FBT002	15 17 19 35 69 75 87 104 109 140 163 174 192-193 198-199

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			207 220 228 239 252 256-258
fetal heart	Invitrogen	FHR001	3 8 19 32 41 48 77-79 91 114 119 126 163 165-166 172 174 176 200 218 232 244 263 331 351-352 360-361
fetal kidney	Clontech	FKD001	16-17 36 46 53 74 82 95 104 111 117 169 189
fetal kidney	Clontech	FKD002	26-27 165-166 218 220 232 238 263 306
fetal kidney	Invitrogen	FKD007	38 74
fetal lung	Clontech	FLG001	32 48 139 173 217
fetal lung	Invitrogen	FLG003	10-11 19 36 58 61 69 74 134 163 168 178 194 249 263 266-267 351-352
fetal liver-spleen	Columbia University	FLS001	1-19 21-38 41-62 68 70 72 74-78 87 90-91 93 100-104 106-121 123-125 127 130-131 133-134 141-142 144 149 155-156 161 163 165-167 169 176 194-196 200 207 210 221 224-225 227 231-233 236 238 263 303 306 313 324 336 342
fetal liver-spleen	Columbia University	FLS002	2 5 7-9 12 14 16-18 22-24 30-33 35-40 43-46 48-50 52-53 57 70 72 76-78 84-85 87 90 92 101-102 106-108 110 112 114 116-120 124 127-128 130-131 134-135 140-142 144 155 163 172 174 187 189-190 192 195-196 199 205-207 210 220-221 223-224 230-234 244 251 258 260-261 263 265 275 296 313-315 331 337-338 345 362
fetal liver-spleen	Columbia University	FLS003	19 30 33 139 174 265 313 339 355
fetal liver	Invitrogen	FLV001	10-11 14 17 19 21 37 46 50 61 63 156 163 165-166 172 200 210 238 253
fetal liver	Clontech	FLV002	19 32 74 163 356
fetal liver	Clontech	FLV004	3 14 19 32-33 37 42 47-48 50 58 60 82 85 121-122 129 131 152 171 193 272 353
fetal muscle	Invitrogen	FMS001	28 32 39-40 45 48 50 57 74 107 121-122 131 137 139-140 147 173 204 230 281
fetal muscle	Invitrogen	FMS002	19 23 32 34 55-56 80-81 98 121-122 124 131-132 158-159 199 212 230 280-281 353 357 360
fetal skin	Invitrogen	FSK001	2 4 14-15 17-19 22 41 46 50 53 59 72 75-76 81-82 84 94 103 106 113 128 135 140 144 156 164 167 170 174 188 209-210 220 227 230 238-239 254 306

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			321-322 333-335
fetal skin	Invitrogen	FSK002	4 34 47 54 79 84 113 126-127 129 134 156 192-193 208 223 230 241 277 285 333
fetal spleen	BioChain	FSP001	32 104
umbilical cord	BioChain	FUC001	4 19 22-23 32 38-40 46 55-56 58 61 73-75 91 98-99 103 106 110 112 116 120 123 129-130 139 160 165-166 175 182 230 234 249 251 302
fetal brain	GIBCO	HFB001	6 9 16 19-20 25 32 35-36 39-41 45 48 53-54 56 60 73 80-81 83-92 98 107 112 114 157-159 163 165-166 172 191 197-198 211 226-227 239 350
infant brain	Columbia University	IB2002	6-8 13 15-17 19 21 32 35 41-42 48 50 60-61 77 81 84-85 88 92 104-106 112-113 116 119 134 139 144 160 165-166 168-169 173 176 191 196 199-201 215 223 225 227-228 239 261 285 290 329 339-340 348
infant brain	Columbia University	IB2003	7-9 13 32 39-41 58 92 103 105-106 144 160 162 199 205-206 219 227-228 271 357
infant brain	Columbia University	IBM002	32 88 340
infant brain	Columbia University	IBS001	6 26-27 32 164 199 340
lung, fibroblast	Stratagene	LFB001	2 4 18-19 25 39-40 46 53 55-56 106 112 124 129 136 139 146 150 164 169 189-190 215 230 239 260 349
adult lung	Invitrogen	LGT002	2 6 8-11 15-16 19 26-28 30 32 39-40 46 48 50 53-56 60-61 66 72 74-75 85 87 92 94 96 98 103-104 108 110 112-113 117 119-120 124 130-131 139-140 149 152-153 155 158-159 167 169 174 176 178 184 189-190 195-196 217 220 229-230 234-239 248-250 263 265-267 280 286 310 329-330 351-352
lymphocyte	ATCC	LPC001	7 13 16 19 32 39-40 54 63 74 82 96 113 120 126 130-131 133 144 150 178 184-186 223 239 241 260 262 294 305 339
leukocytes	GIBCO	LUC001	1 3-4 7-9 13 16-20 26-27 30 32 34-35 38-40 46 48 51 53-56 63 66 70 72-76 78 82 84-85 87 89 91-92 95-96 101 106 108 110-112 114 116 120-122 126-127 129-133 136 139 144 146-152 164 175-179 187 192 232 236

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			239 241 266-267 292-294 306 325-327 329 339 359
leukocytes	Clontech	LUC003	7-8 17 55-56 76 84 112 129 131 161-162 176 180 185-186 329
melanoma	Clontech	MEL004	4 13 17 28 30-31 39-40 83 85 92 113 126 129 139 160 162 182 198 232 239 303 324
mammary gland	Invitrogen	MMG001	8-11 16-21 28 30 32 35 41 45 58-59 61 72 74-75 78 84 87 92 103-104 106-107 110 113 115-116 123 128 131 134-135 144 152 163 176 181 183 210 212 220-221 230 234 236 238-239 248 251 260 272-273 275-276 306 331 351-352 360
neuron	Stratagene	NTD001	18-19 39-40 45 74 78 85 91
neuron	Stratagene	NTR001	19 21 57 246 265
neuronal cells	Stratagene	NTU001	8-9 18-19 21 32 81 85 87 128 164 174 184
pituitary gland	Clontech	PIT004	13 47 82 87 98 112 288 354
placenta	Clontech	PLA003	13 48 50 58 77 100 106 112 126 129 152 178 232
prostate	Clontech	PRT001	16 19 22 26-27 32 34 46-47 76-77 92 98 106 112 124 172 214 239 260 280 294
rectum	Invitrogen	REC001	8 10-11 18 30 54 74-76 106 113 123-124 143 163 172 213 220 232 237 260 322-323 340
salivary gland	Clontech	SAL001	8 19 36 74 83 104 118 124 150 176 260 295 304
skin fibroblast	ATCC	SFB002	239
small intestine	Clontech	SIN001	9 17 19 22 32 34 54 57 59-60 73 75 84-85 96 99 107 113 118 134 139 144 149 151 185-187 189 197 199 217 219 221 230-231 248 250 253-254 260 266-267 295 304 356
skeletal muscle	Clontech	SKM001	17 19 39-40 48 89 104 116 131 281
spinal cord	Clontech	SPC001	8 19 32 34 38-40 47 58 61 74 80 83-84 89 104 108 131 139-140 168 187 213 226 236 239 300 350
adult spleen	Clontech	SPLc01	1 46 54 134 236
stomach	Clontech	STO001	7 32 38-40 51 66 74 76 89 117 124 128 169 229 239 253 280 294 296
thalamus	Clontech	THA002	24 30 50 87 124 127 143 163 201 207 220 223 230 266-267 269 279
thymus	Clontech	THM001	7 13 19 25 32 36 39-40 54-56 72 74 82 96 108 113 119 127

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
			137 139 141-142 146 169 184 192 260 276 296
thymus	Clontech	THMc02	9 17 28 30 32 39-40 48 53 61 72 74-75 77 79 82 91 107 112 119-122 125-126 131 139-142 153 171 175-176 178 184 187 205-206 222-223 227 235-236 269 278 289 297 305 310-311 325 327-329 336
thyroid gland	Clontech	THR001	7-11 15 17 19-20 25-27 32 34 36 46 48 53 59 72 82-87 89 91 96 98-99 104 106 110 118-119 121-122 127 130 136 139 144 151-152 158-159 165-167 179 187 204 208 220 239 249 281 283 295 298-299 312 316 344
trachea	Clontech	TRC001	62-63 73 75 86-87 89 101 147 192 239 266-267 282-283
uterus	Clontech	UTR001	4 8 17 19 22 26-27 32 39-40 46 63 82 98 110 130 151

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	L29075	Dictyostelium discoideum G-box binding factor	173	21
2	AL359215	Streptomyces coelicolor A3(2) putative phosphoglycerate mutase.	133	28
3	AF228713	Homo sapiens EDAG-1	1671	100
4	AC007130	Homo sapiens similar to 3-hydroxyisobutyrate dehydrogenase ; similar to P29266 (PID:g416873)	1557	100
5	AB040926	Homo sapiens KIAA1493 protein	1973	98
6	AF193016	Homo sapiens methyltransferase COQ3	1609	99
7	U95825	Homo sapiens androgen-induced prostate proliferative shutoff associated protein	2968	63
8	AL390081	Homo sapiens SEMA4B, Semaphorin 4B	3560	99
9	AC002130	Arabidopsis thaliana F1N21.9	258	50
10	Z38061	Saccharomyces cerevisiae mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	323	27
11	D88733	Equine herpesvirus 1 membrane glycoprotein	284	24
13	M80783	Homo sapiens B12 protein	1144	70
14	U72678	Mus musculus EF-9	792	92
15	AK026486	Homo sapiens unnamed protein product	427	83
16	AK025813	Homo sapiens unnamed protein product	1010	100
17	AF151036	Homo sapiens HSPC202	722	84
18	AY007148	Homo sapiens similar to Homo sapiens HSPC197 mRNA with GenBank Accession Number AF151031.1	984	100
19	X57432	Rattus rattus ribosomal protein S2	956	97
20	AF164793	Homo sapiens protein x 013	386	100
21	J02642	Homo sapiens glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)	1639	95
22	M34573	Homo sapiens alpha-2 collagen type VI-a	515	100
23	AL109928	Homo sapiens dJ551D2.5 (novel protein)	1999	100
24	AF111858	Homo sapiens dimethylglycine dehydrogenase precursor	3918	99
25	U64854	Caenorhabditis elegans partial CDS	184	25
26	AF151072	Homo sapiens HSPC238	838	99
27	AF151072	Homo sapiens HSPC238	393	96
28	AK024825	Homo sapiens unnamed protein product	1794	99
29	AF285631	Rattus norvegicus secretory carrier membrane protein 4	894	75
30	AK024113	Homo sapiens unnamed protein	3672	99

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		product		
31	AL161515	Arabidopsis thaliana putative protein	146	52
32	AJ007798	Homo sapiens stromal antigen 3, (STAG3)	6320	99
33	D31856	Bacillus subtilis HutI protein, imidazolone-5-propionate hydrolase	667	39
34	AL391145	Arabidopsis thaliana putative protein	423	24
35	AF134726	Homo sapiens G7A	1591	46
36	AJ276485	Homo sapiens integral membrane transporter protein	1502	100
37	J05158	Homo sapiens carboxypeptidase N (EC 3.4.17.3)	2274	88
38	X57351	Homo sapiens 1-8D	673	97
39	AF230904	Homo sapiens c-Cbl-interacting protein	3437	100
40	AF230904	Homo sapiens c-Cbl-interacting protein	2615	99
41	AF276893	Homo sapiens p21-activated protein kinase 6	3550	100
42	AF269255	Homo sapiens lysosomal apyrase-like protein 1	3198	100
43	S85655	Homo sapiens prohibitin	742	84
44	AB040926	Homo sapiens KIAA1493 protein	1973	98
45	AF151063	Homo sapiens HSPC229	1012	100
46	X68277	Homo sapiens protein-tyrosine phosphatase	1886	100
47	Z98745	Homo sapiens dJ29K1.2	889	51
48	AF032668	Rattus norvegicus rsec15	3738	92
50	AF195534	Rattus norvegicus GERp95	4513	99
51	AF161368	Homo sapiens HSPC105	513	98
52	W73147	Amino acid sequence of the soluble complement receptor 1	651	81
53	AF271212	Homo sapiens disrupter of silencing SAS10	2431	100
54	AF116646	Homo sapiens PRO0082	598	100
55	AF145613	Drosophila melanogaster BcDNA.GH03108	817	46
56	AF145613	Drosophila melanogaster BcDNA.GH03108	884	38
57	AL023803	Homo sapiens dJ616B8.3 (novel gene)	2287	100
59	AC024877	Caenorhabditis elegans contains similarity to Pfam families PF00621 (Guanine nucleotide exchange factor for Rho/Rac/Cdc42-like GTPases, score=58.2, E=1.7e-13, N=10 and PF00169 (PH (pleckstrin homology) domain, score=17.0, E=0.00071, N=1)	296	31
60	AL390114	Leishmania major probable proteophosphoglycan	154	30
61	AL031427	Homo sapiens dJ167A19.1 (novel	732	51

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		protein)		
62	AL390935	Leishmania major possible CG17807 protein	151	43
63	J04067	Canis familiaris microsomal signal peptidase	930	99
64	AF062378	Mus musculus calmodulin-binding protein SHA1	1782	60
65	AE001002	Archaeoglobus fulgidus ATP-dependent RNA helicase, putative	195	29
66	X69065	Erythroid ankyrin [Mus musculus]	181	30
68	AF017807	Homo sapiens Arp2/3 complex 16kDa subunit	371	100
69	AC007660	Arabidopsis thaliana putative translation initiation factor	173	29
70	AJ243177	Xenopus laevis Xenopus RPA interacting protein alpha	447	42
71	AF226055	Homo sapiens HTGN29	1367	100
72	AF090930	Homo sapiens PRO0478	180	89
73	AF118084	Homo sapiens PRO1914	350	98
74	AB028893	Homo sapiens ribosomal protein S11	824	100
75	AK024500	Homo sapiens FLJ00109 protein	1514	100
76	AF238866	Mus musculus LNR42	1041	99
77	AC026875	Arabidopsis thaliana T6D22.6	129	30
78	U42436	Caenorhabditis elegans Hypothetical protein C49H3.3	130	32
79	M80902	Homo sapiens AHNAK nucleoprotein	8529	99
80	W90962	Human CSGP-2 protein [homo sapiens]	2346	99
81	AF206661	Gallus gallus neuronal tetraspanin	1066	81
82	S73591	Homo sapiens brain-expressed HHCPA78 homolog VDUP1	800	42
83	AF116650	Homo sapiens PRO0786	302	100
84	L26335	Cavia porcellus zinc finger protein	1493	99
85	AF209198	Homo sapiens zinc finger protein 277	2357	100
86	AE001399	Plasmodium falciparum GAF domain protein (cyclic nt signal transduct.)	178	35
87	Y48226	Human prostate cancer-associated protein 12 [Homo sapiens]	1204	96
88	M94389	Loligo pealei neurofilament protein	165	23
89	AF121775	Homo sapiens nasopharyngeal carcinoma susceptibility protein LZ16	903	58
90	AF116675	Homo sapiens PRO1942	257	100
91	AE002760	Drosophila melanogaster CG14464 gene product	195	43
92	AK000100	Homo sapiens unnamed protein product	841	100
93	AB020236	Homo sapiens ribosomal protein L27A	754	99
94	AF119865	Homo sapiens PRO2176	470	97
96	AF138863	Homo sapiens PRO1677	868	99
97	X14361	Homo sapiens CR-1 receptor SCR9 (or	135	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		16) C-term. (21 is 3rd base in codon) (106 is 1st base in codon)		
98	Z24725	Homo sapiens mitogen inducible gene mig-2	3576	99
99	U64598	Caenorhabditis elegans weakly similar to S. cervisiae PTM1 precursor (SP:P32857)	398	45
100	AC004770	Homo sapiens BC269730_4	1527	84
101	AL139075	Campylobacter jejuni NOL1\NOP2\sun family protein	312	35
102	AF113694	Homo sapiens PRO1359	416	100
103	U15158	Homo sapiens ESP-2	564	41
104	AL020996	Homo sapiens dJ317E23.3 (novel protein)	1818	99
105	AF161370	Homo sapiens HSPC107	824	100
106	AK000161	Homo sapiens unnamed protein product	284	100
107	AK001784	Homo sapiens unnamed protein product	684	100
108	AE000913	Methanobacterium thermoautotrophicum conserved protein	221	25
109	AF165527	Homo sapiens DGCR8	859	100
110	AF230200	Homo sapiens OVN6-2	358	95
111	Z72516	Caenorhabditis elegans T25G3.1	180	36
112	AF201940	Homo sapiens DC6	505	100
113	AK001301	Homo sapiens unnamed protein product	2040	98
114	U23515	Caenorhabditis elegans weakly similar to gastrula zinc finger protein	205	47
115	AF228021	Bos taurus cyclophilin I	345	91
116	AF166124	Homo sapiens selenoprotein X	527	100
117	AF079445	Dictyostelium discoideum TipC	529	30
118	AB032179	Homo sapiens similar to mouse Ehm2	2255	100
119	U89867	Homo sapiens nuclear matrix protein 55	2449	98
120	U29056	Mus musculus Src-like adapter protein	352	47
121	U22015	Mus musculus retinoid X receptor interacting protein	2190	73
122	AF113538	Homo sapiens retinoid x receptor interacting protein	1800	100
123	AK000158	Homo sapiens unnamed protein product	740	100
124	AF260924	Mus musculus UFD2/D4COLE1E fusion protein	1222	82
125	U12465	Homo sapiens ribosomal protein L35	591	97
126	AJ277591	Homo sapiens p15-2a protein	749	100
127	AF205599	Mus musculus transposase-like protein	2406	74
128	U58975	Homo sapiens proto-oncogene	659	90

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
129	X98374	Rattus norvegicus KIS	2193	99
130	AF151049	Homo sapiens HSPC215	627	100
131	M59807	Homo sapiens putative	907	99
132	U12979	Homo sapiens PC4	563	99
133	AF076642	Homo sapiens regulator of G-protein signaling 13	1218	100
134	AF116718	Homo sapiens PRO2900	396	100
135	AC018758	Homo sapiens GPI-anchored metastasis-associated protein homolog	213	31
136	AC025416	Arabidopsis thaliana F5O11.12	135	36
137	M83186	Homo sapiens cytochrome c oxidase subunit VIIa	247	100
138	AF232937	Mus musculus thymic stroma derived lymphopoietin	247	41
139	M15841	Homo sapiens U2 small nuclear ribonucleoprotein B''	638	100
140	AK026916	Homo sapiens unnamed protein product	2612	99
141	Y05317	Human secreted protein bn97_1 [Homo sapiens]	1508	100
142	Y05317	Human secreted protein bn97_1 [Homo sapiens]	851	99
143	AF041083	Rattus norvegicus RoBo-1	139	25
144	AC024260	Arabidopsis thaliana cell division control protein, putative; 15914-18846	194	25
146	AL022398	Homo sapiens dJ434O14.3.2 (putative protein) (isoform 2)	575	100
147	AF212842	Homo sapiens immunoglobulin-like transcript 11 protein	1280	99
148	AB042827	Rattus norvegicus Nadrin	477	66
149	AK001841	Homo sapiens unnamed protein product	1916	100
150	AJ278120	Homo sapiens putative ankyrin-repeat containing protein	540	98
151	AL135959	Homo sapiens dJ233G16.1 (novel protein)	770	100
152	Y58196	[Homo sapiens] Human STRAP-3 protein, encoded by testis EST AI139607	671	100
153	U41060	Homo sapiens LIV-1 protein	373	50
154	AJ007590	Homo sapiens XRP2 protein	1766	100
155	AB046868	Xenopus laevis beta-catenin-interacting protein	125	46
156	AB027258	Homo sapiens basal transcriptional activator hABT1	1408	100
157	AF039656	Homo sapiens neuronal tissue-enriched acidic protein	1109	96
158	AK001425	Homo sapiens unnamed protein product	1695	99
159	AK001425	Homo sapiens unnamed protein	858	98

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		product		
160	AK002030	Homo sapiens unnamed protein product	1029	100
161	X79417	Sus scrofa 40S ribosomal protein S12	510	83
162	X12597	Homo sapiens HMG-1 protein (AA 1-215)	1140	99
163	AK001159	Homo sapiens unnamed protein product	764	100
164	AK000020	Homo sapiens unnamed protein product	1613	100
165	AK001322	Homo sapiens unnamed protein product	1207	100
166	AK001322	Homo sapiens unnamed protein product	892	98
167	AE003822	Drosophila melanogaster CG8493 gene product	357	36
168	AF023451	Bos taurus guanine nucleotide-exchange protein	187	21
169	AK000154	Homo sapiens unnamed protein product	673	100
170	AJ132702	Mus musculus ATFa-associated factor	435	64
172	AL022311	Homo sapiens dJ1014D13.3 (novel protein)	405	38
174	AB017634	Mus musculus ENP	770	65
175	U40407	synthetic construct T cell receptor alpha chain	1119	80
176	AF043179	Homo sapiens T cell receptor beta chain	681	73
177	AF116678	Homo sapiens PRO1995	587	100
178	AF217522	Homo sapiens uncharacterized bone marrow protein BM046	262	42
179	AB046074	Macaca fascicularis unnamed protein product	515	83
180	X79417	Sus scrofa 40S ribosomal protein S12	429	84
181	AF002668	Homo sapiens MLD	1235	65
182	AB036422	Bos taurus molybdopterin cofactor sulfurase	3509	79
184	AF036696	Caenorhabditis elegans contains similarity to Brassica oleracea non-green plastid phosphate/triose-phosphate translocator precursor (GB:U13632)	662	42
185	AJ277276	Homo sapiens rapa-2	5155	99
186	AJ277275	Homo sapiens rapa-1	5086	100
187	U22296	Rattus norvegicus casein kinase 1 gamma 1 isoform	1444	93
188	AE003750	Drosophila melanogaster CG9996 gene product	468	44
189	Z97056	Homo sapiens dJ434P1.2 (KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum	1103	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		protein retention receptor 3)		
190	AF081126	Drosophila melanogaster ER lumen protein retaining receptor	409	75
192	AF226047	Homo sapiens GL002	863	100
193	AF269167	Homo sapiens arsenite related gene 1	906	60
195	U41805	Mus musculus putative T1/ST2 receptor binding protein precursor	162	26
197	AL357374	Homo sapiens bA353C18.2 (novel protein)	404	97
199	M34551	Homo sapiens 52-kD Ro/SSA ribonucleoprotein	964	42
202	AF230201	Homo sapiens OVC10-2	396	100
203	AK001984	Homo sapiens unnamed protein product	658	100
204	AK000530	Homo sapiens unnamed protein product	691	100
205	U37134	Drosophila melanogaster inturned protein	248	23
206	U37134	Drosophila melanogaster inturned protein	244	23
208	AB033130	Mus musculus testis-specific gene	871	85
209	AK000464	Homo sapiens unnamed protein product	221	100
210	AJ277557	Homo sapiens mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2)	617	100
211	AF127564	Arabidopsis thaliana ubiquitin-protein ligase 1	854	42
213	Y17108	Homo sapiens rhomboid-related protein	485	39
214	AL132776	Homo sapiens dJ393D12.2 (novel LIM domain protein)	1660	99
215	U73819	Mus musculus polypeptide GalNAc transferase-T4	1039	42
216	AL035406	Homo sapiens dJ233K16.1 (KIAA0444, a putative chromodomain helicase DNA binding protein 3 (CHD3))	3844	100
217	M15800	Homo sapiens MAL protein	308	42
218	L29554	Rattus norvegicus alpha 2,6-sialyltransferase	942	80
219	AL137315	Homo sapiens hypothetical protein	983	100
220	AK026027	Homo sapiens unnamed protein product	647	100
221	AL137584	Homo sapiens hypothetical protein	246	97
223	AC005498	Homo sapiens R31665_1	1752	78
225	AC010155	Arabidopsis thaliana F3M18.5	171	34
226	AL080276	Homo sapiens dJ101K10.2 (regulator of G-protein signaling 17 (RGS17) (RGSZ2))	1126	100
227	AF042345	Homo sapiens truncated EVI5	1815	64
228	J04214	Bos taurus retinaldehyde-binding protein precursor	504	39

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
230	AF181263	Homo sapiens EH domain containing 2	2816	99
231	AP001660	Homo sapiens putative gene, multidrug resistance associated protein like	1424	100
232	AB000910	Sus scrofa ribosomal protein	542	100
233	AL133404	Homo sapiens dJ238O23.9 (novel protein similar to rat SAC (soluble adenylyl cyclase))	298	100
234	X51397	Mus musculus MyD88 protein (AA 1-243)	136	25
235	X01403	Homo sapiens T-cell receptor alpha-chain	840	90
236	X14254	Rattus rattus invariant chain (AA 1-280)	745	77
238	U23084	Saccharomyces cerevisiae Ynl0470p	344	35
239	X03342	Homo sapiens rpL32 (aa 1-135)	152	96
240	AF116669	Homo sapiens PRO1828	237	100
241	U23181	Caenorhabditis elegans final exon in repeat region; similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein	135	25
242	AF263913	Mus musculus fidgetin	3864	97
243	AF090892	Homo sapiens PRO0106	290	100
244	U21310	Caenorhabditis elegans F40H6.3 gene product	153	27
246	AK001673	Homo sapiens unnamed protein product	3661	100
247	AL022603	Arabidopsis thaliana putative protein	166	43
248	AL023803	Homo sapiens dJ616B8.3 (novel gene)	339	42
249	X52140	Rattus norvegicus precursor polypeptide (AA -28 to 1152)	5429	87
250	AB020755	Arabidopsis thaliana gene_id:MZN1.18~unknown protein	139	46
251	AE003619	Drosophila melanogaster CG7224 gene product	186	43
252	AC004997	Homo sapiens match to ESTs Z43979 (NID:g573097), R19699 (NID:g774333), and C01164 (NID:g1433394); alternatively spliced form of H_DJ130H16.1a (C-terminal truncation confirmed by C01164)	388	67
254	AE003588	Drosophila melanogaster CG13947 gene product	115	42
256	Y50934	Human fetal brain cDNA clone vc30_1 derived protein #1 [Homo sapiens]	498	100
257	AF242768	Homo sapiens mesenchymal stem cell protein DSC43	1554	100
259	M95779	Bos taurus G protein gamma-5 subunit	333	98

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
260	AL035521	Arabidopsis thaliana putative protein	145	28
261	AF247501	Drosophila melanogaster PINEAPPLE EYE	333	36
263	AL034548	Homo sapiens dJ1103G7.2 (novel protein)	262	100
264	AF119851	Homo sapiens PRO1722	143	63
265	L41834	Ensis minor nuclear protein	173	26
266	X97966	Homo sapiens calcyphosine	963	100
267	X97966	Homo sapiens calcyphosine	660	95
269	AF022383	Homo sapiens complexin I	668	99
271	Y10054	Rattus norvegicus 3-hydroxy-3-methylglutaryl CoA lyase	224	67
274	AF153201	Homo sapiens zinc finger protein dp	179	36
275	X85738	Bos taurus novel brain-specific protein	326	55
277	AF250342	Arabidopsis thaliana SMC-related protein MSS2	266	39
278	AL080242	Homo sapiens bA554C12.1 (RBX1 or ROC1 (ring-box or ring finger protein 1))	131	100
279	Z83760	Ciona intestinalis COS41.4	1162	62
280	U41534	Caenorhabditis elegans similar to yeast MAK16 protein (SP:MK16_YEAST,P10962)	721	54
281	AF272975	Gallus gallus smoothelin-C	543	37
282	AL035414	Homo sapiens dJ667H12.2.2 (novel protein (isoform 2))	588	100
283	AF116661	Homo sapiens PRO1438	145	62
285	AK001757	Homo sapiens unnamed protein product	1300	100
287	U20897	Homo sapiens melanoma ubiquitous mutated protein	2133	100
289	U09847	Homo sapiens zinc finger protein	880	100
290	AJ000079	Trypanosoma cruzi glycosylphosphatidylinositol-specific phospholipase C	225	26
291	AF156549	Mus musculus putative E1-E2 ATPase	2108	49
293	AF161345	Homo sapiens HSPC082	439	100
294	AF116694	Homo sapiens PRO2219	351	88
295	M74027	Homo sapiens mucin	461	39
298	AL133640	Homo sapiens hypothetical protein	2149	100
299	M17886	Homo sapiens acidic ribosomal phosphoprotein (P1)	161	76
300	Y99368	Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100 [Homo sapiens]	300	32
303	AE003708	Drosophila melanogaster CG6171 gene product	144	27
304	M32639	Homo sapiens statherin precursor	276	87
305	Z83844	Homo sapiens dJ37E16.2 (SH3-domain binding protein 1)	897	96

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
306	AE003791	Drosophila melanogaster CG18065 gene product	120	32
307	AF135026	Homo sapiens kallikrein-like protein 3 splice variant 1	1392	100
310	AF198257	Felis catus immunoglobulin kappa light chain	678	76
311	X57725	Homo sapiens TCR Vbeta 22a	626	100
312	AC018513	Homo sapiens unknown	818	100
313	X03249	Bos taurus epsilon-4 beta-globin	321	79
314	AB046099	Macaca fascicularis unnamed protein product	395	88
315	AC006033	Homo sapiens T cell receptor gamma chain; match to S08328 (PID:g106470)	1017	95
316	AB046103	Macaca fascicularis unnamed protein product	801	94
317	U88895	Homo sapiens ORF2	399	81
318	U09848	Homo sapiens zinc finger protein	242	49
319	AB003184	Homo sapiens ISLR	880	59
320	AB036921	Chrysophrys major maturation-inducing protein	797	69
322	AF284422	Homo sapiens cation-chloride cotransporter-interacting protein	4694	100
325	AE000659	Homo sapiens TCRAV8S2	577	100
327	R59748	T cell receptor Valpha2.3 chain [homo sapiens]	636	100
328	AJ004871	Homo sapiens TCR alpha chain	1328	94
329	AF043179	Homo sapiens T cell receptor beta chain	1286	92
330	AF090930	Homo sapiens PRO0478	140	50
332	AF077043	Homo sapiens 60S ribosomal protein L36	275	87
333	AL121988	Homo sapiens dJ34M23.3 (gap junction protein, beta 4 (connexin 30.3))	1457	100
334	D86424	Mus musculus high-sulfur keratin protein	521	87
335	AF090434	Fundulus heteroclitus cytochrome P450 2N1	760	40
336	AF116688	Homo sapiens PRO2133	370	98
337	X85372	Homo sapiens Sm protein F	222	84
338	D87009	Homo sapiens putative	1822	99
339	AE000860	Methanobacterium thermoautotrophicum conserved protein	631	35
340	AL049759	Homo sapiens dJ930L11.1 (similar to KIAA0397)	1305	98
341	AE000004	Mycoplasma pneumonia MG207 homolog, from M. genitalium	141	27
342	AF151076	Homo sapiens HSPC242	135	100
343	AB037902	Homo sapiens truncated aldo-keto reductase	670	100

SEQ ID NO:	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
345	M33014	Drosophila melanogaster ubiquitin	153	62
346	AF053356	Homo sapiens leucin rich neuronal protein	580	46
348	AL137512	Homo sapiens hypothetical protein	751	100
349	S68015	Homo sapiens c6.1A	1664	100
350	AF151037	Homo sapiens HSPC203	318	100
351	AB036432	Homo sapiens advanced glycation endproducts receptor	2133	100
352	AB036432	Homo sapiens advanced glycation endproducts receptor	2094	96
353	AC006942	Homo sapiens R31181_2, partial protein	547	100
354	AF125535	Homo sapiens pp21 homolog	502	95
355	AF227130	Homo sapiens candidate taste receptor T2R3	1629	100
357	AB046626	Macaca fascicularis hypothetical protein	291	93
358	Z69597	Canis familiaris Rod transducin alpha subunit	1145	100
359	AE000659	Homo sapiens TCRAV16S1	565	100
360	Y99368	Human PRO1326 (UNQ686) Amino acid sequence SEQ ID NO:100. [Homo sapiens]	2034	100
362	L06499	Homo sapiens ribosomal protein L37a	187	55

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651E 10.53 4.025e-06 60-80
2	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126B 15.20 7.750e-06 208-220
3	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 9.438e-07 285-319
4	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 7.061e-22 151-190 BL00895C 20.10 8.071e-22 200-236 BL00895A 12.61 1.973e-18 42-63
5	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099A 5.17 5.263e-06 409-415
7	PF00598	Influenza Matrix protein (M1).	PF00598C 19.35 3.333e-07 531-563
9	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522A 8.30 3.250e-06 287-297
10	PR00514	5-HYDROXYTRYPTAMINE 1D RECEPTOR SIGNATURE	PR00514C 11.01 9.061e-07 81-100
11	PR00514	5-HYDROXYTRYPTAMINE 1D RECEPTOR SIGNATURE	PR00514C 11.01 9.061e-07 81-100
12	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775G 10.64 3.487e-07 8-27
13	PR00902	VP6 BLUE-TONGUE VIRUS INNER CAPSID PROTEIN SIGNATURE	PR00902K 11.09 1.000e-05 176-200
14	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.127e-07 159-171 PR00875D 5.00 1.000e-05 158-169
15	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 9.200e-07 181-191 DM01803A 10.51 1.000e-06 178-199 DM01803C 7.00 7.337e-06 214-224
16	PF00803	3A movement protein.	PF00803D 14.15 2.622e-06 41-71
17	PR00170	SODIUM CHANNEL SIGNATURE	PR00170G 7.74 1.000e-05 24-53
18	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701E 13.83 5.684e-06 117-133
20	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415A 6.65 6.063e-06 55-68
21	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418A 20.83 7.731e-06 64-112
22	BL00616	Histidine acid phosphatases phosphohistidine proteins.	BL00616D 15.83 7.268e-06 117-133

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611A 7.73 5.826e-06 173-181
24	BL00832	2'-5'-oligoadenylate synthetases proteins.	BL00832D 21.81 5.017e-06 425-449
25	PR00354	7FE FERREDOXIN SIGNATURE	PR00354C 5.72 8.590e-09 543-561
26	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 3.851e-07 89-105
27	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513A 7.75 1.439e-06 168-180
28	DM00552	GROWTH FACTOR AND CYTOKINES RECEPTORS FAMILY.	DM00552A 11.97 1.000e-05 130-152
29	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701I 8.59 3.088e-06 102-126
30	DM00060	338 kw NEUREXIN ALPHA III CYSTEINE.	DM00060 6.92 3.284e-07 680-690
34	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 6.971e-07 484-496
35	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701A 14.28 4.183e-06 722-744
37	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513C 10.79 8.927e-07 287-304
38	PR00166	AROMATIC AMINO ACID PERMEASE SIGNATURE	PR00166I 11.06 1.000e-05 98-118
39	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003A 14.69 3.803e-06 311-321
40	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003A 14.69 3.803e-06 311-321
41	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 8.788e-07 2-14
42	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701F 14.45 7.750e-06 25-46
43	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895B 8.85 4.185e-06 157-167
44	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099A 5.17 5.263e-06 409-415
45	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519A 8.06 8.984e-06 137-154
46	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 1.828e-07 151-168
47	DM00892	3 RETROVIRAL PROTEINASE.	DM00892B 9.78 2.047e-06 21-27
48	BL00832	2'-5'-oligoadenylate synthetases	BL00832B 15.45 6.836e-07 375-416

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	
49	DM00588	8 kw CHO2 ALPHA ANTIGEN PARAMYOSIN.	DM00588A 10.87 7.128e-06 20-31
50	DM00604	2 SHIGA/RICIN RIBOSOMAL INACTIVATING TOXINS.	DM00604D 13.26 8.250e-06 263-273
51	BL01193	Ribosomal protein S8e proteins.	BL01193A 13.21 1.000e-05 19-50
52	PR00172	GLUCOSE TRANSPORTER SIGNATURE	PR00172F 8.47 9.901e-06 69-90
53	PR00297	10 KD CHAPERONIN SIGNATURE	PR00297A 13.91 4.740e-06 379-395
54	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.710e-06 81-96
55	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.126e-07 352-365
56	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.126e-07 352-365
57	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547E 13.94 4.656e-06 229-252
58	PF00506	Influenza virus nucleoprotein.	PF00506I 10.26 3.723e-06 32-68
60	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522B 9.43 7.338e-07 171-185
61	DM01123	5 kw RESISTANCE TETRACYCLINE METHYLENOMYCIN EXPORT.	DM01123B 20.06 3.187e-06 205-244
62	PR00439	11-S SEED STORAGE PROTEIN FAMILY SIGNATURE	PR00439G 17.85 9.239e-07 82-100
63	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652F 11.66 4.767e-06 100-122
64	DM01785	72 PYRUVATE (FLAVODOXIN) DEHYDROGENASE.	DM01785A 14.90 2.196e-06 218-261
65	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652A 8.92 5.104e-06 315-336
67	BL00405	43 Kd postsynaptic protein.	BL00405F 8.07 9.920e-06 13-44
68	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 9.043e-06 44-66
69	PR00683	SPECTRIN PLECKSTRIN HOMOLOGY DOMAIN SIGNATURE	PR00683D 15.87 9.571e-06 46-65
70	PR00753	1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE SIGNATURE	PR00753C 13.93 7.330e-06 192-213
71	PF00602	Influenza RNA-dependant RNA	PF00602J 9.52 9.727e-06 47-102

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polymerase subunit PB1.	
72	DM01855	PROTEIN-GLUTAMATE O-METHYLTRANSFERASE.	DM01855A 11.54 7.594e-06 27-44
74	BL01277	Ribonuclease PH proteins.	BL01277A 17.39 1.000e-05 50-88
75	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517G 16.45 6.919e-06 755-771
77	PF01073	3-beta hydroxysteriod dehydrogenase/isomerase family.	PF01073B 12.26 9.767e-07 102-147
78	PR00351	MAS20 PROTEIN IMPORT RECEPTOR SIGNATURE	PR00351C 7.03 6.182e-06 99-112 PR00351C 7.03 1.000e-05 5-18
79	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611C 11.08 4.549e-06 1489-1501
80	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111C 9.35 2.800e-06 44-73
82	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407B 16.51 1.000e-06 94-111
83	PR00116	ARGINASE SIGNATURE	PR00116D 14.91 9.850e-06 14-44
84	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517F 11.48 7.250e-06 45-62
87	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522B 9.43 3.535e-07 223-237
88	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 8.034e-08 270-320
91	DM01242	3 THREONINE--TRNA LIGASE.	DM01242B 23.57 4.672e-06 71-120
92	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388E 6.66 3.797e-06 124-136
93	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407B 16.51 9.676e-06 15-32
94	PF00506	Influenza virus nucleoprotein.	PF00506I 10.26 4.555e-06 16-52
95	PR00551	2-S GLOBULIN FAMILY SIGNATURE	PR00551H 11.29 8.740e-06 21-39
96	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756E 11.91 9.338e-06 68-81
97	PR00547	X OPIOID RECEPTOR SIGNATURE	PR00547B 6.96 3.268e-06 17-36
98	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR	PR00651A 16.53 4.000e-06 653-674

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
99	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208C 11.51 9.775e-06 54-71
101	PR00451	CHITIN-BINDING DOMAIN SIGNATURE	PR00451A 6.49 1.000e-05 152-161
102	BL00832	2'-5'-oligoadenylate synthetases proteins.	BL00832B 15.45 7.569e-06 1-42
103	BL00405	43 Kd postsynaptic protein.	BL00405J 13.28 6.952e-06 142-176
104	DM01242	3 THREONINE--TRNA LIGASE.	DM01242F 10.61 5.500e-07 187-201
105	DM01834	8 HYDROGENASE (FE) SMALL CHAIN.	DM01834A 4.96 7.097e-06 53-60
107	PR00101	ASPARTATE CARBAMOYLTRANSFERASE SIGNATURE	PR00101E 5.52 1.000e-05 111-117
109	PR00902	VP6 BLUE-TONGUE VIRUS INNER CAPSID PROTEIN SIGNATURE	PR00902K 11.09 9.922e-06 91-115
110	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259A 9.27 9.716e-06 9-33
111	BL00785	5'-nucleotidase proteins.	BL00785B 10.65 6.507e-06 53-67
112	PR00652	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652G 10.94 5.429e-06 14-32
113	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 3.661e-06 372-384
114	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637D 7.09 9.449e-07 32-44
115	DM01235	5 kw T4 55.10 METHYLCYTOSINE TRANSCRIPTASE.	DM01235 20.29 9.832e-06 77-108
116	PR00873	ECHINOIDEA (SEA URCHIN) METALLOTHIONEIN SIGNATURE	PR00873C 6.16 9.906e-06 70-81
117	PR00387	3'5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE SIGNATURE	PR00387D 10.81 4.889e-06 155-172
118	PF00598	Influenza Matrix protein (M1).	PF00598A 14.24 7.158e-06 211-254
119	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 8.036e-06 428-467
120	PR00419	ADRENODOXIN REDUCTASE FAMILY SIGNATURE	PR00419D 10.62 9.430e-06 18-33
121	DM00396	5 kw INTRON COI ND4L	DM00396B 7.85 3.739e-07 381-389

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		ND5.	
122	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 5.500e-06 135-147
123	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554E 10.78 4.208e-06 93-110
124	BL00405	43 Kd postsynaptic protein.	BL00405G 7.78 6.294e-06 130-167
125	PR00298	60 KD CHAPERONIN SIGNATURE	PR00298D 10.23 3.847e-06 14-40
126	PR00317	EPENDYMIN SIGNATURE	PR00317A 13.39 9.897e-06 79-99
127	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513B 17.51 3.971e-06 277-290
130	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516G 15.11 8.811e-06 18-35
131	PR00828	FORMIN SIGNATURE	PR00828F 8.56 1.000e-05 61-81
132	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 7.279e-06 28-56
133	PR00586	PROSTANOID EP4 RECEPTOR SIGNATURE	PR00586B 14.97 7.322e-06 10-28 PR00586H 8.65 9.791e-06 16-40
134	PF00954	S-locus glycoprotein family.	PF00954D 18.68 9.843e-06 9-44
135	PR00018	KRINGLE DOMAIN SIGNATURE	PR00018A 14.52 1.000e-05 120-136
136	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115E 14.13 9.921e-06 40-69
137	PR00521	ANDROGEN RECEPTOR SIGNATURE	PR00521A 17.02 9.729e-06 5-25
138	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701I 8.59 5.267e-07 16-40
139	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 7.085e-08 93-121
140	PR00915	LUTEOVIRUS GROUP 1 COAT PROTEIN SIGNATURE	PR00915D 16.14 1.000e-05 374-392
143	DM00522	499 kw TRYPSIN KINASE KUNITZ PANCREATIC.	DM00522A 8.30 4.441e-06 94-104
144	PF00598	Influenza Matrix protein (M1).	PF00598B 13.10 1.623e-06 89-133
145	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 6.250e-06 24-40
147	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701A 14.28 6.049e-06 266-288
148	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513D 11.06 9.920e-06 103-121
149	PF00603	Influenza RNA-dependant RNA polymerase subunit	PF00603D 8.49 9.319e-07 30-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PA.	
150	DM01688	2 POLY-IG RECEPTOR.	DM01688N 11.93 9.920e-08 72-100
151	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637B 10.68 6.906e-06 186-195
152	BL00461	6-phosphogluconate dehydrogenase proteins.	BL00461A 15.90 1.764e-08 21-57
153	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554A 6.07 2.565e-06 589-599
154	BL00405	43 Kd postsynaptic protein.	BL00405E 8.84 8.125e-06 109-135
155	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637A 15.49 5.179e-06 42-65
156	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 7.339e-06 85-97
157	DM01688	2 POLY-IG RECEPTOR.	DM01688P 13.54 1.925e-07 44-89 DM01688L 4.36 2.367e-07 123-133
159	PR00933	B-LYTIC METALLOENDOPEPTIDASE (M23) SIGNATURE	PR00933D 13.92 1.000e-05 85-106
161	PR00352	3FE-4S FERREDOXIN SIGNATURE	PR00352A 11.15 6.162e-06 94-106
163	BL00785	5'-nucleotidase proteins.	BL00785E 15.85 4.000e-06 95-111
164	PR00916	2C ENDOPEPTIDASE (C24) CYSTEINE PROTEASE FAMILY SIGNATURE	PR00916C 8.02 2.655e-06 121-133
165	BL00785	5'-nucleotidase proteins.	BL00785D 9.89 3.045e-06 154-164
166	BL00785	5'-nucleotidase proteins.	BL00785D 9.89 3.045e-06 123-133
167	DM01023	2 GLYCOSYL HYDROLASES FAMILY 5.	DM01023C 13.51 6.486e-06 149-175
168	PF00803	3A movement protein.	PF00803A 15.38 8.088e-06 255-290
169	PR00282	SNAKE CYTOTOXIN SIGNATURE	PR00282D 11.82 9.882e-06 74-85
170	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 5.787e-06 83-100
172	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 6.804e-06 136-157
173	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701E 13.83 9.724e-06 14-30
174	BL00118	Phospholipase A2 histidine proteins.	BL00118A 16.00 9.842e-06 132-145
175	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 1.825e-06 89-121
176	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930A 7.97 2.403e-07 146-159

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
177	PR00510	NEBULIN SIGNATURE	PR00510F 9.88 8.552e-06 34-51
179	PF00432	Prenyltransferase and squalene oxidase repeat proteins.	PF00432A 11.90 1.000e-05 27-39
180	PR00537	MU OPIOID RECEPTOR SIGNATURE	PR00537A 8.17 1.000e-05 27-41
183	PR00536	MELANOCYTE STIMULATING HORMONE RECEPTOR SIGNATURE	PR00536C 8.58 8.833e-06 64-82
184	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973B 17.81 8.261e-06 158-184
185	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.265e-06 718-731
186	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 4.265e-06 718-731
187	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651A 16.53 6.447e-06 144-165
188	BL01017	Ergosterol biosynthesis ERG4/ERG24 family proteins.	BL01017D 20.82 9.737e-06 21-67
191	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315B 6.84 7.459e-06 95-107
192	PR00930	HIGH MOBILITY GROUP PROTEIN (HMGY) SIGNATURE	PR00930E 5.98 9.740e-06 285-298
193	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794B 22.12 8.967e-06 150-191
194	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517C 5.36 5.853e-06 115-128
196	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 7.031e-07 11-32
197	PR00171	SUGAR TRANSPORTER SIGNATURE	PR00171B 14.73 1.000e-05 15-35
198	PD02407	3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCER.	PD02407J 10.55 6.610e-06 69-81
199	PF00604	Influenza RNA-dependant RNA polymerase subunit PB2.	PF00604F 10.21 2.417e-06 276-331
201	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409D 13.02 9.900e-06 43-58
202	BL00660	Band 4.1 family	BL00660A 31.50 9.595e-06 1-54

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		domain proteins.	
203	PR00745	GLYCOSYL HYDROLASE FAMILY 39 SIGNATURE	PR00745D 15.85 9.700e-06 68-83
204	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364A 6.18 9.667e-06 9-16
205	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 7.690e-07 309-347
206	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 7.690e-07 309-347
207	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895E 15.72 3.170e-06 241-266
208	PR00517	5-HYDROXYTRYPTAMINE 2C RECEPTOR SIGNATURE	PR00517D 7.66 4.835e-06 59-71
209	PD02365	CHAIN FACTOR INTERLEUKIN-12 BETA PRECURSOR IL-1.	PD02365C 7.89 9.719e-06 20-50
210	PR00551	2-S GLOBULIN FAMILY SIGNATURE	PR00551E 10.27 9.432e-06 19-34
211	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418B 22.51 3.289e-06 527-569
213	DM01785	72 PYRUVATE (FLAVODOXIN) DEHYDROGENASE.	DM01785E 12.98 6.400e-06 165-216
214	DM01834	8 HYDROGENASE (FE) SMALL CHAIN.	DM01834B 15.29 3.382e-06 64-90
215	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 4.583e-06 407-423
216	DM00547	1 kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547F 23.43 6.538e-36 628-675 DM00547E 13.94 2.400e-18 387-410 DM00547C 17.30 9.486e-16 266-288 DM00547B 11.28 9.217e-15 237-251 DM00547D 11.60 4.951e-12 357-371 DM00547A 12.38 6.455e-11 216-228
217	BL00407	Connexins proteins.	BL00407D 17.61 1.000e-05 57-87
218	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 9.481e-06 74-86
219	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417B 15.47 3.550e-06 90-102
220	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519E 3.58 2.404e-07 184-199
221	PD01313	INTRON PROBABLE MATURASE CHLOROPLAST MR.	PD01313B 23.27 1.000e-05 10-45
222	PR00047	C4-TYPE STEROID	PR00047A 15.70 9.878e-06 99-116

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		RECEPTOR ZINC FINGER SIGNATURE	
223	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554C 11.76 3.571e-06 255-271
224	DM01123	5 kw RESISTANCE TETRACYCLINE METHYLENOMYCIN EXPORT.	DM01123B 20.06 5.206e-06 28-67
226	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 8.630e-07 28-40
227	BL00895	3-hydroxyisobutyrate dehydrogenase proteins.	BL00895B 21.14 5.173e-06 185-224
229	PR00907	THROMBOMODULIN SIGNATURE	PR00907G 11.63 9.794e-06 13-40
230	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651B 9.95 6.416e-06 62-77
231	DM00611	9 kw LECTIN HTPG SERINE GNTR.	DM00611C 11.08 9.113e-06 214-226
232	PR00582	PROSTANOID EP3 RECEPTOR SIGNATURE	PR00582B 9.74 1.000e-05 76-95
233	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407E 13.51 9.438e-06 176-192
234	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 9.913e-06 6-40
235	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 4.450e-06 94-126 DM01688J 14.69 6.000e-06 34-71
236	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 1.000e-05 80-106
237	PR00076	6-PHOSPHOGLUCONATE DEHYDROGENASE SIGNATURE	PR00076B 11.24 6.418e-07 14-44
239	PR00243	MUSCARINIC ACETYLCHOLINE RECEPTOR SIGNATURE	PR00243F 16.45 9.182e-06 7-18
240	BL00854	Proteasome B-type subunits proteins.	BL00854B 10.97 1.000e-05 1-9
241	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513B 17.51 5.263e-07 876-889
242	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111I 15.32 2.473e-07 522-552
243	BL00415	Synapsins proteins.	BL00415B 9.91 9.778e-06 53-89
244	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514E 14.28 1.000e-05 221-238
245	PR00187	ARTHROPOD HAEMOCYANIN SIGNATURE	PR00187B 15.70 1.000e-05 37-55

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
246	PF00637	7-fold repeat proteins in Clathrin, also in VPS proteins.	PF00637C 27.33 1.184e-06 368-415
247	BL00785	5'-nucleotidase proteins.	BL00785A 9.73 7.557e-06 57-68
248	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651D 12.56 2.615e-06 228-249
249	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516B 10.78 1.811e-06 310-325
250	BL00461	6-phosphogluconate dehydrogenase proteins.	BL00461C 18.34 9.495e-06 30-58
251	BL00888	Cyclic nucleotide-binding domain proteins.	BL00888A 18.03 9.667e-06 20-37
252	DM01242	3 THREONINE--TRNA LIGASE.	DM01242E 23.00 6.215e-07 119-161
253	DM00250	kw ANNEXIN ANTIGEN PROLINE TUMOR.	DM00250A 10.52 6.488e-06 16-32
254	BL00291	Prion protein.	BL00291A 4.49 2.469e-07 51-86 BL00291A 4.49 6.878e-07 40-75 BL00291A 4.49 5.330e-06 22-57 BL00291A 4.49 1.000e-05 30-65
255	PF00506	Influenza virus nucleoprotein.	PF00506F 9.40 5.459e-08 17-55
256	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126A 27.56 6.026e-06 25-62
257	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003D 8.10 5.131e-06 291-300
258	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 7.061e-06 10-20
259	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 8.071e-06 3-13
260	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775D 8.91 3.831e-06 147-165
261	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 1.167e-06 75-91
262	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388D 14.87 8.079e-06 69-83
263	PR00023	ZONA PELLUCIDA SPERM-BINDING PROTEIN SIGNATURE	PR00023A 17.17 9.036e-06 24-39
264	BL00024	Hemopexin domain proteins.	BL00024F 11.30 9.894e-06 3-24
265	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 6.294e-06 177-227
266	PR00652	5-HYDROXYTRYPTAMINE	PR00652A 8.92 9.224e-07 69-90

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		7 RECEPTOR SIGNATURE	
267	PR00652 .	5-HYDROXYTRYPTAMINE 7 RECEPTOR SIGNATURE	PR00652A 8.92 9.224e-07 69-90
268	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 1.673e-06 14-35
270	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875C 8.64 9.550e-06 65-77
271	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 7.308e-06 21-42
272	PF00598	Influenza Matrix protein (M1).	PF00598A 14.24 4.383e-06 46-89
273	PR00113	ALKALINE PHOSPHATASE SIGNATURE	PR00113D 6.87 9.260e-06 8-19
274	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841E 18.60 9.446e-06 80-118
275	PF00600	Influenza non-structural protein (NS1).	PF00600A 20.40 1.563e-06 40-67
276	PR00877	PLANT PEC FAMILY METALLOTHIONEIN SIGNATURE	PR00877B 4.74 9.878e-06 31-38
277	PR00076	6-PHOSPHOGLUCONATE DEHYDROGENASE SIGNATURE	PR00076E 12.73 6.417e-06 71-99
279	BL00101	Hexapeptide-repeat containing-transferases proteins.	BL00101A 10.95 1.000e-05 71-78
280	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111M 10.67 2.629e-06 163-187
282	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.934e-06 35-50
283	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519C 9.73 1.227e-06 22-37
284	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304E 7.79 1.000e-05 54-67
285	BL00197	2Fe-2S ferredoxins, iron-sulfur binding region proteins.	BL00197A 18.23 9.866e-07 49-79
286	PR00753	1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE SIGNATURE	PR00753D 6.85 8.636e-06 61-83
287	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003B 7.64 1.300e-06 166-174
288	BL00940	Gamma-thionins family proteins.	BL00940A 20.51 9.671e-06 16-40
289	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.609e-11 122-135 PD00066 13.92 1.900e-09 94-107 PD00066 13.92 2.703e-07 66-79

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD00066 13.92 1.000e-05 38-51
291	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516F 10.18 9.609e-07 761-779
293	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651E 10.53 8.487e-06 51-71
296	PR00635	AT1 ANGIOTENSIN II RECEPTOR SIGNATURE	PR00635C 7.44 8.602e-06 28-45
297	PF00915	Calicivirus coat protein.	PF00915E 5.71 1.000e-05 102-112
298	PR00519	5-HYDROXYTRYPTAMINE 5B RECEPTOR SIGNATURE	PR00519B 9.99 3.968e-06 495-512
299	PR00784	MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE	PR00784D 15.86 9.730e-06 22-40
300	DM00973	3 kw RESISTANCE BENOMYL YLL028W CYCLOHEXIMIDE.	DM00973A 21.17 1.273e-06 7-44
301	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.752e-06 42-57
302	BL00283	Soybean trypsin inhibitor (Kunitz) protease inhibitors family.	BL00283B 16.55 1.000e-05 15-30
303	DM01753	6 kw OSTEOBLAST MAJOR IMMUNOGENIC MPB70.	DM01753A 21.93 9.830e-06 59-94
304	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516E 14.87 6.516e-06 20-38
305	DM01554	1 THYROLIBERIN PRECURSOR.	DM01554E 10.78 5.452e-07 20-37
306	PR00331	HAEMAGGLUTININ HA2 CHAIN SIGNATURE	PR00331E 18.67 1.000e-05 75-93
307	PR00651	5-HYDROXYTRYPTAMINE 2B RECEPTOR SIGNATURE	PR00651H 5.59 8.858e-06 152-175
308	BL00208	Plant hemoglobins proteins.	BL00208A 18.41 1.000e-05 5-47
309	PR00240	ALPHA-1A ADRENERGIC RECEPTOR SIGNATURE	PR00240E 9.25 9.391e-06 36-56
310	PR00701	60KD INNER MEMBRANE PROTEIN SIGNATURE	PR00701C 10.53 8.255e-06 55-76
311	PR00423	CELL DIVISION PROTEIN FTSZ SIGNATURE	PR00423B 7.15 1.000e-05 5-26
312	PF00602	Influenza RNA-dependant RNA polymerase subunit PB1.	PF00602C 12.16 2.068e-07 26-66
313	PR00246	SOMATOSTATIN RECEPTOR SIGNATURE	PR00246D 7.36 1.000e-05 4-14

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
314	BL00216	Sugar transport proteins.	BL00216A 13.29 9.526e-06 26-38
316	PF00721	Tobacco mosaic virus coat.	PF00721A 14.59 9.845e-06 131-167
317	PD00489	PROTEIN TRANSMEMBRANE TRANSPORT C.	PD00489A 15.57 1.000e-05 55-71
318	PR00163	RUBREDOXIN SIGNATURE	PR00163A 10.47 9.888e-06 59-76
319	PR00513	5-HYDROXYTRYPTAMINE 1B RECEPTOR SIGNATURE	PR00513A 7.75 9.149e-07 205-217
320	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418C 20.48 5.142e-06 377-419
321	BL00067	3-hydroxyacyl-CoA dehydrogenase proteins.	BL00067D 21.49 7.441e-06 9-42
322	DM01857	5 kw NUCLEOSIDE TRANSPORT DEPENDENT NA.	DM01857B 14.94 7.821e-08 52-80
323	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803C 7.00 5.133e-06 43-53
324	PD01672	+ TRANSPORT EXCHANGER NA H TRANS.	PD01672B 15.16 1.000e-05 6-55
325	DM01688	2 POLY-IG RECEPTOR.	DM01688J 14.69 5.538e-06 31-68
327	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.	DM00372A 19.18 1.000e-05 9-54
328	DM01688	2 POLY-IG RECEPTOR.	DM01688J 14.69 4.308e-06 31-68
329	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930A 7.97 2.403e-07 144-157
330	PF00685	Sulfotransferase proteins.	PF00685A 19.12 9.370e-06 49-82
331	PR00347	PATHOGENESIS-RELATED PROTEIN SIGNATURE	PR00347A 13.98 9.649e-06 55-68
332	PR00538	MUSCARINIC M1 RECEPTOR SIGNATURE	PR00538F 10.59 8.667e-06 30-48
334	PR00159	2FE-2S FERREDOXIN SIGNATURE	PR00159A 9.58 1.153e-06 23-32
336	PR00554	ADENOSINE A2B RECEPTOR SIGNATURE	PR00554B 12.52 9.778e-06 41-50
337	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111G 10.39 7.250e-06 3-44
338	PR00516	5-HYDROXYTRYPTAMINE 2A RECEPTOR SIGNATURE	PR00516B 10.78 7.649e-06 214-229
340	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 5.050e-06 141-160
342	DM01664	kw.	DM01664D 16.63 1.000e-05 22-47

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
343	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841K 14.81 1.000e-05 65-95
344	PR00416	EUKARYOTIC DNA TOPOISOMERASE I SIGNATURE	PR00416D 12.12 9.772e-06 23-40
345	BL00726	AP endonucleases family 1 proteins.	BL00726C 19.90 1.000e-05 7-33
346	BL00305	11-S plant seed storage proteins.	BL00305D 21.08 4.566e-06 465-507
347	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE	PR00332A 10.15 9.890e-06 16-33
348	PR00518	5-HYDROXYTRYPTAMINE 5A RECEPTOR SIGNATURE	PR00518A 8.62 7.807e-06 19-36
349	BL00305	11-S plant seed storage proteins.	BL00305D 21.08 4.736e-06 276-318
350	PR00503	BROMODOMAIN SIGNATURE	PR00503C 19.84 9.731e-06 28-47
351	DM01688	2 POLY-IG RECEPTOR.	DM01688K 17.19 9.066e-07 81-120
352	DM01688	2 POLY-IG RECEPTOR.	DM01688K 17.19 9.066e-07 81-120
353	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415B 13.78 5.273e-06 99-147
354	PR00216	OSTEOPONTIN SIGNATURE	PR00216F 11.79 9.913e-06 50-69
356	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.	DM00895G 3.62 9.913e-06 62-72
357	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126B 15.20 6.329e-06 35-47
358	PR00512	5-HYDROXYTRYPTAMINE 1A RECEPTOR SIGNATURE	PR00512G 6.54 3.139e-06 3-19
359	PD02455	ELEMENT TRANSPOSABLE INSERTION PROTEIN TRANSPOSITION DNA.	PD02455D 18.65 1.000e-05 58-77
360	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415A 6.65 3.250e-07 16-29
361	BL00794	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase proteins.	BL00794C 19.62 9.702e-06 27-65
362	PR00866	RNA-DEPENDENT DNA-POLYMERASE (MSDNA) SIGNATURE	PR00866B 9.86 9.786e-06 60-73

* Results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TABLE 4

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
2	PGAM	Phosphoglycerate mutase family	2.5e-05	23.4
6	Ubie_methyltran	ubiE/COQ5 methyltransferase family	0.035	-133.9
8	Plexin_repeat	Plexin repeat	0.03	18.4
13	K_tetra	K+ channel tetramerisation domain	2.3e-31	117.6
14	EGF	EGF-like domain	7.8e-14	59.4
16	Armadillo_seg	Armadillo/beta-catenin-like repeats	1.3e-05	32.1
19	Ribosomal_S5	Ribosomal protein S5	1.7e-46	167.9
21	gpdh	glyceraldehyde 3-phosphate dehydrogenases	1.3e-230	773.2
24	GCV_T	Glycine cleavage T-protein (aminomethyl tran	9.3e-156	530.9
25	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.015	12.5
26	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	38.4
33	urease	Urease	0.014	11.0
35	tRNA-synt_1e	tRNA synthetases class I (C)	0.0091	12.1
37	LRRNT	Leucine rich repeat N-terminal domain	0.00049	26.8
39	SH3	SH3 domain	3.4e-60	213.4
40	SH3	SH3 domain	3.4e-60	213.4
41	PBD	P21-Rho-binding domain	1e-08	42.4
42	GDA1_CD39	GDA1/CD39 (nucleoside phosphatase) family	9e-94	324.9
43	Band_7	SPFH domain / Band 7 family	1.7e-21	84.9
46	Rhodanese	Rhodanese-like domain	2.9e-24	94.0
47	zf-C2H2	Zinc finger, C2H2 type	6.2e-32	119.5
50	ZAP	ZAP domain	1.6e-50	181.3
52	sushi	Sushi domain (SCR repeat)	9.5e-27	102.3
55	zf-C2H2	Zinc finger, C2H2 type	0.047	20.3
56	zf-C2H2	Zinc finger, C2H2 type	0.00021	28.1
59	PH	PH domain	2.6e-06	27.6
60	PHD	PHD-finger	2e-09	44.8
64	IQ	IQ calmodulin-binding motif	6.4e-42	152.7
66	ank	Ank repeat	2.7e-23	90.8
69	eIF-1a	Eukaryotic initiation factor 1A	0.0047	-2.4
74	Ribosomal_S17	Ribosomal protein S17	6e-43	148.6
75	LIM	LIM domain containing proteins	0.00067	19.0
80	Phosphodiest	Type I phosphodiesterase / nucleotide py	2.7e-49	177.2
81	transmembrane4	Transmembrane 4 family	6.6e-61	197.7
84	zf-C2H2	Zinc finger, C2H2 type	1.6e-64	227.8
85	zf-C2H2	Zinc finger, C2H2 type	1.4e-07	38.6
89	ank	Ank repeat	4e-31	116.8
93	L15	Ribosomal protein L15	3.5e-21	61.9

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
98	Band_41	FERM domain (Band 4.1 family)	0.00015	16.7
101	Nol1_Nop2_Sun	NOL1/NOP2/sun family	4.5e-19	68.6
103	LIM	LIM domain containing proteins	1.3e-30	113.2
113	WD40	WD domain, G-beta repeat	0.00018	28.3
115	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	5.3e-34	120.4
116	DUF25	Domain of unknown function DUF25	1.1e-11	46.9
118	Band_41	FERM domain (Band 4.1 family)	3.2e-77	242.4
119	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	1.1e-33	125.4
120	SH3	SH3 domain	3e-05	30.9
125	Ribosomal_L29	Ribosomal L29 protein	1.6e-15	65.0
126	NTF2	Nuclear transport factor 2 (NTF2) domain	7.6e-06	32.2
129	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	0.0016	25.2
130	Fork_head	Fork head domain	1e-28	108.8
132	PC4	Transcriptional Coactivator p15 (PC4)	2.1e-38	141.0
133	RGS	Regulator of G protein signaling domain	2.6e-45	164.0
137	COX7a	Cytochrome c oxidase subunit VIIa	2.3e-40	147.5
139	rrm	RNA recognition motif. (a.k.a. RRM, RBD, or	3.2e-15	64.0
141	lectin_c	Lectin C-type domain	5.1e-05	30.0
142	lectin_c	Lectin C-type domain	5.1e-05	30.0
147	ig	Immunoglobulin domain	9.1e-07	26.9
150	ank	Ank repeat	8.6e-09	42.6
161	Ribosomal_L7Ae	Ribosomal protein L7Ae	0.03	0.8
162	HMG_box	HMG (high mobility group) box	8e-53	188.9
163	PH	PH domain	3e-13	52.4
168	Peptidase_C6	Helper component proteinase	0.0056	7.9
175	ig	Immunoglobulin domain	2.3e-09	35.2
176	ig	Immunoglobulin domain	9.2e-09	33.3
178	WW	WW domain	0.054	17.2
180	Ribosomal_S12e	Ribosomal protein S12e	1.9e-38	141.1
185	myb_DNA-binding	Myb-like DNA-binding domain	0.00011	29.1
186	myb_DNA-binding	Myb-like DNA-binding domain	0.00011	29.1
187	pkinase	Eukaryotic protein kinase domain	3.4e-26	98.4
189	ER_lumen_recept	ER lumen protein retaining receptor	3.9e-144	492.2
190	ER_lumen_recept	ER lumen protein retaining receptor	2.1e-88	307.1
195	EMP24_GP25L	emp24/gp25L/p24 family	6.9e-06	28.1
199	zf-B_box	B-box zinc finger.	5.2e-07	36.7
211	HECT	HECT-domain (ubiquitin-transferase).	1.1e-115	397.8
213	Rhomboid	Rhomboid family	4.2e-42	153.3
214	LIM	LIM domain containing	8.8e-35	127.8

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
		proteins		
215	Ricin_B_lectin	Similarity to lectin domain of ricin	0.0015	19.2
216	chromo	'chromo' (CHRromatin Organization MOdifier	2.1e-09	37.1
218	Sialyltransf	Sialyltransferase family	7.3e-20	79.4
219	PG_binding_2	Putative peptidoglycan binding domain	5e-06	33.5
223	zf-C2H2	Zinc finger, C2H2 type	1.5e-104	360.7
226	RGS	Regulator of G protein signaling domain	5.1e-52	186.2
227	TBC	TBC domain	7.2e-35	129.3
228	CRAL_TRIO	CRAL/TRIO domain.	4.5e-47	158.6
232	Ribosomal_L44	Ribosomal protein L44	1e-48	175.3
235	ig	Immunoglobulin domain	3.5e-08	31.4
236	thyroglobulin_1	Thyroglobulin type-1 repeat	3.9e-24	93.6
238	TBC	TBC domain	1.2e-54	195.0
241	zf-C2H2	Zinc finger, C2H2 type	3.8e-08	40.5
242	AAA	ATPases associated with various cellular act	2.1e-43	157.6
249	integrin_A	Integrin alpha cytoplasmic region	0.091	18.0
256	PAP2	PAP2 superfamily	0.00084	22.8
257	zf-C2H2	Zinc finger, C2H2 type	1.2e-60	214.9
259	G-gamma	GGL domain	5.5e-30	108.3
266	efhand	EF hand	3.4e-07	37.4
267	efhand	EF hand	3.4e-07	37.4
274	zf-C2H2	Zinc finger, C2H2 type	0.00014	28.6
277	RecF	RecF protein	0.036	11.1
281	CH	Calponin homology (CH) domain	7.9e-22	86.0
285	cyclin	Cyclin	3.9e-07	28.5
289	zf-C2H2	Zinc finger, C2H2 type	1.9e-21	84.7
290	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.073	10.8
299	60s_ribosomal	60s Acidic ribosomal protein	4.1e-07	25.8
307	trypsin	Trypsin	6.9e-81	257.3
310	ig	Immunoglobulin domain	1.3e-10	39.3
311	ig	Immunoglobulin domain	6.1e-07	27.4
313	globin	Globin	3.8e-21	78.2
315	ig	Immunoglobulin domain	1.6e-05	22.8
318	zf-C2H2	Zinc finger, C2H2 type	9e-19	75.8
319	ig	Immunoglobulin domain	0.01	13.8
320	BTB	BTB/POZ domain	5e-17	70.0
322	aa_permeases	Amino acid permease	0.0058	-262.2
325	ig	Immunoglobulin domain	1.6e-10	38.9
327	ig	Immunoglobulin domain	1.9e-09	35.5
328	ig	Immunoglobulin domain	2.9e-09	34.9
329	ig	Immunoglobulin domain	7.4e-14	49.7
332	Ribosomal_L36e	Ribosomal protein L36e	6.3e-17	69.7
333	connexin	Connexin	7.6e-148	504.6
335	p450	Cytochrome P450	2.1e-100	347.0
337	Sm	Sm protein	0.00012	28.8
338	zf-C2H2	Zinc finger, C2H2 type	0.0025	24.5

SEQ ID NO:	pFAM NAME	DESCRIPTION	p-value	pFAM SCORE
343	aldo_ket_red	Aldo/keto reductase family	2.4e-53	190.7
345	ubiquitin	Ubiquitin family	3.1e-13	45.5
346	CH	Calponin homology (CH) domain	0.0017	23.8
351	ig	Immunoglobulin domain	4.8e-18	63.2
352	ig	Immunoglobulin domain	4.8e-18	63.2
358	G-alpha	G-protein alpha subunit	4.5e-148	505.3
359	ig	Immunoglobulin domain	8.9e-09	33.3
362	Ribosomal_L37ae	Ribosomal L37ae protein family	0.00083	-3.0

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	maxS (MAXIMUM SCORE)	meanS (MEAN SCORE)
2	1-29	0.942	0.664
12	1-15	0.909	0.589
14	1-17	0.974	0.943
20	1-22	0.932	0.802
25	1-16	0.988	0.881
28	1-13	0.896	0.771
37	1-21	0.992	0.929
42	1-46	0.978	0.754
52	1-34	0.954	0.756
63	1-31	0.960	0.773
71	1-45	0.981	0.652
80	1-22	0.982	0.882
81	1-42	0.993	0.715
83	1-30	0.966	0.767
95	1-18	0.997	0.971
102	1-13	0.981	0.764
107	1-45	0.890	0.631
110	1-27	0.992	0.969
138	1-33	0.961	0.864
144	1-45	0.987	0.658
145	1-20	0.992	0.967
175	1-20	0.957	0.874
176	1-21	0.989	0.945
179	1-42	0.980	0.577
184	1-20	0.972	0.771
189	1-28	0.941	0.755
190	1-28	0.941	0.755
191	1-12	0.907	0.779
195	1-21	0.958	0.779
200	1-15	0.970	0.875
211	1-20	0.895	0.595
215	1-31	0.987	0.895
218	1-30	0.971	0.889
225	1-17	0.884	0.588
235	1-23	0.965	0.817
237	1-29	0.933	0.725
249	1-28	0.972	0.870
251	1-17	0.966	0.905
260	1-26	0.921	0.587
270	1-20	0.938	0.631
283	1-18	0.901	0.763
288	1-20	0.940	0.693
293	1-26	0.937	0.784
295	1-22	0.972	0.745
296	1-15	0.930	0.748
297	1-35	0.906	0.600
300	1-29	0.981	0.864
307	1-19	0.976	0.916
308	1-27	0.973	0.931

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	maxS (MAXIMUM SCORE)	meanS (MEAN SCORE)
309	1-29	0.950	0.629
310	1-19	0.969	0.913
311	1-21	0.956	0.823
315	1-17	0.976	0.938
317	1-19	0.943	0.837
319	1-18	0.991	0.978
324	1-26	0.968	0.806
325	1-20	0.972	0.828
326	1-27	0.893	0.567
327	1-21	0.994	0.959
328	1-20	0.945	0.891
329	1-21	0.984	0.858
330	1-27	0.891	0.593
333	1-40	0.955	0.703
347	1-22	0.968	0.806
351	1-23	0.982	0.945
352	1-23	0.982	0.945
355	1-32	0.955	0.617
356	1-23	0.936	0.677
359	1-20	0.937	0.859
360	1-29	0.956	0.765
361	1-23	0.968	0.819

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 362, a mature protein coding portion of SEQ ID NO: 1 – 362, an active domain of SEQ ID NO: 1 – 362, and complementary sequences thereof.

2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to comprise the polynucleotide of claim 1.

9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

    (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1 – 362.

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-362, a mature protein coding portion of SEQ ID NO: 1-362, an active domain of SEQ ID NO: 1-362, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-362, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 – 362.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

ABSTRACT OF THE INVENTION

The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

Express Mail No.:. EF415382545US
Docket No.: 797

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As [a] below named inventor(s), I/we hereby declare that:

Y. Tom Tang, Ping Zhou, Ryle Goodrich, Chenghua Liu, Vinod Asundi, Feiyan Ren, Jie Zhang, Qing A. Zhao, Aidong J. Xue, Yonghong Yang, Tom Wehrman, Radoje T. Drmanac

My/our residence, post office address and citizenship is/are as stated below next to my/our name(s).

I/we believe I/we am/are an/the original, first and sole/joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES, the specification of which

_X_ is attached hereto.

____ was filed on [date] as Application Serial Number [ ] and was amended on [date].

I/We hereby state that I/we have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above.

I/We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I/We hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate, listed below and so identified, and I/we have also identified below any foreign application for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns and having a filing date before that of the application on which priority is claimed:

NUMBER	COUNTRY	DAY/MONTH/ YEAR FILED	PRIORITY CLAIMED - YES OR NO

I/We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I/we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

SERIAL NUMBER	FILING DATE	STATUS

I/We hereby declare that all statements made herein of my/our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I/We hereby appoint the following attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls with respect to this application be directed to Leslie A. Mooi, HYSEQ, INC., 670 Almanor Avenue, Sunnyvale, CA 94085, Telephone No. (408) 524-8100:

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Citizenship:	Yugoslavia		

Express Mail No.: EF415382545US
Docket No.: 797

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s):	Tang, et al.
Serial No:	Not Yet Assigned
Filed:	Herewith
For:	NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

CERTIFICATE OF MAILING
BY "EXPRESS MAIL" UNDER 37 CFR § 1 10

"Express Mail" Mailing Label Numbers
EF415382559US

Date of Deposit November 17, 2000

I hereby certify that this paper and all enclosures are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" under 37 CFR § 1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C., 20231

Type or Print Name of Person Mailing. Sandy Fong

Signature of Person Mailing

STATEMENT REGARDING SEQUENCE LISTING UNDER 37 CFR §1.821(f)

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Dated: November 17, 2000 By: Leslie Mooi

Leslie A. Mooi
Attorney for Applicants
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SEQUENCE LISTING

<110> Tang, Y. Tom
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  Liu, Chenghua
  Asundi, Vinod
  Ren, Feiyan
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  Xue, Aidong J.
  Yang, Yonghong
  Wehrman, Tom
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aaa aca aca cag ctg gag cac aag tca caa atg tac caa gtt gaa atg       1961
Lys Thr Thr Gln Leu Glu His Lys Ser Gln Met Tyr Gln Val Glu Met
        250                 255                 260

aat caa ggg cag tcc caa ggt aca gtg gac caa cat ctc cag ttc caa       2009
Asn Gln Gly Gln Ser Gln Gly Thr Val Asp Gln His Leu Gln Phe Gln
    265                 270                 275

aaa ccc tca cac cag gtg cac ttc tcc aaa aca gac cat tta cca aaa       2057
Lys Pro Ser His Gln Val His Phe Ser Lys Thr Asp His Leu Pro Lys
280                 285                 290                 295

gct cat gtg cag tca ctg tgt ggc act aga ttt cat ttt caa caa aga       2105
Ala His Val Gln Ser Leu Cys Gly Thr Arg Phe His Phe Gln Gln Arg
                300                 305                 310

gca gat tcc caa act gaa aaa ctt atg tcc cca gtg ttg aaa cag cac       2153
Ala Asp Ser Gln Thr Glu Lys Leu Met Ser Pro Val Leu Lys Gln His
            315                 320                 325

ttg aat caa cag gct tca gag act gag cca ttt tca aac tca cac ctt       2201
Leu Asn Gln Gln Ala Ser Glu Thr Glu Pro Phe Ser Asn Ser His Leu
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            330                 335                 340

ttg caa cat aag cct cat aaa cag gca gca caa aca caa cca tcc cag      2249
Leu Gln His Lys Pro His Lys Gln Ala Ala Gln Thr Gln Pro Ser Gln
        345                 350                 355

agt tca cat ctc cct caa aac cag caa cag cag caa aaa tta caa ata      2297
Ser Ser His Leu Pro Gln Asn Gln Gln Gln Gln Gln Lys Leu Gln Ile
360                 365                 370                 375

aag aat aaa gag gaa ata ctc cag act ttt cct cac ccc caa agc aac      2345
Lys Asn Lys Glu Glu Ile Leu Gln Thr Phe Pro His Pro Gln Ser Asn
                380                 385                 390

aat gat cag caa aga gaa gga tca ttc ttt ggc cag act aaa gtg gaa      2393
Asn Asp Gln Gln Arg Glu Gly Ser Phe Phe Gly Gln Thr Lys Val Glu
            395                 400                 405

gaa tgt ttt cat ggt gaa aat cag tat tca aaa tca agc gag ttc gag      2441
Glu Cys Phe His Gly Glu Asn Gln Tyr Ser Lys Ser Ser Glu Phe Glu
        410                 415                 420

act cat aat gtc caa atg gga ctg gag gaa gta cag aat ata aat cgt      2489
Thr His Asn Val Gln Met Gly Leu Glu Glu Val Gln Asn Ile Asn Arg
    425                 430                 435

aga aat tcc cct tat agt cag acc atg aaa tca agt gca tgc aaa ata      2537
Arg Asn Ser Pro Tyr Ser Gln Thr Met Lys Ser Ser Ala Cys Lys Ile
440                 445                 450                 455

cag gtt tct tgt tca aac aat aca cac cta gtt tca gag aat aaa gaa      2585
Gln Val Ser Cys Ser Asn Asn Thr His Leu Val Ser Glu Asn Lys Glu
                460                 465                 470

cag act aca cat cct gaa ctt ttt gca gga aac aag acc caa aac ttg      2633
Gln Thr Thr His Pro Glu Leu Phe Ala Gly Asn Lys Thr Gln Asn Leu
            475                 480                 485

cat cac atg caa tat ttt cca aat aat gtg atc cca aag caa gat ctt      2681
His His Met Gln Tyr Phe Pro Asn Asn Val Ile Pro Lys Gln Asp Leu
        490                 495                 500

ctt cac agg tgc ttt caa gaa cag gag cag aag tca caa caa gct tca      2729
Leu His Arg Cys Phe Gln Glu Gln Glu Gln Lys Ser Gln Gln Ala Ser
    505                 510                 515

gtt cta cag gga tat aaa aat aga aac caa gat atg tct ggt caa caa      2777
Val Leu Gln Gly Tyr Lys Asn Arg Asn Gln Asp Met Ser Gly Gln Gln
520                 525                 530                 535

gct gcg caa ctt gct cag caa agg tac ttg ata cat aac cat gca aat      2825
Ala Ala Gln Leu Ala Gln Gln Arg Tyr Leu Ile His Asn His Ala Asn
                540                 545                 550

gtt ttt cct gtg cct gac cag gga gga agt cac act cag acc cct ccc      2873
Val Phe Pro Val Pro Asp Gln Gly Gly Ser His Thr Gln Thr Pro Pro
            555                 560                 565
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cag aag gac act caa aag cat gct gct cta agg tgg cat ctc tta cag      2921
Gln Lys Asp Thr Gln Lys His Ala Ala Leu Arg Trp His Leu Leu Gln
        570                 575                 580

aag caa gaa cag cag caa aca cag caa ccc caa act gag tct tgc cat      2969
Lys Gln Glu Gln Gln Gln Thr Gln Gln Pro Gln Thr Glu Ser Cys His
    585                 590                 595

agt cag atg cac agg cca att aag gtg gaa cct gga tgc aag cca cat      3017
Ser Gln Met His Arg Pro Ile Lys Val Glu Pro Gly Cys Lys Pro His
600                 605                 610                 615

gcc tgt atg cac aca gca cca cca gaa aac aaa aca tgg aaa aag gta      3065
Ala Cys Met His Thr Ala Pro Pro Glu Asn Lys Thr Trp Lys Lys Val
                620                 625                 630

act aag caa gag aat cca cct gca agc tgt gat aat gtg cag caa aag      3113
Thr Lys Gln Glu Asn Pro Pro Ala Ser Cys Asp Asn Val Gln Gln Lys
            635                 640                 645

agc atc att gag acc atg gag cag cat ctg aag cag ttt cac gcc aag      3161
Ser Ile Ile Glu Thr Met Glu Gln His Leu Lys Gln Phe His Ala Lys
        650                 655                 660

tcg tta ttt gac cat aag gct ctt act ctc aaa tca cag aag caa gta      3209
Ser Leu Phe Asp His Lys Ala Leu Thr Leu Lys Ser Gln Lys Gln Val
    665                 670                 675

aaa gtt gaa atg tca ggg cca gtc aca gtt ttg act aga caa acc act      3257
Lys Val Glu Met Ser Gly Pro Val Thr Val Leu Thr Arg Gln Thr Thr
680                 685                 690                 695

gct gca gaa ctt gat agc cac acc cca gct tta gag cag caa aca act      3305
Ala Ala Glu Leu Asp Ser His Thr Pro Ala Leu Glu Gln Gln Thr Thr
                700                 705                 710

tct tca gaa aag aca cca acc aaa aga aca gct gct tct gtt ctc aat      3353
Ser Ser Glu Lys Thr Pro Thr Lys Arg Thr Ala Ala Ser Val Leu Asn
            715                 720                 725

aat ttt ata gag tca cct tcc aaa tta cta gat act cct ata aaa aat      3401
Asn Phe Ile Glu Ser Pro Ser Lys Leu Leu Asp Thr Pro Ile Lys Asn
        730                 735                 740

tta ttg gat aca cct gtc aag act caa tat gat ttc cca tct tgc aga      3449
Leu Leu Asp Thr Pro Val Lys Thr Gln Tyr Asp Phe Pro Ser Cys Arg
    745                 750                 755

tgt gta gat cct gta aaa ttt gaa tgt atc tgt ttt aga tca att cgc      3497
Cys Val Asp Pro Val Lys Phe Glu Cys Ile Cys Phe Arg Ser Ile Arg
760                 765                 770                 775

cta ttt agc tct ttg tat att atc tcc tgg aga gac agc tag              3539
Leu Phe Ser Ser Leu Tyr Ile Ile Ser Trp Arg Asp Ser  *
                780                 785
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                             Met Ala Phe Arg Gln Ala Leu Gln Leu
                              1               5

gcg gcc tgc ggg ctg gcc ggg ggc tcg gcc gcc gtg ctc ttc tcg gcc        99
Ala Ala Cys Gly Leu Ala Gly Gly Ser Ala Ala Val Leu Phe Ser Ala
 10                  15                  20                  25

gtg gcg gta ggg aag ccg cgc gca ggc ggg gac gcg gag cca cgc ccg       147
Val Ala Val Gly Lys Pro Arg Ala Gly Gly Asp Ala Glu Pro Arg Pro
                 30                  35                  40

gct gag ccg ccg gcc tgg gcg ggg ggc gcg cgg ccg ggc ccc ggt gtc       195
Ala Glu Pro Pro Ala Trp Ala Gly Gly Ala Arg Pro Gly Pro Gly Val
             45                  50                  55

tgg gac ccc aac tgg gac agg cga gaa cca ctg tct ctg atc aac gtg       243
Trp Asp Pro Asn Trp Asp Arg Arg Glu Pro Leu Ser Leu Ile Asn Val
         60                  65                  70

cgg aag agg aac gtg gaa tct ggg gaa gaa gag ctg gcg tcc aag ctg       291
Arg Lys Arg Asn Val Glu Ser Gly Glu Glu Glu Leu Ala Ser Lys Leu
     75                  80                  85

gac cac tac aaa gcc aag gcc acg cgg cac atc ttc ctc atc agg cat       339
Asp His Tyr Lys Ala Lys Ala Thr Arg His Ile Phe Leu Ile Arg His
 90                  95                 100                 105

tcc cag tac cac gtg gat ggc tcc ctg gag aag gac cgc act ctg acc       387
Ser Gln Tyr His Val Asp Gly Ser Leu Glu Lys Asp Arg Thr Leu Thr
                110                 115                 120

ccg ctg ggt cgg gag cag gct gaa ctc act ggg ctc cgc ctg gca agc       435
Pro Leu Gly Arg Glu Gln Ala Glu Leu Thr Gly Leu Arg Leu Ala Ser
            125                 130                 135

ttg ggg ttg aag ttt aat aaa atc gtc cat tcg tct atg acg cgc gcc       483
Leu Gly Leu Lys Phe Asn Lys Ile Val His Ser Ser Met Thr Arg Ala
        140                 145                 150

ata gag acc acc gat atc atc agc cgg cac ctg cca ggc gtc tgc aaa       531
Ile Glu Thr Thr Asp Ile Ile Ser Arg His Leu Pro Gly Val Cys Lys
    155                 160                 165
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gtc agc aca gat ctg ctg cgg gaa ggc gcc ccc atc gag cca gac ccg      579
Val Ser Thr Asp Leu Leu Arg Glu Gly Ala Pro Ile Glu Pro Asp Pro
170                 175                 180                 185

ccc gtg tct cat tgg aag ccg gaa gct gtg cag tat tac gaa gac gga      627
Pro Val Ser His Trp Lys Pro Glu Ala Val Gln Tyr Tyr Glu Asp Gly
                190                 195                 200

gcc cgg atc gag gcc gcc ttc cgg aac tac atc cac cgc gca gat gcc      675
Ala Arg Ile Glu Ala Ala Phe Arg Asn Tyr Ile His Arg Ala Asp Ala
            205                 210                 215

agg cag gag gag gac agt tac gag atc ttc atc tgt cac gcc aac gtc      723
Arg Gln Glu Glu Asp Ser Tyr Glu Ile Phe Ile Cys His Ala Asn Val
        220                 225                 230

atc cgc tac atc gtg tgc aga gca ctg cag ttt cct cct gaa ggc tgg      771
Ile Arg Tyr Ile Val Cys Arg Ala Leu Gln Phe Pro Pro Glu Gly Trp
    235                 240                 245

ctc cgg ctc tcc ctc aat aat ggc agc atc acc cac ctg gtg atc cga      819
Leu Arg Leu Ser Leu Asn Asn Gly Ser Ile Thr His Leu Val Ile Arg
250                 255                 260                 265

ccc aac ggc cga gtt gcg ctc agg acc ctc ggg gac acg ggg ttc atg      867
Pro Asn Gly Arg Val Ala Leu Arg Thr Leu Gly Asp Thr Gly Phe Met
                270                 275                 280

cct ccc gac aag atc act cga tcc tga gggct ccggcctctc cttccctctg      919
Pro Pro Asp Lys Ile Thr Arg Ser  *
            285                 290

tcctccctgc acaggccgca cacacttaac gttttgttcc caaggagacc ggcggaaagt     979

agaaacctgc aatgctgcat ctgggaactg acttgtgacc aggctgagaa ggggagagtt    1039

gggatcagac agcctgactt ctctgcaggg ttttatacct gaccatgaac ccccaggatg    1099

gcgtggggtt taaggtgaaa gcgtctcacg cacaagtcag gcctgttgtg gggacttgaa    1159

agaggcctga cccagaccac catgttcgca cccacagctg acccgtgctg agggtccagg    1219

ctccattggc aaagccggtc aggcacgagg gcgactgagg cacgtggatg aggagggcac    1279

ccaggttctg ttcacaactc acttcacttc atacatcctt ttaatttctt aaaaaaaaaa    1339

aaa                                                                  1342
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aaggtattgc agcaag    atg gat ttg gga aag gac caa tct cat ttg aag     169
                     Met Asp Leu Gly Lys Asp Gln Ser His Leu Lys
                     1               5                   10

cac cat cag aca cct gac cct cat caa gaa gag aac cat tct cca gaa      217
His His Gln Thr Pro Asp Pro His Gln Glu Glu Asn His Ser Pro Glu
            15                  20                  25

gtc att gga acc tgg agt ttg aga aac aga gaa cta ctt aga aaa aga      265
Val Ile Gly Thr Trp Ser Leu Arg Asn Arg Glu Leu Leu Arg Lys Arg
        30                  35                  40

aaa gct gaa gtg cat gaa aag gaa aca tca caa tgg cta ttt gga gaa      313
Lys Ala Glu Val His Glu Lys Glu Thr Ser Gln Trp Leu Phe Gly Glu
    45                  50                  55

cag aaa aaa cgc aag cag cag aga aca gga aaa gga aat cga aga ggc      361
Gln Lys Lys Arg Lys Gln Gln Arg Thr Gly Lys Gly Asn Arg Arg Gly
60                  65                  70                  75

aga aag aga caa caa aac aca gaa ttg aag gtg gag cct cag cca cag      409
Arg Lys Arg Gln Gln Asn Thr Glu Leu Lys Val Glu Pro Gln Pro Gln
                80                  85                  90

ata gaa aag gaa ata gtg gag aaa gca ctg gca cct ata gag aaa aaa      457
Ile Glu Lys Glu Ile Val Glu Lys Ala Leu Ala Pro Ile Glu Lys Lys
            95                  100                 105

act gag cca cct ggg agc ata acc aaa gta ttt cct tca gta gcc tcc      505
Thr Glu Pro Pro Gly Ser Ile Thr Lys Val Phe Pro Ser Val Ala Ser
        110                 115                 120

ccg caa aaa gtt gtg cct gag gaa cac ttt tct gaa ata tgt caa gaa      553
Pro Gln Lys Val Val Pro Glu Glu His Phe Ser Glu Ile Cys Gln Glu
    125                 130                 135

agt aac ata tat cag gag aat ttt tct gag tac caa gaa ata gca gta      601
Ser Asn Ile Tyr Gln Glu Asn Phe Ser Glu Tyr Gln Glu Ile Ala Val
140                 145                 150                 155

caa aac cat tct tct gaa aca tgc caa cat gtg tct gaa cct gaa gac      649
Gln Asn His Ser Ser Glu Thr Cys Gln His Val Ser Glu Pro Glu Asp
                160                 165                 170

ctc tct cct aaa atg tac caa gaa ata tct gta ctt caa gac aat tct      697
Leu Ser Pro Lys Met Tyr Gln Glu Ile Ser Val Leu Gln Asp Asn Ser
            175                 180                 185
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tcc aaa ata tgc caa gac atg aag gaa cct gaa gac aac tct cct aac      745
Ser Lys Ile Cys Gln Asp Met Lys Glu Pro Glu Asp Asn Ser Pro Asn
        190                 195                 200

aca tgc caa gta ata tct gta att caa gac cat cct ttc aaa atg tac      793
Thr Cys Gln Val Ile Ser Val Ile Gln Asp His Pro Phe Lys Met Tyr
    205                 210                 215

caa gat atg gct aaa cga gaa gat ctg gct cct aaa atg tgc caa gaa      841
Gln Asp Met Ala Lys Arg Glu Asp Leu Ala Pro Lys Met Cys Gln Glu
220                 225                 230                 235

gct gct gta ccc aaa atc ctt cct tgt cca aca tct gaa gac aca gct      889
Ala Ala Val Pro Lys Ile Leu Pro Cys Pro Thr Ser Glu Asp Thr Ala
                240                 245                 250

gat ctg gca gga tgc tct ctt caa gca tat cca aaa cca gat gtg cct      937
Asp Leu Ala Gly Cys Ser Leu Gln Ala Tyr Pro Lys Pro Asp Val Pro
            255                 260                 265

aaa ggc tat att ctt gac aca gac caa aat cca gca gaa cca gag gaa      985
Lys Gly Tyr Ile Leu Asp Thr Asp Gln Asn Pro Ala Glu Pro Glu Glu
        270                 275                 280

tac aat gaa aca gat caa gga ata gct gag aca gaa ggc ctt ttt cct     1033
Tyr Asn Glu Thr Asp Gln Gly Ile Ala Glu Thr Glu Gly Leu Phe Pro
    285                 290                 295

aaa ata caa gaa ata gct gag cct aaa gac ctt tct aca aaa aca cac     1081
Lys Ile Gln Glu Ile Ala Glu Pro Lys Asp Leu Ser Thr Lys Thr His
300                 305                 310                 315

caa gaa tca gct gaa cct aaa tac ctt cct cat aaa aca tgt aac gaa     1129
Gln Glu Ser Ala Glu Pro Lys Tyr Leu Pro His Lys Thr Cys Asn Glu
                320                 325                 330

att att gtg cct aaa gcc ccc tct cat aaa aca atc caa gaa aca cct     1177
Ile Ile Val Pro Lys Ala Pro Ser His Lys Thr Ile Gln Glu Thr Pro
            335                 340                 345

cat tct gaa gac tat tca att gaa ata aac caa gaa act cct ggg tct     1225
His Ser Glu Asp Tyr Ser Ile Glu Ile Asn Gln Glu Thr Pro Gly Ser
        350                 355                 360

gaa aaa tat tca cct gaa acg tat caa gaa ata cct ggg ctt gaa gaa     1273
Glu Lys Tyr Ser Pro Glu Thr Tyr Gln Glu Ile Pro Gly Leu Glu Glu
    365                 370                 375

tat tca cct gaa ata tac caa gaa aca tcc cag ctt gaa gaa tat tca     1321
Tyr Ser Pro Glu Ile Tyr Gln Glu Thr Ser Gln Leu Glu Glu Tyr Ser
380                 385                 390                 395

cct gaa ata tac caa gaa aca ccg ggg cct gaa gac ctc tct act gag     1369
Pro Glu Ile Tyr Gln Glu Thr Pro Gly Pro Glu Asp Leu Ser Thr Glu
                400                 405                 410

aca tat aaa aat aag gat gtg cct aaa gaa tgc ttt cca gaa cca cac     1417
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Thr Tyr Lys Asn Lys Asp Val Pro Lys Glu Cys Phe Pro Glu Pro His
            415                 420                 425

caa gaa aca ggt ggg ccc caa ggc cag gat cct aaa gca cac cag gaa      1465
Gln Glu Thr Gly Gly Pro Gln Gly Gln Asp Pro Lys Ala His Gln Glu
        430                 435                 440

gat gct aaa gat gct tat act ttt cct caa gaa atg aaa gaa aaa ccc      1513
Asp Ala Lys Asp Ala Tyr Thr Phe Pro Gln Glu Met Lys Glu Lys Pro
    445                 450                 455

aaa gaa gag cca gga ata cca gca att ctg aat gag agt cat cca gaa      1561
Lys Glu Glu Pro Gly Ile Pro Ala Ile Leu Asn Glu Ser His Pro Glu
460                 465                 470                 475

aat gat gtc tat agt tat gtt ttg ttt taa c aatgctcaac cataaagttg      1612
Asn Asp Val Tyr Ser Tyr Val Leu Phe  *
                480                 485

tggtccaatg gaacataaaa aaaaaaaa                                       1640



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     <213> Homo sapiens

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     <222> (100)..(1110)

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ggcggcggag gtcaccgcgg ggagaggggc gggcgcagc   atg gca gcc tcc tta      114
                                             Met Ala Ala Ser Leu
                                               1               5

cgg ctc ctc gga gct gcc tcc ggt ctc cgg tac tgg agc cgg cgg ctg      162
Arg Leu Leu Gly Ala Ala Ser Gly Leu Arg Tyr Trp Ser Arg Arg Leu
                10                  15                  20

cgg ccg gca gcc ggc agc ttt gca gcg gtg tgt tct agg tca gtg gct      210
Arg Pro Ala Ala Gly Ser Phe Ala Ala Val Cys Ser Arg Ser Val Ala
            25                  30                  35

tca aag act cca gtt gga ttc att gga ctg ggc aac atg ggg aat cca      258
Ser Lys Thr Pro Val Gly Phe Ile Gly Leu Gly Asn Met Gly Asn Pro
        40                  45                  50

atg gca aaa aat ctc atg aaa cat ggc tat cca ctt att att tat gat      306
Met Ala Lys Asn Leu Met Lys His Gly Tyr Pro Leu Ile Ile Tyr Asp
    55                  60                  65

gtg ttc cct gat gcc tgc aaa gag ttt caa gat gca ggt gaa cag gta      354
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Val Phe Pro Asp Ala Cys Lys Glu Phe Gln Asp Ala Gly Glu Gln Val
 70                 75                  80                  85

gta tct tcc cca gca gat gtt gct gaa aaa gct gac aga att att aca      402
Val Ser Ser Pro Ala Asp Val Ala Glu Lys Ala Asp Arg Ile Ile Thr
                 90                  95                 100

atg ctg ccc acc agt atc aat gca ata gaa gct tat tcc gga gca aat      450
Met Leu Pro Thr Ser Ile Asn Ala Ile Glu Ala Tyr Ser Gly Ala Asn
            105                 110                 115

ggg att cta aaa aaa gtg aag aag ggc tca tta tta ata gat tcc agc      498
Gly Ile Leu Lys Lys Val Lys Lys Gly Ser Leu Leu Ile Asp Ser Ser
        120                 125                 130

act att gat cct gca gtt tca aaa gaa ttg gcc aaa gaa gtt gag aaa      546
Thr Ile Asp Pro Ala Val Ser Lys Glu Leu Ala Lys Glu Val Glu Lys
    135                 140                 145

atg gga gca gtt ttc atg gat gcc cct gtt tct ggt ggt gta gga gct      594
Met Gly Ala Val Phe Met Asp Ala Pro Val Ser Gly Gly Val Gly Ala
150                 155                 160                 165

gca cga tct ggg aac ctc acg ttt atg gtg gga gga gtt gaa gat gaa      642
Ala Arg Ser Gly Asn Leu Thr Phe Met Val Gly Gly Val Glu Asp Glu
                170                 175                 180

ttt gct gct gcc caa gag ttg ctg ggg tgc atg ggc tcc aac gtg gtg      690
Phe Ala Ala Ala Gln Glu Leu Leu Gly Cys Met Gly Ser Asn Val Val
            185                 190                 195

tac tgt gga gct gtt ggg act ggg cag gcg gca aag atc tgc aac aac      738
Tyr Cys Gly Ala Val Gly Thr Gly Gln Ala Ala Lys Ile Cys Asn Asn
        200                 205                 210

atg ctg tta gct att agt atg att gga act gct gaa gct atg aat ctt      786
Met Leu Leu Ala Ile Ser Met Ile Gly Thr Ala Glu Ala Met Asn Leu
    215                 220                 225

gga atc agg tta ggg ctt gac cca aaa cta ctg gct aaa atc cta aat      834
Gly Ile Arg Leu Gly Leu Asp Pro Lys Leu Leu Ala Lys Ile Leu Asn
230                 235                 240                 245

atg agc tca gga cgg tgt tgg tca agt gac act tat aat cct gta cct      882
Met Ser Ser Gly Arg Cys Trp Ser Ser Asp Thr Tyr Asn Pro Val Pro
                250                 255                 260

gga gtg atg gat ggc gtt ccc tcg gct aat aac tat cag ggt gga ttt      930
Gly Val Met Asp Gly Val Pro Ser Ala Asn Asn Tyr Gln Gly Gly Phe
            265                 270                 275

gga aca aca ctc atg gct aag gat ctg gga ttg gca caa gac tct gct      978
Gly Thr Thr Leu Met Ala Lys Asp Leu Gly Leu Ala Gln Asp Ser Ala
        280                 285                 290

acc agc aca aag agc cca atc ctt ctt ggc agt ctg gcc cat cag atc     1026
Thr Ser Thr Lys Ser Pro Ile Leu Leu Gly Ser Leu Ala His Gln Ile
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    295                 300                 305

tac agg atg atg tgt gca aag ggc tac tca aag aaa gac ttc tca tcc      1074
Tyr Arg Met Met Cys Ala Lys Gly Tyr Ser Lys Lys Asp Phe Ser Ser
310                 315                 320                 325

gtg ttc cag ttc cta cga gag gag gag acc ttc tga gtgt gccctttggc      1124
Val Phe Gln Phe Leu Arg Glu Glu Glu Thr Phe  *
                330                 335

cacggacact gttgggaacc aaactctgtc ttggagcctc cttttagctc actccacaag   1184

taaatggatt taatcaaagg tcacctatct gcttttgatt gtctaggtca cagtaatccc   1244

taggattttt caccgcttat tctttttgtc tttttaacaa acatattatc cgaatttttt   1304

ttctgcaagc cactgatagt ctctgctaac tagcttaatt gaccttttta caaagtttga   1364

tccccaagca tcctcaacta aatcattgaa tacttcaatc aggatattat ctgctttact   1424

ttacaaataa aaccaaatct tttgtcaaca ggatgaaacc catcttaaag gaaagaaaag   1484

gaattggtgt gaagagagaa gttagagaag ggaaatgcag tgaattacta tctgtgtcca   1544

tcaggaagtt tgtcctgtta accaaatggt tactgcacta ccagggttac tggtttattt   1604

tccagggagc tgataaagca ggagaactgt tgctgcatgt tttctatttg gactccgtca   1664

caatatggta ggatatccct caccaactcc cgacactcag cagacttgtt tttatatttt   1724

tttctttctt gttcattctt actacgtatt ttttgactta agaatgacat ctttagatgc   1784

atttcagagc caatgatgat atttgcttta gataattatt atattattat aaatatagcc   1844

atattatttt gaattcaaat aaatttctat actggtaaaa aaaaaaaa                1892


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     <213> Homo sapiens

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                                                             Met
                                                              1

aaa aat ata aaa gca ctt gtg gcc ttt cat agc act gcc ttg gat aag      105
Lys Asn Ile Lys Ala Leu Val Ala Phe His Ser Thr Ala Leu Asp Lys
            5                   10                  15
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gaa att aca tca gca aat tat gct ggt gtc tgt aca tca tct gtg att       153
Glu Ile Thr Ser Ala Asn Tyr Ala Gly Val Cys Thr Ser Ser Val Ile
         20                  25                  30

aaa gaa gaa aac att gat caa cca gga tac tgt tat ctc tca cct gat       201
Lys Glu Glu Asn Ile Asp Gln Pro Gly Tyr Cys Tyr Leu Ser Pro Asp
     35                  40                  45

gga aag aga aaa act atg ctc tgc ttg gct tgt gga caa tcc atg aga       249
Gly Lys Arg Lys Thr Met Leu Cys Leu Ala Cys Gly Gln Ser Met Arg
 50                  55                  60                  65

aca gag aaa gga ctg aaa caa ttg ctt cca ggg gtt cca ttc ctc tgt       297
Thr Glu Lys Gly Leu Lys Gln Leu Leu Pro Gly Val Pro Phe Leu Cys
                 70                  75                  80

att tca ggc acc aag act cag aag ccc ttc tta caa ggg ccc ttc aag       345
Ile Ser Gly Thr Lys Thr Gln Lys Pro Phe Leu Gln Gly Pro Phe Lys
             85                  90                  95

gtc atc agt gtg gct gag gtt gat ttg tcg tgt gac aag gct gaa aaa       393
Val Ile Ser Val Ala Glu Val Asp Leu Ser Cys Asp Lys Ala Glu Lys
        100                 105                 110

act cta agt tac tac caa gca cgt cta ttg tct tta cgg atg aag acc       441
Thr Leu Ser Tyr Tyr Gln Ala Arg Leu Leu Ser Leu Arg Met Lys Thr
    115                 120                 125

tgc acg caa gct gca tct cac agt ggc atg gca gcc aca cac cag aag       489
Cys Thr Gln Ala Ala Ser His Ser Gly Met Ala Ala Thr His Gln Lys
130                 135                 140                 145

gca gtg aaa ata att gca tac aaa aat ggg gat ggg tat cgt aat ggg       537
Ala Val Lys Ile Ile Ala Tyr Lys Asn Gly Asp Gly Tyr Arg Asn Gly
                150                 155                 160

aag tta att gtg gct gga aca ttc ccc atg ctt ctt aca gaa tgc acg       585
Lys Leu Ile Val Ala Gly Thr Phe Pro Met Leu Leu Thr Glu Cys Thr
            165                 170                 175

gaa caa ctt ggg ctt gcc aga gca gcc tcc aaa gta tat acc aaa gat       633
Glu Gln Leu Gly Leu Ala Arg Ala Ala Ser Lys Val Tyr Thr Lys Asp
        180                 185                 190

gga acc cca atc ttt acc ttg cgt gat ttg gtt tta tgg gct cta gat       681
Gly Thr Pro Ile Phe Thr Leu Arg Asp Leu Val Leu Trp Ala Leu Asp
    195                 200                 205

gaa tcc ttt ctc cag aga gac tct gag aaa caa aag caa gat gca gct       729
Glu Ser Phe Leu Gln Arg Asp Ser Glu Lys Gln Lys Gln Asp Ala Ala
210                 215                 220                 225

cct gtt gga aaa gaa cag ata att gtt gaa agt atg gaa gaa aat cca       777
Pro Val Gly Lys Glu Gln Ile Ile Val Glu Ser Met Glu Glu Asn Pro
                230                 235                 240

aga atg aaa gtg aaa aac aga tta ttt gca aaa tct gtg aca tcc gat       825
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Arg Met Lys Val Lys Asn Arg Leu Phe Ala Lys Ser Val Thr Ser Asp
            245                 250                 255

agt ttg gat ggt ata gac aag tct ttg ctt acc ctc atc ctc aga aat      873
Ser Leu Asp Gly Ile Asp Lys Ser Leu Leu Thr Leu Ile Leu Arg Asn
        260                 265                 270

cct att gcc atc tgg gtg tct tgt ggt gaa cca ttt cta cct cca aat      921
Pro Ile Ala Ile Trp Val Ser Cys Gly Glu Pro Phe Leu Pro Pro Asn
    275                 280                 285

gct ttg cag aaa gca gaa aaa tta gag aaa cag aac tgg cta aaa aag      969
Ala Leu Gln Lys Ala Glu Lys Leu Glu Lys Gln Asn Trp Leu Lys Lys
290                 295                 300                 305

gac aga att ttg gct gat cta gat acc atg aga cac aaa atg aga cag     1017
Asp Arg Ile Leu Ala Asp Leu Asp Thr Met Arg His Lys Met Arg Gln
                310                 315                 320

tta aaa ggg cgg cga gta gcg gca tgt cag cca gcc acc atg gtt cct     1065
Leu Lys Gly Arg Arg Val Ala Ala Cys Gln Pro Ala Thr Met Val Pro
            325                 330                 335

acc aag agc cct gtg cag ccc gtg gtg gtt gaa gga ggc tgg acc gaa     1113
Thr Lys Ser Pro Val Gln Pro Val Val Val Glu Gly Gly Trp Thr Glu
        340                 345                 350

cag act caa cag gaa att aaa ctc atg gaa ctt ata aga cat aca gag     1161
Gln Thr Gln Gln Glu Ile Lys Leu Met Glu Leu Ile Arg His Thr Glu
    355                 360                 365

gca cac ctt tct gaa atc caa gaa atg gaa tcc aaa ata aat ttt cca     1209
Ala His Leu Ser Glu Ile Gln Glu Met Glu Ser Lys Ile Asn Phe Pro
370                 375                 380                 385

att gca acc aaa cgt ata gca gtc aag ccg agc aac ctg tat aag cag     1257
Ile Ala Thr Lys Arg Ile Ala Val Lys Pro Ser Asn Leu Tyr Lys Gln
                390                 395                 400

ccc aac aca aaa cga gtg tgg att tat cta aat gga ggc aga cct gaa     1305
Pro Asn Thr Lys Arg Val Trp Ile Tyr Leu Asn Gly Gly Arg Pro Glu
            405                 410                 415

gat ggc act tat gcc tgg ggc aaa act att tca gag ctg ctg caa gac     1353
Asp Gly Thr Tyr Ala Trp Gly Lys Thr Ile Ser Glu Leu Leu Gln Asp
        420                 425                 430

tgc tcc tct cgt ctc aaa atg acc cac cca gct aga gca ctg tac acc     1401
Cys Ser Ser Arg Leu Lys Met Thr His Pro Ala Arg Ala Leu Tyr Thr
    435                 440                 445

ccc agt gga gag cca att cag tcc tgg gac gac ata gag cga gat atg     1449
Pro Ser Gly Glu Pro Ile Gln Ser Trp Asp Asp Ile Glu Arg Asp Met
450                 455                 460                 465

gtc atc tgt gtg tct atg gga cat ggt ttc aaa acc cca aaa gag tta     1497
Val Ile Cys Val Ser Met Gly His Gly Phe Lys Thr Pro Lys Glu Leu
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                470                 475                 480

aaa caa ctg atg gag atc aga gca aat tat gcc aga atc cga agg cag      1545
Lys Gln Leu Met Glu Ile Arg Ala Asn Tyr Ala Arg Ile Arg Arg Gln
            485                 490                 495

cag ggc cct caa gcc aca gac att gtg gtg tca cca tcc acg aag ctg      1593
Gln Gly Pro Gln Ala Thr Asp Ile Val Val Ser Pro Ser Thr Lys Leu
        500                 505                 510

ctg tct ctg gca cat ctc cac aat taa ctcct atcagaacca tcggattttc      1645
Leu Ser Leu Ala His Leu His Asn  *
    515                 520

tgctgtattt ttctggaaag aaaactttct ttacccactt ataaacagaa gactgtgaca    1705

agaaggccaa ttatttccat cgctgaagac tctaaatttg gcaaatcttc taaataacaa    1765

tcctgcatag tttattaaaa aaaattagtc gtaaaattta tccttcaaaa atctgcattt    1825

taaataaacc ctgacagtga tttctcaaga ctgtaaagat attagtctga gaatgcaact    1885

ctaacagact gctctgggca tcttttctct ttgccttggc caggcctctc agaattgagt    1945

gagcgtgtga ctccatttgc acagtgggac agatgagtac aactgaaata aaaagtggag    2005

gcctctgcaa aaaataaaaa aaaaaaa                                        2032



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                                          Met Trp Ser Gly Arg
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aag ctg ggc tcc tcc ggg ggt tgg ttt tta aga gtg ctg ggg cct gga       101
Lys Leu Gly Ser Ser Gly Gly Trp Phe Leu Arg Val Leu Gly Pro Gly
                10                  15                  20

ggc tgt aat aca aaa gct gcg cgt ccc tta att tcc tcg gcg gtt tat       149
Gly Cys Asn Thr Lys Ala Ala Arg Pro Leu Ile Ser Ser Ala Val Tyr
            25                  30                  35

gtg aag aac cag ctc agt ggg act cta cag att aaa cca ggg gtt ttc       197
Val Lys Asn Gln Leu Ser Gly Thr Leu Gln Ile Lys Pro Gly Val Phe
        40                  45                  50
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aat gaa tac aga acc ata tgg ttc aaa tcc tac agg acg atc ttt tcc       245
Asn Glu Tyr Arg Thr Ile Trp Phe Lys Ser Tyr Arg Thr Ile Phe Ser
     55                  60                  65

tgt ttg aac aga ata aag agt ttc agg tac cct tgg gcg aga ctg tac       293
Cys Leu Asn Arg Ile Lys Ser Phe Arg Tyr Pro Trp Ala Arg Leu Tyr
 70                  75                  80                  85

agt act tcc caa acc act gtc gac agc ggt gag gta aaa acc ttc ttg       341
Ser Thr Ser Gln Thr Thr Val Asp Ser Gly Glu Val Lys Thr Phe Leu
                 90                  95                 100

gcc ctg gct cac aaa tgg tgg gat gaa caa gga gta tat gca cct ctt       389
Ala Leu Ala His Lys Trp Trp Asp Glu Gln Gly Val Tyr Ala Pro Leu
            105                 110                 115

cat tcc atg aat gac ctg agg gtg cca ttt att agg gac aat ctt ctg       437
His Ser Met Asn Asp Leu Arg Val Pro Phe Ile Arg Asp Asn Leu Leu
        120                 125                 130

aaa aca att cct aat cac cag cca gga aaa cct ttg ttg ggg atg aag       485
Lys Thr Ile Pro Asn His Gln Pro Gly Lys Pro Leu Leu Gly Met Lys
    135                 140                 145

att ctt gac gtt ggc tgt ggt ggt ggg ctg tta act gaa cct cta ggg       533
Ile Leu Asp Val Gly Cys Gly Gly Gly Leu Leu Thr Glu Pro Leu Gly
150                 155                 160                 165

cgg ctt ggg gct tca gtt att gga atc gac cct gtg gat gag aac att       581
Arg Leu Gly Ala Ser Val Ile Gly Ile Asp Pro Val Asp Glu Asn Ile
                170                 175                 180

aaa aca gca caa tgc cat aaa tca ttt gat cca gtc cgg gat aag aga       629
Lys Thr Ala Gln Cys His Lys Ser Phe Asp Pro Val Arg Asp Lys Arg
            185                 190                 195

ata gag tac aga gtg tgt tcc ctg gaa gag att gtg gaa gag act gca       677
Ile Glu Tyr Arg Val Cys Ser Leu Glu Glu Ile Val Glu Glu Thr Ala
        200                 205                 210

gaa aca ttt gat gct gtt gta gct tct gaa gtt gta gaa cat gtg att       725
Glu Thr Phe Asp Ala Val Val Ala Ser Glu Val Val Glu His Val Ile
    215                 220                 225

gat cta gaa aca ttt tta cag tgc tgc tgt caa gtg tta aaa ccc ggt       773
Asp Leu Glu Thr Phe Leu Gln Cys Cys Cys Gln Val Leu Lys Pro Gly
230                 235                 240                 245

ggt tct tta ttc att act aca atc aac aaa aca caa ctt tcc tat gcc       821
Gly Ser Leu Phe Ile Thr Thr Ile Asn Lys Thr Gln Leu Ser Tyr Ala
                250                 255                 260

ttg gga att gtt ttt tca gag caa att gca ggt att gta cca aaa ggt       869
Leu Gly Ile Val Phe Ser Glu Gln Ile Ala Gly Ile Val Pro Lys Gly
            265                 270                 275

act cat aca tgg gag aag ttt gtt tca cct gaa aca cta gag agc att       917
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Thr His Thr Trp Glu Lys Phe Val Ser Pro Glu Thr Leu Glu Ser Ile
        280                 285                 290

ctg gaa tca aat ggt ctg tca gtt caa aca gtg gta gga atg ctc tat      965
Leu Glu Ser Asn Gly Leu Ser Val Gln Thr Val Val Gly Met Leu Tyr
    295                 300                 305

aac ccc ttc tca ggt tac tgg cat tgg agt gaa aat acc agc ctt aac     1013
Asn Pro Phe Ser Gly Tyr Trp His Trp Ser Glu Asn Thr Ser Leu Asn
310                 315                 320                 325

tat gca gct cat gct gtg aaa tcc agg gtc cag gaa cac cca gcc tct     1061
Tyr Ala Ala His Ala Val Lys Ser Arg Val Gln Glu His Pro Ala Ser
                330                 335                 340

gct gag ttt gtt tta aag gga gaa aca gaa gag ctc caa gct aat gcc     1109
Ala Glu Phe Val Leu Lys Gly Glu Thr Glu Glu Leu Gln Ala Asn Ala
            345                 350                 355

tgc acc aat cca gct gtg cat gaa aag ctg aag aaa tga attgtttctg      1158
Cys Thr Asn Pro Ala Val His Glu Lys Leu Lys Lys  *
        360                 365                 370

agaactatag taatatggct tggatatctg atgttttcaa atacaagaaa tgtacaattt   1218

atcctttgag agagaatcat gaagaaaaga aggtcaataa aaagggctaa aaccttggac   1278

aaaagttttt gttatttcgt ctaatagcta ctttcaaggg attctgtgaa taaaaagttt   1338

tgtcaagaaa aaaaaaaaa                                                1357



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tgcgtctcct tgtagcatgt tgtttggctg atatctttcg tatctatgcc ccagaagctc    120

catatacttc ccatgataaa cttaagtggc gagtaagaaa agaagct atg atg ggt      176
                                                    Met Met Gly
                                                      1

ctg gct cag ctt tat aag aaa tac tgt ctt cat ggt gaa gca gga aag      224
Leu Ala Gln Leu Tyr Lys Lys Tyr Cys Leu His Gly Glu Ala Gly Lys
    5                  10                  15

gaa gct gca gag aaa gtc agc tgg ata aag gac aaa ctt ctg cat att      272
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Glu Ala Ala Glu Lys Val Ser Trp Ile Lys Asp Lys Leu Leu His Ile
 20                  25                  30                  35

tat tat cag aac agc att gac gac aaa ctg ttg gta gag aaa atc ttt       320
Tyr Tyr Gln Asn Ser Ile Asp Asp Lys Leu Leu Val Glu Lys Ile Phe
                 40                  45                  50

gct cag tat ctt gtc ccc cac aac ctg gaa aca gaa gag aga atg aaa       368
Ala Gln Tyr Leu Val Pro His Asn Leu Glu Thr Glu Glu Arg Met Lys
             55                  60                  65

tgc tta tat tac tta tat gct agt ttg gat cca aat gct gta aaa gct       416
Cys Leu Tyr Tyr Leu Tyr Ala Ser Leu Asp Pro Asn Ala Val Lys Ala
         70                  75                  80

ctc aac gaa atg tgg aag tgt cag aac atg ctt cgg agc cat gta cgc       464
Leu Asn Glu Met Trp Lys Cys Gln Asn Met Leu Arg Ser His Val Arg
     85                  90                  95

gaa cta ttg gat ttg cac aag cag cct aca tca gag gct aac tgt tct       512
Glu Leu Leu Asp Leu His Lys Gln Pro Thr Ser Glu Ala Asn Cys Ser
100                 105                 110                 115

gcc atg ttt gga aaa ctg atg acc ata gca aag aat ttg cct gac ccc       560
Ala Met Phe Gly Lys Leu Met Thr Ile Ala Lys Asn Leu Pro Asp Pro
                120                 125                 130

ggg aaa gca caa gat ttt gtg aag aaa ttt aac cag gtt ctc ggc gat       608
Gly Lys Ala Gln Asp Phe Val Lys Lys Phe Asn Gln Val Leu Gly Asp
            135                 140                 145

gat gag aaa ctt cgg tct cag ttg gag tta tta att agc cca acc tgt       656
Asp Glu Lys Leu Arg Ser Gln Leu Glu Leu Leu Ile Ser Pro Thr Cys
        150                 155                 160

tct tgc aaa caa gca gat att tgt gtg aga gaa ata gcc cgg aaa ctt       704
Ser Cys Lys Gln Ala Asp Ile Cys Val Arg Glu Ile Ala Arg Lys Leu
    165                 170                 175

gca aat cct aag caa cca aca aat cct ttt cta gag atg gtc aaa ttt       752
Ala Asn Pro Lys Gln Pro Thr Asn Pro Phe Leu Glu Met Val Lys Phe
180                 185                 190                 195

ctg ttg gaa aga atc gca cct gtg cac att gat tca gaa gcc ata agt       800
Leu Leu Glu Arg Ile Ala Pro Val His Ile Asp Ser Glu Ala Ile Ser
                200                 205                 210

gcg cta gtg aaa ttg atg aat aag tca ata gag ggg aca gca gat gat       848
Ala Leu Val Lys Leu Met Asn Lys Ser Ile Glu Gly Thr Ala Asp Asp
            215                 220                 225

gaa gag gag ggt gta agt cca gat aca gct atc cgt tca gga ctt gaa       896
Glu Glu Glu Gly Val Ser Pro Asp Thr Ala Ile Arg Ser Gly Leu Glu
        230                 235                 240

ctt ctt aag gtt ctg tct ttt aca cat cct acc tcg ttc cac tct gca       944
Leu Leu Lys Val Leu Ser Phe Thr His Pro Thr Ser Phe His Ser Ala
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    245                 250                 255

gag aca tat gag tcc ttg tta cag tgc cta aga atg gag gat gac aag         992
Glu Thr Tyr Glu Ser Leu Leu Gln Cys Leu Arg Met Glu Asp Asp Lys
260                 265                 270                 275

gta gca gaa gct gct att caa att ttt aga aat aca ggt cac aaa ata        1040
Val Ala Glu Ala Ala Ile Gln Ile Phe Arg Asn Thr Gly His Lys Ile
                280                 285                 290

gaa aca gac ctt ccc cag ata cga tcg acc tta att ccc att tta cat        1088
Glu Thr Asp Leu Pro Gln Ile Arg Ser Thr Leu Ile Pro Ile Leu His
            295                 300                 305

caa aaa gca aag agg ggt act cca cac caa gca aaa cag gct gtg cac        1136
Gln Lys Ala Lys Arg Gly Thr Pro His Gln Ala Lys Gln Ala Val His
        310                 315                 320

tgt ata cac gcc ata ttc aca aat aaa gaa gtc cag ctt gca cag att        1184
Cys Ile His Ala Ile Phe Thr Asn Lys Glu Val Gln Leu Ala Gln Ile
    325                 330                 335

ttt gag cca ctc agt agg agt ctg aat gct gat gtg cca gaa caa ctt        1232
Phe Glu Pro Leu Ser Arg Ser Leu Asn Ala Asp Val Pro Glu Gln Leu
340                 345                 350                 355

ata act cca tta gtt tca ttg ggc cac att tct atg tta gca cca gat        1280
Ile Thr Pro Leu Val Ser Leu Gly His Ile Ser Met Leu Ala Pro Asp
                360                 365                 370

cag ttt gct tcc cca atg aaa tct gta gta gca aat ttt att gtg aaa        1328
Gln Phe Ala Ser Pro Met Lys Ser Val Val Ala Asn Phe Ile Val Lys
            375                 380                 385

gat ctg cta atg aat gac agg tca aca ggt gaa aag aat gga aaa ctg        1376
Asp Leu Leu Met Asn Asp Arg Ser Thr Gly Glu Lys Asn Gly Lys Leu
        390                 395                 400

tgg tct cca gat gaa gag gtt tcc cct gaa gta cta gca aag gta cag        1424
Trp Ser Pro Asp Glu Glu Val Ser Pro Glu Val Leu Ala Lys Val Gln
    405                 410                 415

gca att aaa ctt ctg gta agg tgg ctg ttg ggt atg aaa aac aac cag        1472
Ala Ile Lys Leu Leu Val Arg Trp Leu Leu Gly Met Lys Asn Asn Gln
420                 425                 430                 435

tct aaa tct gcc aat tca acc ctt cgg tta tta tca gcg atg ttg gtt        1520
Ser Lys Ser Ala Asn Ser Thr Leu Arg Leu Leu Ser Ala Met Leu Val
                440                 445                 450

agt gag ggt gac ctg aca gag caa aag agg atc agt aaa tct gat atg        1568
Ser Glu Gly Asp Leu Thr Glu Gln Lys Arg Ile Ser Lys Ser Asp Met
            455                 460                 465

tct cgc ttg cga tta gct gct ggt agt gcc ata atg aag ctt gct cag        1616
Ser Arg Leu Arg Leu Ala Ala Gly Ser Ala Ile Met Lys Leu Ala Gln
        470                 475                 480
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gaa cct tgt tac cat gaa att att acc cca gaa cag ttt cag ctc tgt      1664
Glu Pro Cys Tyr His Glu Ile Ile Thr Pro Glu Gln Phe Gln Leu Cys
    485                 490                 495

gca ctt gtt att aat gat gag tgt tac caa gta agg cag ata ttt gct      1712
Ala Leu Val Ile Asn Asp Glu Cys Tyr Gln Val Arg Gln Ile Phe Ala
500                 505                 510                 515

cag aag ctg cat aag gca ctt gtg aag tta ctg ctc cca ttg gag tat      1760
Gln Lys Leu His Lys Ala Leu Val Lys Leu Leu Leu Pro Leu Glu Tyr
            520                 525                 530

atg gcg atc ttt gcc ttg tgt gcc aaa gat cct gtg aag gag aga aga      1808
Met Ala Ile Phe Ala Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg
        535                 540                 545

gca cac gca cga caa tgt tta ctg aaa aat atc agt ata cgc agg gaa      1856
Ala His Ala Arg Gln Cys Leu Leu Lys Asn Ile Ser Ile Arg Arg Glu
    550                 555                 560

tac att aag cag aat cct atg gct act gag aaa tta tta tca ctg ttg      1904
Tyr Ile Lys Gln Asn Pro Met Ala Thr Glu Lys Leu Leu Ser Leu Leu
565                 570                 575

cct gaa tat gta gtt cca tac atg att cac ctg cta gcc cat gat cca      1952
Pro Glu Tyr Val Val Pro Tyr Met Ile His Leu Leu Ala His Asp Pro
580                 585                 590                 595

gat ttt aca aga tca caa gat gtt gat cag ctt cgt gat atc aaa gag      2000
Asp Phe Thr Arg Ser Gln Asp Val Asp Gln Leu Arg Asp Ile Lys Glu
                600                 605                 610

tgc cta tgg ttc atg ctt gaa gtt tta atg aca aag aat gaa aac aat      2048
Cys Leu Trp Phe Met Leu Glu Val Leu Met Thr Lys Asn Glu Asn Asn
            615                 620                 625

agc cat gcc ttt atg aag aag atg gca gag aac atc aag tta acc aga      2096
Ser His Ala Phe Met Lys Lys Met Ala Glu Asn Ile Lys Leu Thr Arg
        630                 635                 640

gat gcc cag tct cca gat gaa tcc aag aca aat gaa aaa ctg tat aca      2144
Asp Ala Gln Ser Pro Asp Glu Ser Lys Thr Asn Glu Lys Leu Tyr Thr
    645                 650                 655

gta tgt gat gtg gct ctc tgt gtt ata aat agt aaa agt gct ttg tgc      2192
Val Cys Asp Val Ala Leu Cys Val Ile Asn Ser Lys Ser Ala Leu Cys
660                 665                 670                 675

aat gca gat tca cca aag gac cca gtc ctc cca atg aaa ttt ttt aca      2240
Asn Ala Asp Ser Pro Lys Asp Pro Val Leu Pro Met Lys Phe Phe Thr
                680                 685                 690

caa cct gaa aag gac ttc tgt aac gat aag agt tat att tca gaa gag      2288
Gln Pro Glu Lys Asp Phe Cys Asn Asp Lys Ser Tyr Ile Ser Glu Glu
            695                 700                 705
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aca aga gta ctt ctg tta aca gga aag cca aag cct gct gga gta cta       2336
Thr Arg Val Leu Leu Leu Thr Gly Lys Pro Lys Pro Ala Gly Val Leu
        710                 715                 720

ggt gca gta aat aag cct tta tca gca acg gga agg aaa ccc tat gtt       2384
Gly Ala Val Asn Lys Pro Leu Ser Ala Thr Gly Arg Lys Pro Tyr Val
    725                 730                 735

aga agc act ggc act gag act gga agc aat att aat gta aat tca gag       2432
Arg Ser Thr Gly Thr Glu Thr Gly Ser Asn Ile Asn Val Asn Ser Glu
740                 745                 750                 755

ctg aac cct tca acc gga aat cga tca agg gaa cag agt tca gag gca       2480
Leu Asn Pro Ser Thr Gly Asn Arg Ser Arg Glu Gln Ser Ser Glu Ala
                760                 765                 770

gca gaa act gga gtt agt gaa aat gaa gag aac cct gtg agg att att       2528
Ala Glu Thr Gly Val Ser Glu Asn Glu Glu Asn Pro Val Arg Ile Ile
            775                 780                 785

tca gtc aca cct gta aag aat att gac cca gta aag aat aag gaa att       2576
Ser Val Thr Pro Val Lys Asn Ile Asp Pro Val Lys Asn Lys Glu Ile
        790                 795                 800

aat tct gat cag gct acc cag ggc aac atc agc agt gac cga gga aag       2624
Asn Ser Asp Gln Ala Thr Gln Gly Asn Ile Ser Ser Asp Arg Gly Lys
    805                 810                 815

aaa aga aca gta aca gca gct ggt gca gag aat atc caa caa aaa aca       2672
Lys Arg Thr Val Thr Ala Ala Gly Ala Glu Asn Ile Gln Gln Lys Thr
820                 825                 830                 835

gat gag aaa gta gat gaa tcg gga cct ccc gcc cct tcc aaa ccc agg       2720
Asp Glu Lys Val Asp Glu Ser Gly Pro Pro Ala Pro Ser Lys Pro Arg
                840                 845                 850

aga gga cgt cga ccc aag tct gaa tct cag ggc aat gct acc aaa aat       2768
Arg Gly Arg Arg Pro Lys Ser Glu Ser Gln Gly Asn Ala Thr Lys Asn
            855                 860                 865

gat gat cta aat aaa cct att aac aag gga agg aag aga gct gca gtg       2816
Asp Asp Leu Asn Lys Pro Ile Asn Lys Gly Arg Lys Arg Ala Ala Val
        870                 875                 880

ggt cag gag agc cct ggg ggt ttg gaa gca ggt aat gcc aaa gca ccc       2864
Gly Gln Glu Ser Pro Gly Gly Leu Glu Ala Gly Asn Ala Lys Ala Pro
    885                 890                 895

aaa ctg caa gat tta gcc aaa aag gca gca cca gca gaa aga caa att       2912
Lys Leu Gln Asp Leu Ala Lys Lys Ala Ala Pro Ala Glu Arg Gln Ile
900                 905                 910                 915

gac tta caa agg taa aaatgcattt gcaaagggag aaaatgaagg ccaaacagaa       2967
Asp Leu Gln Arg  *
                920

gcaggctcca gcttctgcaa aaacttggat tcacaaatgt ccctgaacag aaaatgaagc    3027
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tcacttcaga acacacactc tctgccttga aaactaaaga gactattact tccttttcac 3087

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ttctgtccca cacacctcac ctgcctgcag agttgccttc tcctgcacgc ctctctcttt    240

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cagaac   atg gag aac ttc acc ctg gca agg gac gag aag ggg aat gtc     348
         Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
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ctc ctg gaa gat ggc aag ggc cgt tgt ccc ttc gac ccg aat ttc aag      396
Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
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tcc act gcc ctg gtg gtt gat ggc gag ctc tac act gga aca gtc agc      444
Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser
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agc ttc caa ggg aat gac ccg gcc atc tcg cgg agc caa agc ctt cgc      492
Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg
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ccc acc aag acc gag agc tcc ctc aac tgg ctg caa gac cca gct ttt      540
Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
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gtg gcc tca gcc tac att cct gag agc ctg ggc agc ttg caa ggc gat      588
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp
     80                  85                  90

gat gac aag atc tac ttt ttc ttc agc gag act ggc cag gaa ttt gag      636
Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu
 95                 100                 105                 110

ttc ttt gag aac acc att gtg tcc cgc att gcc cgc atc tgc aag ggc      684
Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly
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gat gag ggt gga gag cgg gtg cta cag cag cgc tgg acc tcc ttc ctc      732
Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu
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aag gcc cag ctg ctg tgc tca cgg ccc gac gat ggc ttc ccc ttc aac      780
Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn
        145                 150                 155

gtg ctg cag gat gtc ttc acg ctg agc ccc aag ccc cag gac tgg cgt      828
Val Leu Gln Asp Val Phe Thr Leu Ser Pro Lys Pro Gln Asp Trp Arg
    160                 165                 170

gac acc ctt ttc tat ggg gtc ttc act tcc cag tgg cac agg gga act      876
Asp Thr Leu Phe Tyr Gly Val Phe Thr Ser Gln Trp His Arg Gly Thr
175                 180                 185                 190

aca gaa ggc tct gcc gtc tgt gtt ttc aca atg aag gat gtg cag aga      924
Thr Glu Gly Ser Ala Val Cys Val Phe Thr Met Lys Asp Val Gln Arg
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Val Phe Ser Gly Leu Tyr Lys Glu Val Asn Arg Glu Thr Gln Gln Trp
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tac acc gtg acc cac ccg gtg ccc aca ccc cgg cct gga gcg tgc atc     1020
Tyr Thr Val Thr His Pro Val Pro Thr Pro Arg Pro Gly Ala Cys Ile
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acc aac agt gcc cgg gaa agg aag atc aac tca tcc ctg cag ctc cca     1068
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Thr Asn Ser Ala Arg Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro
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gac cgc gtg ctg aac ttc ctc aag gac cac ttc ctg atg gac ggg cag      1116
Asp Arg Val Leu Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln
255                 260                 265                 270

gtc cga agc cgc atg ctg ctg ctg cag ccc cag gct cgc tac cag cgc      1164
Val Arg Ser Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg
                275                 280                 285

gtg gct gta cac cgc gtc cct ggc ctg cac cac acc tac gat gtc ctc      1212
Val Ala Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu
            290                 295                 300

ttc ctg ggc act ggt gac ggc cgg ctc cac aag gca gtg agc gtg ggc      1260
Phe Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
        305                 310                 315

ccc cgg gtg cac atc att gag gag ctg cag atc ttc tca tcg gga cag      1308
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly Gln
    320                 325                 330

ccc gtg cag aat ctg ctc ctg gac acc cac agg ggg ctg ctg tat gcg      1356
Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu Tyr Ala
335                 340                 345                 350

gcc tca cac tcg ggc gta gtc cag gtg ccc atg gcc aac tgc agc ctg      1404
Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn Cys Ser Leu
                355                 360                 365

tac agg agc tgt ggg gac tgc ctc ctc gcc cgg gac ccc tac tgt gct      1452
Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp Pro Tyr Cys Ala
            370                 375                 380

tgg agc ggc tcc agc tgc aag cac gtc agc ctc tac cag cct cag ctg      1500
Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu Tyr Gln Pro Gln Leu
        385                 390                 395

gcc acc agg ccg tgg atc cag gac atc gag gga gcc agc gcc aag gac      1548
Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu Gly Ala Ser Ala Lys Asp
    400                 405                 410

ctt tgc agc gcg tct tcg gtt gtg tcc ccg tct ttt gta cca aca ggg      1596
Leu Cys Ser Ala Ser Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly
415                 420                 425                 430

gag aag cca tgt gag caa gtc cag ttc cag ccc aac aca gtg aac act      1644
Glu Lys Pro Cys Glu Gln Val Gln Phe Gln Pro Asn Thr Val Asn Thr
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ttg gcc tgc ccg ctc ctc tcc aac ctg gcg acc cga ctc tgg cta cgc      1692
Leu Ala Cys Pro Leu Leu Ser Asn Leu Ala Thr Arg Leu Trp Leu Arg
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aac ggg gcc ccc gtc aat gcc tcg gcc tcc tgc cac gtg cta ccc act      1740
Asn Gly Ala Pro Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr
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        465                 470                 475

ggg gac ctg ctg ctg gtg ggc acc caa cag ctg ggg gag ttc cag tgc      1788
Gly Asp Leu Leu Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys
    480                 485                 490

tgg tca cta gag gag ggc ttc cag cag ctg gta gcc agc tac tgc cca      1836
Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro
495                 500                 505                 510

gag gtg gtg gag gac ggg gtg gca gac caa aca gat gag ggt ggc agt      1884
Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser
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gta ccc gtc att atc agc aca tcg cgt gtg agt gca cca gct ggt ggc      1932
Val Pro Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly
            530                 535                 540

aag gcc agc tgg ggt gca gac agg tcc tac tgg aag gag ttc ctg gtg      1980
Lys Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val
        545                 550                 555

atg tgc acg ctc ttt gtg ctg gcc gtg ctg ctc cca gtt tta ttc ttg      2028
Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe Leu
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ctc tac cgg cac cgg aac agc atg aaa gtc ttc ctg aag cag ggg gaa      2076
Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu
575                 580                 585                 590

tgt gcc agc gtg cac ccc aag acc tgc cct gtg gtg ctg ccc cct gag      2124
Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu
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acc cgc cca ctc aac ggc cta ggg ccc cct agc acc ccg ctc gat cac      2172
Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His
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cga ggg tac cag tcc ctg tca gac agc ccc ccg ggg gcc cga gtc ttc      2220
Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro Gly Ala Arg Val Phe
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act gag tca gag aag agg cca ctc agc atc caa gac agc ttc gtg gag      2268
Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu
    640                 645                 650

gta tcc cca gtg tgc ccc cgg ccc cgg gtc cgc ctt ggc tcg gag atc      2316
Val Ser Pro Val Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile
655                 660                 665                 670

cgt gac tct gtg gtg tga gagctg acttccagag gacgctgccc tggcttcagg      2370
Arg Asp Ser Val Val  *
                675

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Ser Ser Glu Glu Ser Cys Asp Ser Phe Asp Ser Leu Glu Ser Gly Lys
 5                  10                  15                  20

cag gtc gcg gag tca gat ttg agt gat gat ggc aaa gca tct ttg gtg      151
Gln Val Ala Glu Ser Asp Leu Ser Asp Asp Gly Lys Ala Ser Leu Val
                25                  30                  35

agc gag gaa gag gaa gat gaa gaa gaa gat aag gct acc cct aga aga      199
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Ser Glu Glu Glu Glu Asp Glu Glu Glu Asp Lys Ala Thr Pro Arg Arg
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agc agg tct aga aga agt agt att ggt ctt cga gta gcc ttt cag ttc       247
Ser Arg Ser Arg Arg Ser Ser Ile Gly Leu Arg Val Ala Phe Gln Phe
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ccc acc aag aag ctg gcc aac aaa cca gat aaa aac agt tct tcc gag       295
Pro Thr Lys Lys Leu Ala Asn Lys Pro Asp Lys Asn Ser Ser Ser Glu
     70                  75                  80

cag ttg ttt tct agc gca cgc tta cag aat gag aaa aaa aca att ctt       343
Gln Leu Phe Ser Ser Ala Arg Leu Gln Asn Glu Lys Lys Thr Ile Leu
 85                  90                  95                 100

gaa aga aag aaa gac tgt aga cag gtg ata caa agg gaa gat tct acc       391
Glu Arg Lys Lys Asp Cys Arg Gln Val Ile Gln Arg Glu Asp Ser Thr
                105                 110                 115

tct gag tct gag gat gac tct cgg gat gag agc cag gag agt tca gat       439
Ser Glu Ser Glu Asp Asp Ser Arg Asp Glu Ser Gln Glu Ser Ser Asp
            120                 125                 130

gct ttg ctg aaa agg acc atg aac atc aag gag aac aaa gcc atg ctt       487
Ala Leu Leu Lys Arg Thr Met Asn Ile Lys Glu Asn Lys Ala Met Leu
        135                 140                 145

gcc cag tta ttg gcg gaa ttg aac tcg atg cca gat ttc ttc cca gta       535
Ala Gln Leu Leu Ala Glu Leu Asn Ser Met Pro Asp Phe Phe Pro Val
    150                 155                 160

cga acc cca acc tca gct tct agg aag aag aca gtg agg cgg gcc ttc       583
Arg Thr Pro Thr Ser Ala Ser Arg Lys Lys Thr Val Arg Arg Ala Phe
165                 170                 175                 180

tcg gag gga cag atc acg cgg cgt atg aac cca acc cgg agt gcg cgg       631
Ser Glu Gly Gln Ile Thr Arg Arg Met Asn Pro Thr Arg Ser Ala Arg
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cct cct gag aag ttt gct cta gag aac ttc act gtc tca gcc gct aaa       679
Pro Pro Glu Lys Phe Ala Leu Glu Asn Phe Thr Val Ser Ala Ala Lys
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ttt gcg gaa gag ttt tac agc ttc cga aga agg aag aca att ggg ggg       727
Phe Ala Glu Glu Phe Tyr Ser Phe Arg Arg Arg Lys Thr Ile Gly Gly
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aaa tgc cgg gag tac aga cga cgt cac cgt ata tct tct ttt cgg cca       775
Lys Cys Arg Glu Tyr Arg Arg Arg His Arg Ile Ser Ser Phe Arg Pro
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gtg gag gat atc acc gaa gag gac tta gaa aat gtt gcc ata act gtt       823
Val Glu Asp Ile Thr Glu Glu Asp Leu Glu Asn Val Ala Ile Thr Val
245                 250                 255                 260

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Arg Asp Lys Ile Tyr Asp Lys Val Leu Gly Asn Thr Cys His Gln Cys
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cga caa aag acc atc gac acc aag aca gtg tgt cgg aac cag ggt tgc      919
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tgt ggt gtg cga gga cag ttc tgt gga cca tgc ctg cgg aac cgc tat      967
Cys Gly Val Arg Gly Gln Phe Cys Gly Pro Cys Leu Arg Asn Arg Tyr
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ggg gag gat gtc aga tcg gca ttg ctg gac ccg gat tgg gtg tgt ccc     1015
Gly Glu Asp Val Arg Ser Ala Leu Leu Asp Pro Asp Trp Val Cys Pro
    310                 315                 320

ccc tgt cgt ggg atc tgc aat tgc agc tac tgt cgg aag cgt gac ggc     1063
Pro Cys Arg Gly Ile Cys Asn Cys Ser Tyr Cys Arg Lys Arg Asp Gly
325                 330                 335                 340

cgc tgt gcc aca gga atc ctc att cat ctg gcc aag ttt tat ggt tat     1111
Arg Cys Ala Thr Gly Ile Leu Ile His Leu Ala Lys Phe Tyr Gly Tyr
                345                 350                 355

gac aat gtt aag gaa tat ctg gag agc tta caa aag gag ctg gta gaa     1159
Asp Asn Val Lys Glu Tyr Leu Glu Ser Leu Gln Lys Glu Leu Val Glu
            360                 365                 370

gac aat taa gaggaaa acaaacagaa ccagccacct caccatagag tactccaaca     1215
Asp Asn  *
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agctccatgg ctgccacaca ggcctgggct tcccaggact gcctccttct tgttcgctta    240

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gggtgtaaat gcaatagctt gtgtgaagtc cactggaacc caggctcacc aagtcagtct    360

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                                                 Met Thr Thr Asp
                                                   1

gac aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg      461
Asp Thr Glu Val Pro Ala Met Thr Leu Ala Pro Gly His Ala Ala Leu
  5                  10                  15                  20

gaa act caa acg ctg agc gct gag acc tct tct agg gcc tca acc cca      509
Glu Thr Gln Thr Leu Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro
                 25                  30                  35

gcc ggc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc      557
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cct gca aga gag acc agg agt ttc aca aaa aca tct ccc aac ttc atg       605
Pro Ala Arg Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met
        55                  60                  65

gtg ctg atc gcc acc tcc gtg gag aca tca gcc gcc agt ggc agc ccc       653
Val Leu Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro
    70                  75                  80

gag gga gct gga atg acc aca gtt cag acc atc aca ggc agt gat ccc       701
Glu Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro
85                  90                  95                  100

gag gaa gcc atc ttt gac acc ctt tgc acc gat gac agc tct gaa gag       749
Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu
                105                 110                 115

gca aag aca ctc aca atg gac ata ttg aca ttg gct cac acc tcc aca       797
Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr
            120                 125                 130

gaa gct aag ggc ctg tcc tca gag agc agt gcc tct tcc gac ggc ccc       845
Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro
        135                 140                 145

cat cca gtc atc acc ccg tca cgg gcc tca gag agc agc gcc tct tcc       893
His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser
    150                 155                 160

gac ggc ccc cat cca gtc atc acc ccg tca cgg gcc tca gag agc agc       941
Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser
165                 170                 175                 180

gcc tct tcc gac ggc ccc cat cca gtc atc acc ccg tca cgg gcc tca       989
Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser
                185                 190                 195

gag agc agc gcc tct tcc gac ggc ccc cat cca gtc atc acc ccg tca      1037
Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser
            200                 205                 210

cgg gcc tca gag agc agc gcc tct tcc gac ggc ctc cat cca gtc atc      1085
Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Leu His Pro Val Ile
        215                 220                 225

acc ccg tca cgg gcc tca gag agc agc gcc tct tcc gac ggc ccc cat      1133
Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His
    230                 235                 240

cca gtc atc acc ccc tca tgg tcc ccg gga tct gac gtc act ctc ctc      1181
Pro Val Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu
245                 250                 255                 260

gct gaa gcc ctg gtg act gtc aca aac atc gag gtt att aat tgc agc      1229
Ala Glu Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser
```

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                265                 270                 275

atc aca gaa ata gaa aca acg act tcc agc atc cct ggg gcc tca gac      1277
Ile Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp
            280                 285                 290

aca gat ctc atc ccc acg gaa ggg gtg aag gcc tcg tcc acc tcc gat      1325
Thr Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser Asp
        295                 300                 305

cca cca gct ctg cct gac tcc act gaa gca aaa cca cac atc act gag      1373
Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile Thr Glu
    310                 315                 320

gtc aca gcc tct gcc gag acc ctg tcc aca gcc ggc acc aca gag tca      1421
Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr Thr Glu Ser
325                 330                 335                 340

gct gca cct cat gcc acg gtt ggg acc cca ctc ccc act aac agc gcc      1469
Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro Thr Asn Ser Ala
                345                 350                 355

aca gaa aga gaa gtg aca gca ccc ggg gcc acg acc ctc agt gga gct      1517
Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr Thr Leu Ser Gly Ala
            360                 365                 370

ctg gtc aca gtt agc agg aat ccc ctg gaa gaa acc tca gcc ctc tct      1565
Leu Val Thr Val Ser Arg Asn Pro Leu Glu Glu Thr Ser Ala Leu Ser
        375                 380                 385

gtt gag aca cca agt tac gtc aaa gtc tca gga gca gct ccg gtc tcc      1613
Val Glu Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val Ser
    390                 395                 400

ata gag gct ggg tca gca gtg ggc aaa aca act tcc ttt gct ggg agc      1661
Ile Glu Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly Ser
405                 410                 415                 420

tct gct tcc tcc tac agc ccc tcg gaa gcc gcc ctc aag aac ttc acc      1709
Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu Lys Asn Phe Thr
                425                 430                 435

cct tca gag aca ccg acc atg gac atc gca acc aag ggg ccc ttc ccc      1757
Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe Pro
            440                 445                 450

acc agc agg gac cct ctt cct tct gtc cct ccg act aca acc aac agc      1805
Thr Ser Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Thr Asn Ser
        455                 460                 465

agc cga ggg acg aac agc acc tta gcc aag atc aca acc tca gcg aag      1853
Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys
    470                 475                 480

acc acg atg aag ccc cca aca gcc acg ccc acg act gcc cgg acg agg      1901
Thr Thr Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr Arg
485                 490                 495                 500
```

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ccg acc aca gac gtg agt gca ggt gaa aat gga ggt ttc ctc ctc ctg      1949
Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu Leu
                505                 510                 515

cgg ctg agt gtg gct tcc ccg gaa gac ctc act gac ccc aga gtg gca      1997
Arg Leu Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val Ala
            520                 525                 530

gaa agg ctg atg cag cag ctc cac cgg gaa ctc cac gcc cac gcg cct      2045
Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala Pro
        535                 540                 545

cac ttc cag gtc tcc tta ctg cgt gtc agg aga ggc taa cggacatcag       2094
His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly  *
    550                 555                 560

ctgcagccag gcatgtcccg tatgccaaaa gagggtgctg cccctagcct gggcccccac    2154

cgacagactg cagctgcgtt actgtgctga gaggtaccca gaaggttccc atgaagggca    2214

gcatgtccaa gcccctaacc ccagatgtgg caacaggacc ctcgctcaca tccaccggag    2274

tgtatgtatg gggaggggct tcacctgttc ccagaggtgt ccttggactc accttggcac    2334

atgttctgtg tttcagtaaa gagagacctg atcacccaaa aaaaaaaaa                2383



     <210> 11
     <211> 2098
     <212> DNA
     <213> Homo sapiens

     <220>
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     <222> (402)..(1799)

     <400> 11
accaactcaa agctctgcga gtcctggacg ctggtctgcc ttcttggctc accctggaag      60

gtggacgctg gccccacaca tcccctctta aagacgcagg ccgatagcca gcagatcctg     120

gggcttgctg gccccaagtg agttgtcagg gtttcagagg acaccagtca tggcaacccc     180

agctccatgg ctgccacaca ggcctgggct tcccaggact gcctccttct tgttcgctta     240

tgtagatgaa aaatgaggta acggcactcc cctgccccac cctcctccca gaagtgccca     300

gggtgtaaat gcaatagctt gtgtgaagtc cactggaacc caggctcacc aagtcagtct     360

taaccaacac aggccccagc acccgcagag cagacactgc g    atg aca acg gac     413
                                                 Met Thr Thr Asp
                                                  1

gac aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg      461
```

```
Asp Thr Glu Val Pro Ala Met Thr Leu Ala Pro Gly His Ala Ala Leu
  5                  10                  15                  20

gaa act caa acg ctg agc gct gag acc tct tct agg gcc tca acc cca       509
Glu Thr Gln Thr Leu Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro
                 25                  30                  35

gcc ggc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc       557
Ala Gly Pro Ile Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser
             40                  45                  50

cct gca aga gag acc agg agt ttc aca aaa aca tct ccc aac ttc atg       605
Pro Ala Arg Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met
         55                  60                  65

gtg ctg atc gcc acc tcc gtg gag aca tca gcc gcc agt ggc agc ccc       653
Val Leu Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro
     70                  75                  80

gag gga gct gga atg acc aca gtt cag acc atc aca ggc agt gat ccc       701
Glu Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro
 85                  90                  95                 100

gag gaa gcc atc ttt gac acc ctt tgc acc gat gac agc tct gaa gag       749
Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu
                105                 110                 115

gca aag aca ctc aca atg gac ata ttg aca ttg gct cac acc tcc aca       797
Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr
            120                 125                 130

gaa gct aag ggc ctg tcc tca gag agc agt gcc tct tcc gac ggc ccc       845
Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro
        135                 140                 145

cat cca gtc atc acc ccc tca tgg tcc ccg gga tct gac gtc act ctc       893
His Pro Val Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu
    150                 155                 160

ctc gct gaa gcc ctg gtg act gtc aca aac atc gag gtt att aat tgc       941
Leu Ala Glu Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys
165                 170                 175                 180

agc atc aca gaa ata gaa aca acg act tcc agc atc cct ggg gcc tca       989
Ser Ile Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser
                185                 190                 195

gac aca gat ctc atc ccc acg gaa ggg gtg aag gcc tcg tcc acc tcc      1037
Asp Thr Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser
            200                 205                 210

gat cca cca gct ctg cct gac tcc act gaa gca aaa cca cac atc act      1085
Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile Thr
        215                 220                 225

gag gtc aca gcc tct gcc gag acc ctg tcc aca gcc ggc acc aca gag      1133
Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr Thr Glu
```

```
    230                 235                 240

tca gct gca cct cat gcc acg gtt ggg acc cca ctc ccc act aac agc      1181
Ser Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro Thr Asn Ser
245                 250                 255                 260

gcc aca gaa aga gaa gtg aca gca ccc ggg gcc acg acc ctc agt gga      1229
Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr Thr Leu Ser Gly
                265                 270                 275

gct ctg gtc aca gtt agc agg aat ccc ctg gaa gaa acc tca gcc ctc      1277
Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu Glu Thr Ser Ala Leu
            280                 285                 290

tct gtt gag aca cca agt tac gtc aaa gtc tca gga gca gct ccg gtc      1325
Ser Val Glu Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val
        295                 300                 305

tcc ata gag gct ggg tca gca gtg ggc aaa aca act tcc ttt gct ggg      1373
Ser Ile Glu Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly
    310                 315                 320

agc tct gct tcc tcc tac agc ccc tcg gaa gcc gcc ctc aag aac ttc      1421
Ser Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu Lys Asn Phe
325                 330                 335                 340

acc cct tca gag aca ccg acc atg gac atc gca acc aag ggg ccc ttc      1469
Thr Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe
                345                 350                 355

ccc acc agc agg gac cct ctt cct tct gtc cct ccg act aca acc aac      1517
Pro Thr Ser Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Thr Asn
            360                 365                 370

agc agc cga ggg acg aac agc acc tta gcc aag atc aca acc tca gcg      1565
Ser Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala
        375                 380                 385

aag acc acg atg aag ccc cca aca gcc acg ccc acg act gcc cgg acg      1613
Lys Thr Thr Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr
    390                 395                 400

agg ccg acc aca gac gtg agt gca ggt gaa aat gga ggt ttc ctc ctc      1661
Arg Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu
405                 410                 415                 420

ctg cgg ctg agt gtg gct tcc ccg gaa gac ctc act gac ccc aga gtg      1709
Leu Arg Leu Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val
                425                 430                 435

gca gaa agg ctg atg cag cag ctc cac cgg gaa ctc cac gcc cac gcg      1757
Ala Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala
            440                 445                 450

cct cac ttc cag gtc tcc tta ctg cgt gtc agg aga ggc taa cggacat      1806
Pro His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly  *
        455                 460                 465
```

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cagctgcagc caggcatgtc ccgtatgcca aaagagggtg ctgcccctag cctgggcccc   1866

caccgacaga ctgcagctgc gttactgtgc tgagaggtac ccagaaggtt cccatgaagg   1926

gcagcatgtc caagccccta accccagatg tggcaacagg accctcgctc acatccaccg   1986

gagtgtatgt atggggaggg gcttcacctg ttcccagagg tgtccttgga ctcaccttgg   2046

cacatgttct gtgtttcagt aaagagagac ctgatcaccc aaaaaaaaaa aa           2098




     <210> 12
     <211> 636
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (394)..(618)

     <400> 12
actagtccag tgcggcggaa ttcgctggct gcacccctca aaccatgaag ctgagaagca     60

cccactttac aagtgcagca tccggagagg aggctctcat cagtgcaggc tcatccacac    120

cagccgtgtt ttggggactt aaggaggtca ttcgcgctca gaggctgtcc cgggcaccat    180

gcggcgtctg ccggggtctt tctcctgccc agcctcattt gcctgtgcat gcacttggtt    240

atccaacaag agctagaaca ttctgggaga agcccacggt ggctccttgc cgggctggtc    300

agactccgtg gttgtcctga gacacccacc ctctgctgcc ctgagggtgg cccaggaaag    360

tttgtgtgac cttccacacg gatcccctgg gac atg cag gtg tgg ctc ttg aca     414
                                     Met Gln Val Trp Leu Leu Thr
                                      1               5

ctg gaa agg ctg agg gtt ctg ccc aaa cct agg agt gaa ttc gac ttc      462
Leu Glu Arg Leu Arg Val Leu Pro Lys Pro Arg Ser Glu Phe Asp Phe
         10                  15                  20

ttt ccc atc tca cac aca cac ccg aga cgt cac ccg aat cca cgt att      510
Phe Pro Ile Ser His Thr His Pro Arg Arg His Pro Asn Pro Arg Ile
     25                  30                  35

tcc cac gtt cgg ctg cca ctg cct ccc agg tgg gct ttg cag gac cca      558
Ser His Val Arg Leu Pro Leu Pro Pro Arg Trp Ala Leu Gln Asp Pro
 40                  45                  50                  55

cca tcg cat ccc ctc tca ctc cac aga aaa ctc gtg ggg ccg tgt tcc      606
Pro Ser His Pro Leu Ser Leu His Arg Lys Leu Val Gly Pro Cys Ser
                 60                  65                  70

ccc tgc cac tga ccacgctttc cttgcaga                                  636
```

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Pro Cys His  *
             75




     <210> 13
     <211> 2905
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (314)..(1279)

     <400> 13
ccccttgtgcc tgcagggtcg acaggcaggg tcagtgtatg aggctttttg ggtgggtttt      60

gggacaaact aggggatgca tggccctctc taggggtcat ccaatacccc agctctgacc     120

agttgttccc ctgctagccc agttggcctc tgattttagg agaagccaga agtccagatt     180

tttctgtgag ctctccttag ttgtccacat tggaagcaaa cttttaaatg ctgtgtatgc     240

gtggcccaag caaaacacat ctggaggcca gattgaatcc acaggctgaa agcagtcaac     300

caggcctgat gtc   atg acc ctg tat cct ctc cac tgg cag gaa gag atg      349
                 Met Thr Leu Tyr Pro Leu His Trp Gln Glu Glu Met
                  1               5                   10

tca gga gaa agt gtg gtg agc tca gcg gtg cca gcg gct gct acc cgc      397
Ser Gly Glu Ser Val Val Ser Ser Ala Val Pro Ala Ala Ala Thr Arg
        15                  20                  25

acc act tcc ttc aag ggc acg agc ccc agc tcc aaa tac gtg aag ctg      445
Thr Thr Ser Phe Lys Gly Thr Ser Pro Ser Ser Lys Tyr Val Lys Leu
    30                  35                  40

aat gtg ggt gga gcc ctc tac tat acc acc atg cag acg ctg acc aag      493
Asn Val Gly Gly Ala Leu Tyr Tyr Thr Thr Met Gln Thr Leu Thr Lys
45                  50                  55                  60

cag gac acc atg ctg aag gcc atg ttc agc ggg cgc atg gaa gtg ctc      541
Gln Asp Thr Met Leu Lys Ala Met Phe Ser Gly Arg Met Glu Val Leu
                65                  70                  75

acc gac agt gaa ggc tgg atc ctc att gac cgc tgt ggg aag cac ttt      589
Thr Asp Ser Glu Gly Trp Ile Leu Ile Asp Arg Cys Gly Lys His Phe
            80                  85                  90

ggt acg ata ctc aac tac ctt cga gac ggg gcg gtg cct tta ccc gag      637
Gly Thr Ile Leu Asn Tyr Leu Arg Asp Gly Ala Val Pro Leu Pro Glu
        95                  100                 105

agc cgc cgg gag atc gag gag ctg cta gca gaa gcc aag tac tac cta      685
Ser Arg Arg Glu Ile Glu Glu Leu Leu Ala Glu Ala Lys Tyr Tyr Leu
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    110                 115                 120

gtc caa ggc ctg gtg gaa gag tgc cag gcg gcc cta caa aac aaa gat      733
Val Gln Gly Leu Val Glu Glu Cys Gln Ala Ala Leu Gln Asn Lys Asp
125                 130                 135                 140

act tat gag cct ttc tgc aag gtc cct gtg atc acc tca tcc aag gaa      781
Thr Tyr Glu Pro Phe Cys Lys Val Pro Val Ile Thr Ser Ser Lys Glu
                145                 150                 155

gaa caa aaa ctt ata gcg act tca aat aag cca gcc gtg aag ttg ctc      829
Glu Gln Lys Leu Ile Ala Thr Ser Asn Lys Pro Ala Val Lys Leu Leu
            160                 165                 170

tac aac aga agt aac aac aaa tac tca tat acc agc aat tct gac gac      877
Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser Asn Ser Asp Asp
        175                 180                 185

aat atg ttg aaa aac att gaa ctg ttt gat aag ctg tct ctg cgc ttt      925
Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu Ser Leu Arg Phe
    190                 195                 200

aac gga agg gtc ctg ttc ata aag gat gtt att ggg gat gaa atc tgc      973
Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly Asp Glu Ile Cys
205                 210                 215                 220

tgc tgg tcc ttt tat ggt cag ggc cgg aag att gct gaa gtc tgt tgt     1021
Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala Glu Val Cys Cys
                225                 230                 235

acc tcc atc gtc tat gcc act gag aag aaa cag acc aag gtg gag ttt     1069
Thr Ser Ile Val Tyr Ala Thr Glu Lys Lys Gln Thr Lys Val Glu Phe
            240                 245                 250

ccc gaa gcc cgg att tat gag gag acc ctg aac att ttg ctg tat gag     1117
Pro Glu Ala Arg Ile Tyr Glu Glu Thr Leu Asn Ile Leu Leu Tyr Glu
        255                 260                 265

gcc cag gat ggc cgg gga cct gac aat gcg ctc ctg gag gcc aca ggc     1165
Ala Gln Asp Gly Arg Gly Pro Asp Asn Ala Leu Leu Glu Ala Thr Gly
    270                 275                 280

ggg gcg gcg ggg cgc tcc cac cac ctg gac gag gac gag gag cgg gag     1213
Gly Ala Ala Gly Arg Ser His His Leu Asp Glu Asp Glu Glu Arg Glu
285                 290                 295                 300

cgg atc gag cgc gtg cgg agg atc cac atc aag cgc cct gat gac cgg     1261
Arg Ile Glu Arg Val Arg Arg Ile His Ile Lys Arg Pro Asp Asp Arg
                305                 310                 315

gcc cac ctc cac cag tga gcaggc aagagaccga gccgccctcc tctcaccgcc     1315
Ala His Leu His Gln  *
            320

cccactccct gccgtgctac acccagatcc tgtgcaggct gccgggcccc ttctgcttcc   1375

cttggagcct ggagatactt ttgtaacaag ccagatgatt attttggtat tgcttgacaa   1435
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ggcaaattga ttgtcttgac ccaggcgtat gacccctgtc gttgaacaag ctgtgtctaa 1495

gatctctact tttcatgaga atctgagact ctttggagcc aggctttctc ggttctcaga 1555

ggaaaagtat gaatgagtgt gaagtgtatg tgagaacttt tgtttgcaat atttattttt 1615

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tatttcataa tcctccagcc ccagcaggtc cactcctggt tcctgtgtgt ttggcccggg 1795

cacaatcccc actgctttgc tagacgtgct ttctgccatg tggctttggg cctagagctt 1855

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accagtgcaa ctttgggtgc aaggctttgt ttagggatca agccttttgc caccttgggc 1975

tggtctttgg cctggtgctc actgggaccc catatgtctg cgtaggagca gaactttcca 2035

tggcagtaag tgtccagctc tgtttctggt tctttcccca actccagccc cgtccagttg 2095

ttctcctgat tgacccgact ccactccagg aaggccatct gaccctgtga caggcatagc 2155

tcataaacta cccctccctg ggatcccgct cctcttcagc ctccttcccc atgaagctgg 2215

gctaactttc taagtcattt tgcttagaaa ttcagtgtgg cccataccct ttgtcctccc 2275

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aaacacagac ccccttgtct ttgcctctga tttttacaca gtgtagagtg gccagcagtg 2395

aacaggttga ggatgtgcgg gtagatagat aactttgggt ctggtttgtg tctgtgttca 2455

tgtttgttta agggatatgt gtgactgtgg gtggggacgt gtgcttgtgg ggcacaggtg 2515

gcccctgctg gagcccggct gggcgcagcg cctatgtagg acgggtgttc tcagtgacct 2575

acctcccagg ctcctctgca cctgcaaagg aacaggagtg agtcgtgact gacaggggtg 2635

gttgagacta gactaggtag agtagttacc aggagatgtg aatgtgcgtc aggtgatgga 2695

tgggtttgtc aagggaatcg ttaccgtttt ataccaaagg tattaacatg ggcagccttt 2755

gacacatgta ttccaaaaac gagtttatat tttcaaacgg tttttacagc ttagactttg 2815

tacttactgc cctgcctgtg acagttgtat gccttcattt tgtatccaac agcaaagtct 2875

acaataaaac tttaaaacaa aaaaaaaaaa 2905

<210> 14
<211> 2444
<212> DNA

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<213> Homo sapiens

<220>
<221> CDS
<222> (287)..(1924)

<400> 14
gcaccggtcc ggaattcccg ggtcgacttc gctgtcgacg atttcgtcgt aagcttggat      60

cctctagagc gtccgctcgc gatctagaac ccaaggccag agctgtggac accttatccc     120

actcatcctc atcctcttcc tctgataaag cccctaccag tgctgataaa gtctttctcg     180

tgagagccta gaggccttaa aaaaaaaagt gcttgaaaga gaaggggaca aaggaacacc     240

agtattaaga ggattttcca gtgtttctgg cagttggtcc agaagg   atg cct cca     295
                                                     Met Pro Pro
                                                       1

ttc ctg ctt ctc acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc       343
Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro
    5                   10                  15

gtg gcc cta gat cct tgt tct gct tac atc agc ctg aat gag ccc tgg       391
Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp
 20                  25                  30                  35

agg aac act gac cac cag ttg gat gag tct caa ggt cct cct cta tgt       439
Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys
                40                  45                  50

gac aac cat gtg aat ggg gag tgg tac cac ttc acg ggc atg gcg gga       487
Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly
            55                  60                  65

gat gcc atg cct acc ttc tgc ata cca gaa aac cac tgt gga acc cac       535
Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His
        70                  75                  80

gca cct gtc tgg ctc aat ggc agc cac ccc cta gaa ggc gac ggc att       583
Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile
    85                  90                  95

gtg caa cgc cag gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg       631
Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp
100                 105                 110                 115

aac acc acg gtg gaa gtc aag gct tgc cct gga ggc tac tat gtg tat       679
Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr
                120                 125                 130

cgt ctg acc aag ccc agc gtc tgc ttc cac gtc tac tgt ggt cat ttt       727
Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys Gly His Phe
            135                 140                 145

tat gac atc tgc gac gag gac tgc cat ggc agc tgc tca gat acc agc       775
Tyr Asp Ile Cys Asp Glu Asp Cys His Gly Ser Cys Ser Asp Thr Ser
```

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        150                 155                 160

gag tgc aca tgc gct cca gga act gtg cta ggc cct gac agg cag aca      823
Glu Cys Thr Cys Ala Pro Gly Thr Val Leu Gly Pro Asp Arg Gln Thr
    165                 170                 175

tgc ttt gat gaa aat gaa tgt gag caa aac aac ggt ggc tgc agt gag      871
Cys Phe Asp Glu Asn Glu Cys Glu Gln Asn Asn Gly Gly Cys Ser Glu
180                 185                 190                 195

atc tgt gtg aac ctc aaa aac tcc tac cgc tgt gag tgt ggg gtt ggc      919
Ile Cys Val Asn Leu Lys Asn Ser Tyr Arg Cys Glu Cys Gly Val Gly
                200                 205                 210

cgt gtg cta aga agt gat ggc aag act tgt gaa gac gtt gaa gga tgc      967
Arg Val Leu Arg Ser Asp Gly Lys Thr Cys Glu Asp Val Glu Gly Cys
            215                 220                 225

cac aat aac aat ggt ggc tgc agc cac tct tgc ctt gga tct gag aaa     1015
His Asn Asn Asn Gly Gly Cys Ser His Ser Cys Leu Gly Ser Glu Lys
        230                 235                 240

ggc tac cag tgt gaa tgt ccc cgg ggc ctg gtg ctg tct gag gat aac     1063
Gly Tyr Gln Cys Glu Cys Pro Arg Gly Leu Val Leu Ser Glu Asp Asn
    245                 250                 255

cac act tgc caa gtc cct gtg ttg tgc aaa tca aat gcc att gaa gtg     1111
His Thr Cys Gln Val Pro Val Leu Cys Lys Ser Asn Ala Ile Glu Val
260                 265                 270                 275

aac atc ccc agg gag ctg gtt ggt ggc ctg gag ctc ttc ctg acc aac     1159
Asn Ile Pro Arg Glu Leu Val Gly Gly Leu Glu Leu Phe Leu Thr Asn
                280                 285                 290

acc tcc tgc cga gga gtg tcc aac ggc acc cat gtc aac atc ctc ttc     1207
Thr Ser Cys Arg Gly Val Ser Asn Gly Thr His Val Asn Ile Leu Phe
            295                 300                 305

tct ctc aag aca tgt ggt aca gtg gtc gat gtg gtg aat gac aag att     1255
Ser Leu Lys Thr Cys Gly Thr Val Val Asp Val Val Asn Asp Lys Ile
        310                 315                 320

gtg gcc agc aac ctc gtg aca ggt cta ccc aag cag acc ccg ggg agc     1303
Val Ala Ser Asn Leu Val Thr Gly Leu Pro Lys Gln Thr Pro Gly Ser
    325                 330                 335

agc ggg gac ttc atc atc cga acc agc aag ctg ctg atc ccg gtg acc     1351
Ser Gly Asp Phe Ile Ile Arg Thr Ser Lys Leu Leu Ile Pro Val Thr
340                 345                 350                 355

tgc gag ttt cca cgc ctg tac acc att tct gaa gga tac gtt ccc aac     1399
Cys Glu Phe Pro Arg Leu Tyr Thr Ile Ser Glu Gly Tyr Val Pro Asn
                360                 365                 370

ctt cga aac tcc cca ctg gaa atc atg agc cga aat cat ggg atc ttc     1447
Leu Arg Asn Ser Pro Leu Glu Ile Met Ser Arg Asn His Gly Ile Phe
            375                 380                 385
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cca ttc act ctg gag atc ttc aag gac aat gag ttt gaa gag cct tac      1495
Pro Phe Thr Leu Glu Ile Phe Lys Asp Asn Glu Phe Glu Glu Pro Tyr
        390                 395                 400

cgg gaa gct ctg ccc acc ctc aag ctt cgt gac tcc ctc tac ttt ggc      1543
Arg Glu Ala Leu Pro Thr Leu Lys Leu Arg Asp Ser Leu Tyr Phe Gly
    405                 410                 415

att gag ccc gtg gtg cac gtg agc ggc ttg gaa agc ttg gtg gag agc      1591
Ile Glu Pro Val Val His Val Ser Gly Leu Glu Ser Leu Val Glu Ser
420                 425                 430                 435

tgc ttt gcc acc ccc acc tcc aag atc gac gag gtc ctg aaa tac tac      1639
Cys Phe Ala Thr Pro Thr Ser Lys Ile Asp Glu Val Leu Lys Tyr Tyr
                440                 445                 450

ctc atc cgg gat ggc tgt gtt tca gat gac tcg gta aag cag tac aca      1687
Leu Ile Arg Asp Gly Cys Val Ser Asp Asp Ser Val Lys Gln Tyr Thr
            455                 460                 465

tcc cgg gat cac cta gca aag cac ttc cag gtc cct gtc ttc aag ttt      1735
Ser Arg Asp His Leu Ala Lys His Phe Gln Val Pro Val Phe Lys Phe
        470                 475                 480

gtg ggc aaa gac cac aag gaa gtg ttt ctg cac tgc cgg gtt ctt gtc      1783
Val Gly Lys Asp His Lys Glu Val Phe Leu His Cys Arg Val Leu Val
    485                 490                 495

tgt gga gtg ttg gac gag cgt tcc cgc tgt gcc cag ggt tgc cac cgg      1831
Cys Gly Val Leu Asp Glu Arg Ser Arg Cys Ala Gln Gly Cys His Arg
500                 505                 510                 515

cga atg cgt cgt ggg gca gga gga gag gac tca gcc ggt cta cag ggc      1879
Arg Met Arg Arg Gly Ala Gly Gly Glu Asp Ser Ala Gly Leu Gln Gly
                520                 525                 530

cag acg cta aca ggc ggc ccg atc cgc atc gac tgg gag gac tag ttc      1927
Gln Thr Leu Thr Gly Gly Pro Ile Arg Ile Asp Trp Glu Asp  *
            535                 540                 545

gtagccatac ctcgagtccc tgcattggac ggctctgctc tttggagctt ctccccccac    1987

cgccctctaa gaacatctgc caacagctgg gttcagactt cacactgtga gttcagactc    2047

ccagcaccaa ctcactctga ttctggtcca ttcagtgggc acaggtcaca gcactgctga    2107

acaatgtggc ctgggtgggg tttcatcttt ctagggttga aaactaaact gtccacccag    2167

aaagacactc accccatttc cctcatttct ttcctacact taaatacctc gtgtatggtg    2227

caatcagacc acaaaatcag aagctgggta taatatttca agttacaaac cctagaaaaa    2287

ttaaacagtt actgaaatta tgacttaaat acccaatgac tccttaaata tgtaaattat    2347

agttatacct tgaaatttca attcaaatgc agactaatta tagggaattt ggaagtgtat    2407
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caataaaaca gtatataatt ttaaaaaaaa aaaaaaa                            2444




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gggttgaggc tgcctgaccc cagcctaatg gggtaggtag gccttgggaa gtggagc       117
atg ggg gca aag gat cca agc att gag cct tca tcc tct att ccc cat      165
Met Gly Ala Lys Asp Pro Ser Ile Glu Pro Ser Ser Ser Ile Pro His
  1               5                  10                  15

cca gtg ggg tgc cga ggc tca ggc agc atg acg acg gag acc ttt gtg      213
Pro Val Gly Cys Arg Gly Ser Gly Ser Met Thr Thr Glu Thr Phe Val
             20                  25                  30

aag gat atc aag cct ggg ctc aag aat ctg aac ctt atc ttc att gtg      261
Lys Asp Ile Lys Pro Gly Leu Lys Asn Leu Asn Leu Ile Phe Ile Val
         35                  40                  45

ctg gag aca ggc cga gtg acc aag aca aag gac ggg cat gag gtt cgg      309
Leu Glu Thr Gly Arg Val Thr Lys Thr Lys Asp Gly His Glu Val Arg
     50                  55                  60

acc tgc aaa gtg gcg gac aaa aca ggc agc atc aat atc tct gtc tgg      357
Thr Cys Lys Val Ala Asp Lys Thr Gly Ser Ile Asn Ile Ser Val Trp
 65                  70                  75                  80

gac gat gtt ggc aat ctg atc cag cct ggg gac att atc cgg ctc acc      405
Asp Asp Val Gly Asn Leu Ile Gln Pro Gly Asp Ile Ile Arg Leu Thr
                 85                  90                  95

aaa ggg tac gct tca gtt ttc aaa ggt tgt ctg aca cta tat act ggc      453
Lys Gly Tyr Ala Ser Val Phe Lys Gly Cys Leu Thr Leu Tyr Thr Gly
            100                 105                 110

cgt ggg ggt gat ctg cag aag att gga gaa ttc tgt atg gtt tat tct      501
Arg Gly Gly Asp Leu Gln Lys Ile Gly Glu Phe Cys Met Val Tyr Ser
        115                 120                 125

gag gtt cct aac ttc agt gag cca aac cca gag tac agc acc cag cag      549
Glu Val Pro Asn Phe Ser Glu Pro Asn Pro Glu Tyr Ser Thr Gln Gln
    130                 135                 140

gca ccc aac aag gcg gtg cag aac gac agc aac cct tca gct tcc cag      597
Ala Pro Asn Lys Ala Val Gln Asn Asp Ser Asn Pro Ser Ala Ser Gln
145                 150                 155                 160
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cct acc act gga ccc tct gct gcc tct cca gcc tct gag aac cag aat      645
Pro Thr Thr Gly Pro Ser Ala Ala Ser Pro Ala Ser Glu Asn Gln Asn
                165                 170                 175

ggg aat gga ctg agt gcc cca cca ggt ccc ggt ggt ggc cca cat ccc      693
Gly Asn Gly Leu Ser Ala Pro Pro Gly Pro Gly Gly Gly Pro His Pro
            180                 185                 190

cct cat act ccc tcc cac cca ccc agc acc cga atc act cga agc cag      741
Pro His Thr Pro Ser His Pro Pro Ser Thr Arg Ile Thr Arg Ser Gln
        195                 200                 205

ccc aac cac aca cct gca ggc ccg cct ggc cct ttc agc aac cct gtt      789
Pro Asn His Thr Pro Ala Gly Pro Pro Gly Pro Phe Ser Asn Pro Val
    210                 215                 220

agt aac ggc aaa gaa acc cgg agg agc agc aag aga tag catgacattc       838
Ser Asn Gly Lys Glu Thr Arg Arg Ser Ser Lys Arg  *
225                 230                 235

tttcttcctg ccaccaacca catcccaagt gtcccctgga gagcaagata gccttccact    898

gattggctgg tgtagcagta ttttagccac tgaacttcag tggagggtgg tgagcagtgt    958

ccttatccac cctaatctca tactccctca ttgtccagct gaactacctg tcccctggga   1018

gtcaggaccc tctgcctgct ctctttcctc tttagaaatg gcagttactg gctgggcgca   1078

gtggctcacg cttgtaatcc cagcactttg ggaagccgag gtgggcggat cacctgaggt   1138

cgggagttca agaccagcct gaccaacatg gagaaacccc gtgtctacta aaaatacaga   1198

attagccagg catggtggcg tatgcctgta atcccagcta cttaggaggc tgaggcagga   1258

gaatctcttg aaaccgggag gcggaggttg aggtgagccg aaattgcacc attgcactcc   1318

agcctgggca ataagagcga aactccatct caaaaaaaaa agaaagaaag aaagaaagaa   1378

atggcagtta ccatctgttt cttctgtgtg agacatggga gtctaactga agtctctcct   1438

tcctaataaa tgttaccact ctaaaaaaaa aaaa                               1472


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     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (301)..(897)

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gcgccccaat ttcgattttc aaacgcaact cctacaggat tctgagaccc cgtcccatct     120

cccatatccc atttccagct gcaaattact gcagaatctg aacccaggaa agaaacccat     180

ttgccgaccc cctcttccct ctccagacag gtggagagcg ggtgagggtc tcgctcggct     240

ttccccctgc acctttccca ccctcccgcc cgtccctggg ggtcctccgt caccgcggcc     300

atg gcc cag aag ccg aag gtg gac ccc cac gtc ggg cgg ctg gga tac       348
Met Ala Gln Lys Pro Lys Val Asp Pro His Val Gly Arg Leu Gly Tyr
 1               5                   10                  15

ctg cag gcg ctg gtc acg gaa ttc cag gag acc caa agc caa gac gcc       396
Leu Gln Ala Leu Val Thr Glu Phe Gln Glu Thr Gln Ser Gln Asp Ala
             20                  25                  30

aag gag caa gtc ctc gcc aac ctc gcc aac ttc gct tat gac ccc agc       444
Lys Glu Gln Val Leu Ala Asn Leu Ala Asn Phe Ala Tyr Asp Pro Ser
         35                  40                  45

aac tac gag tat ctg cgg cag ctg cag gtc ctg gat tta ttt ctc gat       492
Asn Tyr Glu Tyr Leu Arg Gln Leu Gln Val Leu Asp Leu Phe Leu Asp
     50                  55                  60

tcg ctg tcg gag gag aat gag acc ctg gtg gag ttt gct att gga ggc       540
Ser Leu Ser Glu Glu Asn Glu Thr Leu Val Glu Phe Ala Ile Gly Gly
 65                  70                  75                  80

ctg tgc aac ctg tgc cca gac agg gcc aac aag gag cac atc ctg cac       588
Leu Cys Asn Leu Cys Pro Asp Arg Ala Asn Lys Glu His Ile Leu His
                 85                  90                  95

gca gga ggt gtc cca ctc atc atc aac tgc cta tcc agc ccc aat gag       636
Ala Gly Gly Val Pro Leu Ile Ile Asn Cys Leu Ser Ser Pro Asn Glu
            100                 105                 110

gag acg gtg ctg tct gcc atc acc acg ctc atg cac ctg agc ccg ccg       684
Glu Thr Val Leu Ser Ala Ile Thr Thr Leu Met His Leu Ser Pro Pro
        115                 120                 125

ggc cgc agc ttt ctc cca gag ctg acc gcc acg ccc gtg gtg cag tgc       732
Gly Arg Ser Phe Leu Pro Glu Leu Thr Ala Thr Pro Val Val Gln Cys
    130                 135                 140

atg ctt cgc ttc tcc ctc tcg gcc agc gcc agg ctc cgg aac ctg gca       780
Met Leu Arg Phe Ser Leu Ser Ala Ser Ala Arg Leu Arg Asn Leu Ala
145                 150                 155                 160

cag atc ttc ctg gag gac ttc tgc tcc ccc cgc cag gtg gcc gag gcc       828
Gln Ile Phe Leu Glu Asp Phe Cys Ser Pro Arg Gln Val Ala Glu Ala
                165                 170                 175

cgc agc cgg cag gcg cac tct gcc ctg ggt atc cca ctg ccg agg agc       876
Arg Ser Arg Gln Ala His Ser Ala Leu Gly Ile Pro Leu Pro Arg Ser
            180                 185                 190
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gtg gcc cca cgg cag cgc tga tc catggagact gcgagaccgt ggcacccta      929
Val Ala Pro Arg Gln Arg  *
        195

ctgctgggga ccacagtcct gatgtggacg cagggaacgg ggagcacata ctgccccatt    989

ggtgcctttt cagccatctg aaaggcgggt tctttcagca ggacaggcat ttacactgat   1049

gaaacgccac tgggagtgag gaagccagac tccagagaca cggagaagat caaactggag   1109

ctgcgttcat aggctggcac tctcaatcct acatcaggtg ccaccaccac cagactcagg   1169

ccctggtgta agaagcggcc aagtgcctgg acccagaggc tttgcaggac agtgttctca   1229

ggagctgggc ctgaggctta ggagagctgc cttcgctgca ggaaatcagg gattatccct   1289

taacagaagt gtctggagta gttttcaggt ataggaatga gatgcctcgt ggtgaaagga   1349

tctcaccctg ggaagatgtg gtgcccctc cagggctctg gaggatggat gcctccccca   1409

ggggctctcc aagctgggca tttgggcctg gtggatgcca acctggataa cctgtggccc   1469

agcattgact gtccacccag ccttgctgtt aggcaccatg actccaagat gaagatgtgg   1529

tccctgccct tgagtgacag cccagggact taatgtggcc atcgggcatc aagcacaagg   1589

ccatgcaggt gatgatacgt cggaatagag gcaccagccc tggtaactgc atcttctccc   1649

cttgccaccc catggccccg gctgaaagct tcggccctcc tctgctgtca ctcaatgatg   1709

gggagcccta ccccagaagt gtatcccacg agggcatcag ggacgcagtg agtgttgctc   1769

aagggagtca ggaagagacg gcaacgtaaa ggatgtggct ccatgtccat ggtgcccct    1829

ggtcaacata aggagcgtgg gatccgatgg aaaggtggag ctcagggaaa atgggggtcc   1889

ttgcctctcg tgtacccct caaggctgac ccttagatg gcccaggaat ggcaggtgct     1949

acaaaaatgg tacccacgtg ggcatggaaa tggggcagat taggggacca ctggactcag   2009

aggggaggga agggctcatc agcacccgct cagggagcct gtccctttat gttcccaaat   2069

aaagggtcct agaagaaaaa aaaaaaaaa                                      2098
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<210> 17
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<212> DNA
<213> Homo sapiens

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<222> (119)..(580)

<400> 17
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ccgggaaccg ttcccgggcc gttgatcttc ggccccacac gcagagaggg gcagcagg      118
atg aat gtg ggc aca gcg cac agc gag gtg aac ccc aac acg cgg gtg      166
Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
  1               5                  10                  15

atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc      214
Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
             20                  25                  30

ctc cac atc gtg ctg ctg agc atc ccg ttt gtg agt gtc cct gtc gtc      262
Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
         35                  40                  45

tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc ctg      310
Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
     50                  55                  60

cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag gcg      358
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65                  70                  75                  80

agg ctg cta acc cac tgg gag cag atg gat tat ggg gtc cag ttc acg      406
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr
                 85                  90                  95

gcc tct cgg aag ttc ttg acc atc aca ccc atc gtg ctg tac ttc ctc      454
Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu
            100                 105                 110

acc agc ttc tac act aag tac gac cag atc cat ttt gtg ctc aac acc      502
Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr
        115                 120                 125

gtg tcc ctg atg agc gtg ctt atc ccc aag ctg ccc cag ctc cac gga      550
Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly
    130                 135                 140

gtc cgg att ttt gga atc aat aag tac tga g agtgcagccc cttcccctgc      601
Val Arg Ile Phe Gly Ile Asn Lys Tyr  *
145                 150

ccagggtggc aggggagggg tagggtaaaa ggcatgtgct gcaacactga agacagaaag    661

aagaagcctc tggacactgc cagagatggg ggttgagcct ctggcctaat ttcccccctc    721

gcttcccccca gtagccaact tggagtagct tgtagtgggg ttggggtagg ccccctgggc   781

tctgaccttt tctgaatttt ttgatctttt ccttttgctt tttgaataga gactccatgg    841

agttggtcat ggaatgggct gggctcctgg gctgaacatg gaccacgcag ttgcgacagg    901

aggccagggg aaaaacccct gctcacttgt ttgccctcag gcagccaaag cactttaacc    961

cctgcatagg gagcagaggg cggtacggct tctggattgt ttcactgtga ttcctaggtt   1021
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ttttcgatgc cacgcagtgt gtgcttttgt gtatggaagc aagtgtggga tgggtctttg 1081

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ccaccgtggg tcctggttgg gagtggggag ggtcaggttg gggaaagatg gggtagagtg 1201

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ggaaaaggcc cgtgagtcat tgtaagcaca ggtccaactt ggccctgact cctgcggggg 1561

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tgtgaggcca ccccatgtgg ggtctgtggt gagagtcctg taggatccct gctcaagcag 1741

cacagaggaa ggggcaagac gtggcctgta ggcactgtct cagcctgcag agaagaaagt 1801

gaggccggga gcctgagcct gggctggagc cttctcccct ccccagttgg actaggggca 1861

gtgttaattt tgaaaaggtg tgggtccctg tgtcctcttc caggggtcca agggaacagg 1921

agaggtcact gggcctgttt tctccctcct gaccctgcat ctcccacccc gtgtatcata 1981

gggaactttc accttaaaat ctttctaagc aaagtgtgaa taggattttt actccctttg 2041

tacagtattc tgagaaacgc aaataaaagg gcaacatgtt tctgttaaaa aaaaaaaa 2099

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gctggtaact ttggcgcctc cgccaagccc tgccagactc ccctggctgt gatggcattc 180

tgtgccatcc tccttgtccc cagcctctgc aggatgccct ccctacccac ctctccctgg 240

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gccttccctg tccactgggc tggattcatg ttcaaaccac tggactggca gggcaacgac      300

ttcttcccac ctcaagatga ggtcctcgcc cccttgtctt ggcataaaaa cacctttaaa      360

gcatgagcca tgtgcttctt tgcccttctc tgtcctgttc caatcttctg cctcccagtc      420

actccctggg gactatggga tcactgtccc cccacctgtg tggccacacc atgtgtcctg      480

tcaatccaga actgcctctg agctccaggc tgaccacaga tcagccacag cctg  atg        537
                                                             Met
                                                               1

cct gca gcc cca ctt tgc tca ccc ttc ccc tcc cct cct cct tcc ttc        585
Pro Ala Ala Pro Leu Cys Ser Pro Phe Pro Ser Pro Pro Pro Ser Phe
              5                  10                  15

cac aca gca agc cta cct ttc tcc atc cat gct cac cat agc ccc ctt        633
His Thr Ala Ser Leu Pro Phe Ser Ile His Ala His His Ser Pro Leu
         20                  25                  30

cct tgt gac ttg gac cct cca ttg tac ctg gct gag act gtc agc ctc        681
Pro Cys Asp Leu Asp Pro Pro Leu Tyr Leu Ala Glu Thr Val Ser Leu
     35                  40                  45

ctg gag gag tgg ggt cca cct tct tct tgc cct atg cag tgc aag ctc        729
Leu Glu Glu Trp Gly Pro Pro Ser Ser Cys Pro Met Gln Cys Lys Leu
 50                  55                  60                  65

act tct cac cca gca agg ttg act cat ctg cct cca tgt ctc tgg ggc        777
Thr Ser His Pro Ala Arg Leu Thr His Leu Pro Pro Cys Leu Trp Gly
                 70                  75                  80

ttt gct gtt gcc ctg aaa cct agc tgg gct ggt ctt gct ccc agc ttg        825
Phe Ala Val Ala Leu Lys Pro Ser Trp Ala Gly Leu Ala Pro Ser Leu
             85                  90                  95

ctt ccc cct cct cgg atg tcc ctt tgc agg ccc ctg tcg ttc ctc cgg        873
Leu Pro Pro Pro Arg Met Ser Leu Cys Arg Pro Leu Ser Phe Leu Arg
        100                 105                 110

cac cag tgt cct tgg ctg cca tgg caa gct cat cag ggg ctt gta ccc        921
His Gln Cys Pro Trp Leu Pro Trp Gln Ala His Gln Gly Leu Val Pro
    115                 120                 125

tgg tca cca agc atg gta gca gct gcc tgc att gta tct cca tct ggt        969
Trp Ser Pro Ser Met Val Ala Ala Ala Cys Ile Val Ser Pro Ser Gly
130                 135                 140                 145

cac tgc agg tgc caa ccc ttc atc ccc cat gtt ttc ctg ggc cat gga       1017
His Cys Arg Cys Gln Pro Phe Ile Pro His Val Phe Leu Gly His Gly
                150                 155                 160

ggg ctg acc tcc gtt tct ggg gaa tgt ggc tga gctgtggt aaccagctac       1068
Gly Leu Thr Ser Val Ser Gly Glu Cys Gly  *
            165                 170

accccaggtg ctctttccat ggtggtgcct gctcatcttg ctgatgcaaa ctaggaagtt     1128
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aggctgcatc tcggagtggc tttcgctgga gaggtgcttt gctgtctctc agactcagtc   1188

actgtgttcc ctccccgcct ctcttatctc catggctgtt tgcagctctc ccaggtactt   1248

tggggtctga gctggaattc ctttgtggtt tgctcttctg cttctcactc ttgtattaag   1308

aaggattcca caaagggaga gtggcatccc tgctgctgct gtgccagacc agagtttcct   1368

gaggggccct gaccctaacc ctccagctca gccctgtaca cctgaccctg taaatgagtg   1428

gggtttgctg actgtaatcc ctgacaccag taaaaccaaa aggactcttg ggggctcagt   1488

gtgagagcca gggttaccta ctctgccaag tgaggacaaa ctgctaggct gtatcccata   1548

atttcaggat gagaaacatt aacaataaaa atttgtagta aacataaaaa aaaaaaa      1605



     <210> 19
     <211> 1497
     <212> DNA
     <213> Homo sapiens

     <220>
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     <222> (210)..(1172)

     <400> 19
agttcgggcg acgaggacaa aacactgtga gtcgctgttg gtcgctgcag cgggcctctg     60

cgtgggcggc gggaatccgc ggacatcggg tcgggtctag gctcccgagt ccgcgctccc    120

tgggcgggag cccttgtctg ggtctcgcgg ggggctgcca gatgcgtagg ccacactgac    180

tagttccttc ttgtcgcttt tcccagcaa  atg gcg gat gac gcc ggt gca gcg    233
                                 Met Ala Asp Asp Ala Gly Ala Ala
                                   1               5

ggg ggg ccc ggg ggc cct ggt ggc cct ggg atg ggg aac cgc ggt ggc      281
Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Met Gly Asn Arg Gly Gly
     10                  15                  20

ttc cgc gga ggt ttc ggc agt ggc atc cgg ggc cgg ggt cgc ggc cgt      329
Phe Arg Gly Gly Phe Gly Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg
 25                  30                  35                  40

gga cgg ggc cgg ggc cga ggc cgc gga gct cgc gga ggc aag gcc gag      377
Gly Arg Gly Arg Gly Arg Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu
                 45                  50                  55

gat aag gag tgg atg ccc gtc acc aag ttg ggc cgc ttg gtc aag gac      425
Asp Lys Glu Trp Met Pro Val Thr Lys Leu Gly Arg Leu Val Lys Asp
             60                  65                  70

atg aag atc aag tcc ctg gag gag atc tat ctc ttc tcc ctg ccc att      473
```

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Met Lys Ile Lys Ser Leu Glu Glu Ile Tyr Leu Phe Ser Leu Pro Ile
         75                  80                  85

aag gaa tca gag atc att gat ttc ttc ctg ggg gcc tct ctc aag gat       521
Lys Glu Ser Glu Ile Ile Asp Phe Phe Leu Gly Ala Ser Leu Lys Asp
     90                  95                 100

gag gtt ttg aag att atg cca gtg cag aag cag acc cgt gcc ggc cag       569
Glu Val Leu Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln
105                 110                 115                 120

cgc acc agg ttc aag gca ttt gtt gct atc ggg gac tac aat ggc cac       617
Arg Thr Arg Phe Lys Ala Phe Val Ala Ile Gly Asp Tyr Asn Gly His
                125                 130                 135

gtc ggt ctg ggt gtt aag tgc tcc aag gag gtg gcc acc gcc atc cgt       665
Val Gly Leu Gly Val Lys Cys Ser Lys Glu Val Ala Thr Ala Ile Arg
            140                 145                 150

ggg gcc atc atc ctg gcc aag ctc tcc atc gtc ccc gtg cgc aga ggc       713
Gly Ala Ile Ile Leu Ala Lys Leu Ser Ile Val Pro Val Arg Arg Gly
        155                 160                 165

tac tgg ggg aac aag atc ggc aag ccc cac act gtc cct tgc aag gtg       761
Tyr Trp Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys Lys Val
    170                 175                 180

aca gcg tgg ggc cat cat cct ggc caa gct ctc cat cgt ccc cgt gcg       809
Thr Ala Trp Gly His His Pro Gly Gln Ala Leu His Arg Pro Arg Ala
185                 190                 195                 200

cag agg cta ctg ggg gaa caa gat cgg caa gcc cca cac tgt cac ctt       857
Gln Arg Leu Leu Gly Glu Gln Asp Arg Gln Ala Pro His Cys His Leu
                205                 210                 215

gca agg gac agt gtg ggg ctt gcc gat ctt gtt ccc cca gta gcc tct       905
Ala Arg Asp Ser Val Gly Leu Ala Asp Leu Val Pro Pro Val Ala Ser
            220                 225                 230

gcg cac ggg gac gat gga gag ctt ggc cag gat gat ggc ccc acg gat       953
Ala His Gly Asp Asp Gly Glu Leu Gly Gln Asp Asp Gly Pro Thr Asp
        235                 240                 245

ggc ggt ggc cac ctc ctt gga gca ctt aac acc cag acc gac gtg gcc      1001
Gly Gly Gly His Leu Leu Gly Ala Leu Asn Thr Gln Thr Asp Val Ala
    250                 255                 260

att gta gtc ccc gat agc aac aaa tgc ctt gaa cct ggt gcg ctg gcc      1049
Ile Val Val Pro Asp Ser Asn Lys Cys Leu Glu Pro Gly Ala Leu Ala
265                 270                 275                 280

ggc acg ggt ctg ctt ctg cac tgg cat aat ctt caa aac ctc atc ctt      1097
Gly Thr Gly Leu Leu Leu His Trp His Asn Leu Gln Asn Leu Ile Leu
                285                 290                 295

gag aga ggg cac cac aca gtg aac gaa agt caa atg agt gct gct gat      1145
Glu Arg Gly His His Thr Val Asn Glu Ser Gln Met Ser Ala Ala Asp
```

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           300                 305                 310

tcc tta ata ggc agg gag aag aga tag atcac cactccaggg acttagatct      1197
Ser Leu Ile Gly Arg Glu Lys Arg  *
        315                 320

tcatgtcctt ggaccaagcg gccacaactt cggtgacggg gcatccactc cttatcgctc   1257

ggccttgcgc tccagcgagc tccgcaggca catcggccca caggccacac agtcacacag   1317

gccgcagacc accaggccac cagagtgcac agcatgcaca gaaacactgc cgcaggaagc   1377

acacacagcg gcttcccaca tcacaagggc cacaatgggc ccccagggcc caccccgctg   1437

taccggcgta tccagccatt tggtgttttg acaacccagg atcgtacact agccgtaatt   1497




     <210> 20
     <211> 907
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (114)..(338)

     <400> 20
gcttcttcca gtcacctcgg cccggatcgg gaagtgtcaa gcgggcgctc ccccatctcc      60

gccgctatta ccactgaacc cggacccccct acccaggtcc agggccagcc gcc   atg      116
                                                              Met
                                                               1

acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt       164
Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe
            5                   10                  15

gtt tgc acc tgt gcc tac ttc aag aaa gta cct cgt ctc aaa acc tgg       212
Val Cys Thr Cys Ala Tyr Phe Lys Lys Val Pro Arg Leu Lys Thr Trp
        20                  25                  30

ctg cta tca gag aag aag ggt gtt tgg ggt gtg ttt tac aaa gcc gct       260
Leu Leu Ser Glu Lys Lys Gly Val Trp Gly Val Phe Tyr Lys Ala Ala
    35                  40                  45

gtg att gga acc agg ctg cat gct gct gtg gca att gct tgt gtt gta       308
Val Ile Gly Thr Arg Leu His Ala Ala Val Ala Ile Ala Cys Val Val
50                  55                  60                  65

atg gcc ttt tac gtc ctg ttt ata aaa tga a ttccaaagca cccaagtcat       359
Met Ala Phe Tyr Val Leu Phe Ile Lys  *
                70                  75

caactgccaa ccaaggggac ggggatgaag aacctgttgg agacctgaac ccagtgtagg    419
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agagttcagc tgaaatcatc ggtccccagg atgacaccac agcatctgcc cctgctatat     479

gtggggaaaa ctcatggtca cgaacattat ttatgcttca ggggactaca gaaagccagc     539

ttcctttgat ctatgtgtaa atcagtcctt ggcagagtgc atataatgtc cggataaatt     599

acacccctcg gtgataagat tacatacctc cttcataaaa acctgtcatc ctgtttgttc     659

ttcagctcct catcaggatc ttttcaaact gggctcatta gggaaggaac taggcttgtg     719

ttcagacttc tttgagagcg agaatttcca gacttctttt cctccttgat tggtctggca     779

ttggggcggg gatgctgggt gggaacccgt ttgaattgcc aggaaattct tgggttagaa     839

ttctcttcat gtccatccgg accttaggag gctggggctt gcaaggaccc gtcctcccgg     899

ttggccgg                                                              907



     <210> 21
     <211> 1329
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (103)..(1116)

     <400> 21
aaggatcctt aattaaatta atcccccccc ccggctcctc ctgttcgaca gtcagccgca      60

tcttcttttg cgtcgccagc cgagccacat cgctcagaca cc   atg ggg aag gtg      114
                                                 Met Gly Lys Val
                                                   1

aag gtc gga gtc aac gga ttt ggt cgt att ggg cgc ctg gtc acc agg      162
Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val Thr Arg
  5                  10                  15                  20

gct gct ttt aac tct ggt aaa gtg gat att gtt gcc atc aat gac ccc      210
Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala Ile Asn Asp Pro
                 25                  30                  35

ttc att gac ctc aac tac atg gtt tac atg ttc caa tat gat tcc acc      258
Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp Ser Thr
             40                  45                  50

cat ggc aaa ttc cat ggc acc gtc aag gct gag aac ggg aag ctt gtc      306
His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn Gly Lys Leu Val
         55                  60                  65

atc aat gga aat ccc atc acc atc ttc cag gag cga gat ccc tcc aaa      354
Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro Ser Lys
     70                  75                  80
```

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atc aag tgg ggc gat gct ggc gct gag tac gtc gtg gag tcc act ggc       402
Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val Glu Ser Thr Gly
 85                  90                  95                 100

gtc ttc acc acc atg gag aag gct ggg gct cat ttg cag ggg gga gcc       450
Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu Gln Gly Gly Ala
                105                 110                 115

aaa agg gtc atc atc tct gcc ccc tct gct gat gcc ccc atg ttc gtc       498
Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Phe Val
            120                 125                 130

atg ggt gtg aac cat gag aag tat gac aac agc ctc aag atc atc agc       546
Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu Lys Ile Ile Ser
        135                 140                 145

aat gcc tcc tgc acc acc aac tgc tta gca ccc ctg gcc aag gtc atc       594
Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile
    150                 155                 160

cat gac aac ttt ggt atc gtg gaa gga ctc atg acc aca gtc cat gcc       642
His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala
165                 170                 175                 180

atc act gcc acc cag aag act gtg gga tgg ccc ctt ccg gga aac tgt       690
Ile Thr Ala Thr Gln Lys Thr Val Gly Trp Pro Leu Pro Gly Asn Cys
                185                 190                 195

ggc gtg atg gcc gcg ggg gcg tct gcc aga aac atc atc cct gcc tct       738
Gly Val Met Ala Ala Gly Ala Ser Ala Arg Asn Ile Ile Pro Ala Ser
            200                 205                 210

act ggc gct gcc aag gct gtg ggc aag gtc atc cct gag ctg aac ggg       786
Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly
        215                 220                 225

aag ctc act ggc atg gcc ttc cgt gtc ccc act gcc aac gtg tca gtg       834
Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val Ser Val
    230                 235                 240

gtg gac ctg acc tgc cgt cta gaa aaa cct gcc aaa tat gat gac atc       882
Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile
245                 250                 255                 260

aag aag gtg gtg aag cag gcg tcg gag ggc ccc ctc aag ggc atc ctg       930
Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly Ile Leu
                265                 270                 275

ggc tac act gag cac cag gtg gtc tcc tct gac ttc aac agc gac acc       978
Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser Asp Thr
            280                 285                 290

cac tcc tcc acc ttt gac gct ggg gct ggc att gcc ctc aac gac cac      1026
His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn Asp His
        295                 300                 305

ttt gtc aag ctc att tcc tgg tat gac aac gaa ttt ggc tac agc aac      1074
```

```
Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn
    310                 315                 320

agg gtg gtg gac ctc atg gcc cac atg gcc tcc aag gag taa gacccct     1123
Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu  *
325                 330                 335

ggaccaccag ccccagcaag agcacaagag gaagagagag accctcactg ctggggagtc   1183

cctgccacac tcagtccccc accacactga atctcccctc ctcacagttg ccatgtagac   1243

cccttgaaga ggggaggggc ctagggagcc gcaccttgtc atgtaccatc aataaagtac   1303

cctgtgctca accaaaaaaa aaaaaa                                        1329



     <210> 22
     <211> 1251
     <212> DNA
     <213> Homo sapiens

     <220>
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     <222> (532)..(930)

     <400> 22
gagttctcag ttgcgtgggg accagagggt gctggagaaa caaaccagac gcagctgaag     60

gcagtcaggg cagggcgcaa tcagcgataa gagctgcata ggggccacag cgtaacctga    120

gctccagtcg gtggaaagaa aaggcagaga cgttgcagag gccaggtctg ctcaggggaa    180

gacagttctg ggtgtagagg actcacatcc cagagaggct gaggaagggt ttaccaccgc    240

aagctttctc aggcgggctc ttgaggggtg gctggggtct tcctggcgac gggcctgcgg    300

cactggaagc cctactggag tttggcctgt ctccggcaca ggtttggacg gagctgtttt    360

gtgctgaaag gttttctcgg ggtccgtggt gtcccccaaa ggtgccaccg tgcgggtctc    420

ctagctccct gccagcttcc tgtccctgtg ctcactgccc ccacgcctcc tgccaaggcc    480

gagccacaca cccgctccac ctgcatttcc tctaccgact cgccagccca a atg ccg     537
                                                         Met Pro
                                                          1

ctc ttc act ctg gcc tcg ctg agc ggc tgc ccg agg agg agc tct agg      585
Leu Phe Thr Leu Ala Ser Leu Ser Gly Cys Pro Arg Arg Ser Ser Arg
        5                   10                  15

ccg acg ccc acc gca ggc ctt aca gtc ttc tct gga cgc tcc ctt gca      633
Pro Thr Pro Thr Ala Gly Leu Thr Val Phe Ser Gly Arg Ser Leu Ala
    20                  25                  30

gat gca ccg tgg cct ggc ggc gag ccc ccg gtc acc ttc ctc cgc acg      681
```

Asp Ala Pro Trp Pro Gly Gly Glu Pro Pro Val Thr Phe Leu Arg Thr
35 40 45 50

gaa gag ggg ccg gac gcc acc ttc ccc agg acc att ccc ctg atc caa 729
Glu Glu Gly Pro Asp Ala Thr Phe Pro Arg Thr Ile Pro Leu Ile Gln
55 60 65

cag ttg cta aac gcc acg gag ctc acg cag gac ccg gcc gcc tac tcc 777
Gln Leu Leu Asn Ala Thr Glu Leu Thr Gln Asp Pro Ala Ala Tyr Ser
70 75 80

cag ctg gtg gcc gtg ctg gtc tac acc gcc gag cgg gcc aag ttc gcc 825
Gln Leu Val Ala Val Leu Val Tyr Thr Ala Glu Arg Ala Lys Phe Ala
85 90 95

acc ggg gta gag cgg cag gac tgg atg gag ctg ttc att gac acc ttt 873
Thr Gly Val Glu Arg Gln Asp Trp Met Glu Leu Phe Ile Asp Thr Phe
100 105 110

aag ctg gtg cac agg gac atc gtg ggg gac ccc gag acc gcg ctg gcc 921
Lys Leu Val His Arg Asp Ile Val Gly Asp Pro Glu Thr Ala Leu Ala
115 120 125 130

ctc tgc taa agcccgg gcacccgccc agccgggctg ggccctccct gccacactag 977
Leu Cys *

cttcccaggg ctgcccccga caggctggct ctcagtggag gccagagatc tggaatcggg 1037

gtcagcgggg ctacagtcct tccaggggct ctggggcagc tcccagcctc ttcccatgct 1097

ggtggccacc gtgtcccttg ctgcggctgc atcttccagt ctctcctccg tcttccagtg 1157

gccgctctct ttataagaac cctggtcatt gaatttaagg cccaccccaa gtccagaatg 1217

acctcgcaag acccttaact caaaaaaaaa aaaa 1251

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<211> 1566
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (291)..(1442)

<400> 23
cgcgccgcag ccgggcgtcc ccgcgcgggc gccggagagg aaggaaggct ggcagcctcg 60

tcacgtgtcc gctgcagtcg cgaaacagtt ccggtggtga ggagaccttt ccaaatataa 120

gaggaataaa gaagtcacct ccccagctgt catcatcttc cagcagattg agcaagaata 180

ttttgagcac tacaggaaag acagtccatc aaacccgaga tgatgatcag ccacgtgatt 240

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ttttcaagaa gaggaatagg gtgaatgaat ctcatcagaa aagcagcaat   atg aat      296
                                                         Met Asn
                                                          1

gct ggc cca tct tgg aat aaa gtg caa cat tca aag aat tct tca gga      344
Ala Gly Pro Ser Trp Asn Lys Val Gln His Ser Lys Asn Ser Ser Gly
         5                   10                  15

aaa agg cag agt aaa tcc caa gta ccc cac gct tct tcc cag ccg aga      392
Lys Arg Gln Ser Lys Ser Gln Val Pro His Ala Ser Ser Gln Pro Arg
     20                  25                  30

agc agc ctc aca gct gtc acc cag cct act gaa gaa aaa ctt aaa gaa      440
Ser Ser Leu Thr Ala Val Thr Gln Pro Thr Glu Glu Lys Leu Lys Glu
 35                  40                  45                  50

agc att tcc ccg gaa gca aga cgc aaa agg aat cca ctc ggt tcc agg      488
Ser Ile Ser Pro Glu Ala Arg Arg Lys Arg Asn Pro Leu Gly Ser Arg
                 55                  60                  65

tgt cag ggg gcc tca ggg aat aaa ctg ttt ctt gat ttt cag tca atg      536
Cys Gln Gly Ala Ser Gly Asn Lys Leu Phe Leu Asp Phe Gln Ser Met
             70                  75                  80

aaa att att aaa gag aat gct gat gag gac agt gca agt gat ctc tct      584
Lys Ile Ile Lys Glu Asn Ala Asp Glu Asp Ser Ala Ser Asp Leu Ser
         85                  90                  95

gat tcg gaa aga att ccc att cct cct tct ccc ctc aca cct cca gat      632
Asp Ser Glu Arg Ile Pro Ile Pro Pro Ser Pro Leu Thr Pro Pro Asp
    100                 105                 110

ctc aat ctt cga gct gaa gaa att gat cca gtt tac ttt gat ctt cac      680
Leu Asn Leu Arg Ala Glu Glu Ile Asp Pro Val Tyr Phe Asp Leu His
115                 120                 125                 130

cct ggt cag ggc cat aca aaa cct gaa tac tat tat cct aat ttc ctt      728
Pro Gly Gln Gly His Thr Lys Pro Glu Tyr Tyr Tyr Pro Asn Phe Leu
                135                 140                 145

cca tcc cct ttc agc tcc tgg gac cta cga gat atg gcc ctg ctt ctg      776
Pro Ser Pro Phe Ser Ser Trp Asp Leu Arg Asp Met Ala Leu Leu Leu
            150                 155                 160

aac gca gag aac aaa acg gaa gcc gtg ccc cga gtg gga gga ctt ctt      824
Asn Ala Glu Asn Lys Thr Glu Ala Val Pro Arg Val Gly Gly Leu Leu
        165                 170                 175

ggg aag tat atc gat aga ctt att cag ctt gag tgg ctg caa gtc cag      872
Gly Lys Tyr Ile Asp Arg Leu Ile Gln Leu Glu Trp Leu Gln Val Gln
    180                 185                 190

act gta cag tgt gaa aaa gca aag ggg ggc aaa gca agg ccc ccc act      920
Thr Val Gln Cys Glu Lys Ala Lys Gly Gly Lys Ala Arg Pro Pro Thr
195                 200                 205                 210
```

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gcc cct ggg acc tca ggg gca ctg aaa agc cct ggg aga agt aag cta      968
Ala Pro Gly Thr Ser Gly Ala Leu Lys Ser Pro Gly Arg Ser Lys Leu
                215                 220                 225

att gct agt gct ctg tcc aag cca cta cct cac cag gaa ggg gct tca     1016
Ile Ala Ser Ala Leu Ser Lys Pro Leu Pro His Gln Glu Gly Ala Ser
            230                 235                 240

aag tca ggc cct tcc cga aag aaa gct ttt cac cat gaa gaa atc cac     1064
Lys Ser Gly Pro Ser Arg Lys Lys Ala Phe His His Glu Glu Ile His
        245                 250                 255

cca tca cat tat gca ttt gag act tcc cct aga ccc att gat gtg ctt     1112
Pro Ser His Tyr Ala Phe Glu Thr Ser Pro Arg Pro Ile Asp Val Leu
    260                 265                 270

ggt ggt acc agg ttt tgt tct cag agg caa acc ctt gaa atg agg aca     1160
Gly Gly Thr Arg Phe Cys Ser Gln Arg Gln Thr Leu Glu Met Arg Thr
275                 280                 285                 290

gaa gaa aaa aaa aaa aaa tca agt aag agt acg aag ctg cag cgc tgg     1208
Glu Glu Lys Lys Lys Lys Ser Ser Lys Ser Thr Lys Leu Gln Arg Trp
                295                 300                 305

gat ctg tcc ggc agt gga agc agc tct aag gtg gaa acc agc ggt cac     1256
Asp Leu Ser Gly Ser Gly Ser Ser Ser Lys Val Glu Thr Ser Gly His
            310                 315                 320

att cga gtt ccc aaa cag gca gct gtg att ctg gac tca gca gat tcc     1304
Ile Arg Val Pro Lys Gln Ala Ala Val Ile Leu Asp Ser Ala Asp Ser
        325                 330                 335

tgt aag gcc tcc aaa aca caa gca cat gca cat cct agg aaa aag gga     1352
Cys Lys Ala Ser Lys Thr Gln Ala His Ala His Pro Arg Lys Lys Gly
    340                 345                 350

aag gca gag agc tgt ggt cat gcc act gta tcg agt gag aaa aaa ctg     1400
Lys Ala Glu Ser Cys Gly His Ala Thr Val Ser Ser Glu Lys Lys Leu
355                 360                 365                 370

aaa aca aac gga gta aag caa aac aca tat aaa cta aaa taa atatcta     1449
Lys Thr Asn Gly Val Lys Gln Asn Thr Tyr Lys Leu Lys  *
                375                 380

aaatgctgaa ttgccaagac ctgcaggtac ctcaatgtta gagcgcttcc aaaagtcaaa   1509

atactgtgaa ttttaaggaa ttttacaaat actgacattt aagtaaaaaa aaaaaaa      1566


     <210> 24
     <211> 2851
     <212> DNA
     <213> Homo sapiens

     <220>
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<221> CDS
<222> (70)..(2322)

<400> 24
atttggccct cgaggccaag aattcggcac gaggaaccat gtttgagtac caaacaatga      60

cttatttat    atg ctc tca ctg gaa tta ttg tca cag gtg gtg gga ttc      108
             Met Leu Ser Leu Glu Leu Leu Ser Gln Val Val Gly Phe
               1               5                  10

cat cag cca ggt agt atc aga ctt gct acc acc cct gta agg gta gat      156
His Gln Pro Gly Ser Ile Arg Leu Ala Thr Thr Pro Val Arg Val Asp
     15                  20                  25

gaa ttt aaa tat caa atg act cgg act ggc tgg cat gca aca gaa cag      204
Glu Phe Lys Tyr Gln Met Thr Arg Thr Gly Trp His Ala Thr Glu Gln
 30                  35                  40                  45

tat ctc att gaa cct gaa aaa att caa gag atg ttc cct tta ctc aac      252
Tyr Leu Ile Glu Pro Glu Lys Ile Gln Glu Met Phe Pro Leu Leu Asn
                 50                  55                  60

atg aat aag gtt tta gct gga ttg tat aat cct gga gat ggt cac att      300
Met Asn Lys Val Leu Ala Gly Leu Tyr Asn Pro Gly Asp Gly His Ile
             65                  70                  75

gat cct tat tct cta act atg gca ctg gct gct ggg gct agg aaa tgt      348
Asp Pro Tyr Ser Leu Thr Met Ala Leu Ala Ala Gly Ala Arg Lys Cys
         80                  85                  90

ggt gcc ctt tta aaa tat cct gca cca gta act tct ctg aaa gcc agg      396
Gly Ala Leu Leu Lys Tyr Pro Ala Pro Val Thr Ser Leu Lys Ala Arg
     95                 100                 105

tca gat gga aca tgg gac gtt gaa aca cca cag ggg tct atg aga gca      444
Ser Asp Gly Thr Trp Asp Val Glu Thr Pro Gln Gly Ser Met Arg Ala
110                 115                 120                 125

aat aga att gtg aat gct gca gga ttt tgg gct cgt gaa gta ggt aaa      492
Asn Arg Ile Val Asn Ala Ala Gly Phe Trp Ala Arg Glu Val Gly Lys
                130                 135                 140

atg att gga cta gaa cat cct ctc att ccg gtt caa cat caa tat gtt      540
Met Ile Gly Leu Glu His Pro Leu Ile Pro Val Gln His Gln Tyr Val
            145                 150                 155

gtt aca tcg act ata tct gaa gtg aaa gct ttg aaa cga gaa ctg cct      588
Val Thr Ser Thr Ile Ser Glu Val Lys Ala Leu Lys Arg Glu Leu Pro
        160                 165                 170

gtg ctc cgt gac ctg gaa gga tca tat tat ctc cga cag gaa agg gat      636
Val Leu Arg Asp Leu Glu Gly Ser Tyr Tyr Leu Arg Gln Glu Arg Asp
    175                 180                 185

ggg ctt ttg ttt ggt cca tat gaa agt caa gag aaa atg aaa gtt cag      684
Gly Leu Leu Phe Gly Pro Tyr Glu Ser Gln Glu Lys Met Lys Val Gln
190                 195                 200                 205
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gac tcc tgg gtc acc aat gga gtt cct cca ggt ttt gga aag gaa ctc        732
Asp Ser Trp Val Thr Asn Gly Val Pro Pro Gly Phe Gly Lys Glu Leu
                210                 215                 220

ttt gag tct gat cta gat cga atc atg gaa cac atc aaa gct gcc atg        780
Phe Glu Ser Asp Leu Asp Arg Ile Met Glu His Ile Lys Ala Ala Met
            225                 230                 235

gaa atg gtt cct gtc ttg aaa aag gct gac atc atc aat gtt gtc aat        828
Glu Met Val Pro Val Leu Lys Lys Ala Asp Ile Ile Asn Val Val Asn
        240                 245                 250

ggt cct atc acg tat tct cct gac att ctg cct atg gtg ggg ccc cat        876
Gly Pro Ile Thr Tyr Ser Pro Asp Ile Leu Pro Met Val Gly Pro His
    255                 260                 265

cag ggg gtc aga aac tac tgg gtg gct ata ggc ttt gga tat ggc ata        924
Gln Gly Val Arg Asn Tyr Trp Val Ala Ile Gly Phe Gly Tyr Gly Ile
270                 275                 280                 285

atc cac gct ggt ggg gta ggg aaa tat ctc agt gac tgg atc ctg cat        972
Ile His Ala Gly Gly Val Gly Lys Tyr Leu Ser Asp Trp Ile Leu His
                290                 295                 300

gga gaa cct cct ttt gat ctg ata gaa ttg gat cct aat cgc tat ggc       1020
Gly Glu Pro Pro Phe Asp Leu Ile Glu Leu Asp Pro Asn Arg Tyr Gly
            305                 310                 315

aaa tgg aca aca acc cag tac act gag gcc aaa gca aga gaa tca tat       1068
Lys Trp Thr Thr Thr Gln Tyr Thr Glu Ala Lys Ala Arg Glu Ser Tyr
        320                 325                 330

gga ttc aac aat att gtt ggt tat cct aaa gaa gaa cgg ttt gct ggg       1116
Gly Phe Asn Asn Ile Val Gly Tyr Pro Lys Glu Glu Arg Phe Ala Gly
    335                 340                 345

agg ccg act caa cga gtc agt ggg ctc tat caa agg ctg gag tct aag       1164
Arg Pro Thr Gln Arg Val Ser Gly Leu Tyr Gln Arg Leu Glu Ser Lys
350                 355                 360                 365

tgt tcc atg ggg ttc cat gct ggc tgg gag cag ccg cac tgg ttc tac       1212
Cys Ser Met Gly Phe His Ala Gly Trp Glu Gln Pro His Trp Phe Tyr
                370                 375                 380

aaa cca ggc cag gac act cag tac agg cca agt ttt cgc cac aca aac       1260
Lys Pro Gly Gln Asp Thr Gln Tyr Arg Pro Ser Phe Arg His Thr Asn
            385                 390                 395

tgg ttt gag cct gtg ggc tcg gag tat aaa cag gtt atg caa aga gta       1308
Trp Phe Glu Pro Val Gly Ser Glu Tyr Lys Gln Val Met Gln Arg Val
        400                 405                 410

ggg gta act gac cta tca cca ttt ggc aag ttt aac atc aaa ggc caa       1356
Gly Val Thr Asp Leu Ser Pro Phe Gly Lys Phe Asn Ile Lys Gly Gln
    415                 420                 425
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gat tcc att aga cta ctg gac cat ctc ttt gca aat gtc att cca aag      1404
Asp Ser Ile Arg Leu Leu Asp His Leu Phe Ala Asn Val Ile Pro Lys
430                 435                 440                 445

gtg ggt ttt aca aat ata agt cac atg tta aca ccc aag ggt cga gtg      1452
Val Gly Phe Thr Asn Ile Ser His Met Leu Thr Pro Lys Gly Arg Val
                450                 455                 460

tat gct gag ctg act gtt tct cac caa tct cct ggg gag ttt ctt tta      1500
Tyr Ala Glu Leu Thr Val Ser His Gln Ser Pro Gly Glu Phe Leu Leu
            465                 470                 475

att act ggc tct gga tca gaa ctt cat gat ctt aga tgg att gaa gaa      1548
Ile Thr Gly Ser Gly Ser Glu Leu His Asp Leu Arg Trp Ile Glu Glu
        480                 485                 490

gaa gca gtc aaa ggt gga tat gat gtt gaa att aaa aac ata act gat      1596
Glu Ala Val Lys Gly Gly Tyr Asp Val Glu Ile Lys Asn Ile Thr Asp
    495                 500                 505

gag ctt gga gtt ctt gga gtt gct ggg cca cag gca aga aag gtc ctt      1644
Glu Leu Gly Val Leu Gly Val Ala Gly Pro Gln Ala Arg Lys Val Leu
510                 515                 520                 525

cag aaa ctg acc cct gaa gat ctt agt gat gat gtt ttc aag ttt ctt      1692
Gln Lys Leu Thr Pro Glu Asp Leu Ser Asp Asp Val Phe Lys Phe Leu
                530                 535                 540

caa acc aag tcc tta aag gtt tcc aac att cct gtc act gct att agg      1740
Gln Thr Lys Ser Leu Lys Val Ser Asn Ile Pro Val Thr Ala Ile Arg
            545                 550                 555

ata tct tat act ggt gag ctg ggt tgg gag ctg tat cac aga aga gaa      1788
Ile Ser Tyr Thr Gly Glu Leu Gly Trp Glu Leu Tyr His Arg Arg Glu
        560                 565                 570

gat tct gtg gcg ctg tat gac gct atc atg aat gca ggc cag gag gag      1836
Asp Ser Val Ala Leu Tyr Asp Ala Ile Met Asn Ala Gly Gln Glu Glu
    575                 580                 585

gga atc gac aat ttt gga acc tat gcc atg aat gcc tta cgc ctg gag      1884
Gly Ile Asp Asn Phe Gly Thr Tyr Ala Met Asn Ala Leu Arg Leu Glu
590                 595                 600                 605

aaa gcc ttc aga gcc tgg ggg tta gag atg aac tgt gat aca aat cct      1932
Lys Ala Phe Arg Ala Trp Gly Leu Glu Met Asn Cys Asp Thr Asn Pro
                610                 615                 620

ttg gaa gct gga ctg gaa tat ttt gtg aag tta aat aag cca gca gac      1980
Leu Glu Ala Gly Leu Glu Tyr Phe Val Lys Leu Asn Lys Pro Ala Asp
            625                 630                 635

ttc ata gga aag caa gca ctg aaa cag att aaa gcc aag ggg ctg aaa      2028
Phe Ile Gly Lys Gln Ala Leu Lys Gln Ile Lys Ala Lys Gly Leu Lys
        640                 645                 650

cga aga ctg gtc tgc ctc acc ttg gca acg gat gat gtt gat cca gag      2076
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Arg Arg Leu Val Cys Leu Thr Leu Ala Thr Asp Asp Val Asp Pro Glu
    655                 660                 665

gga aat gaa agc atc tgg tac aat ggc aag gtg gtt ggc aac acg aca      2124
Gly Asn Glu Ser Ile Trp Tyr Asn Gly Lys Val Val Gly Asn Thr Thr
670                 675                 680                 685

tct gga agc tat agc tac agc atc cag aag agt ctg gct ttc gca tat      2172
Ser Gly Ser Tyr Ser Tyr Ser Ile Gln Lys Ser Leu Ala Phe Ala Tyr
                690                 695                 700

gtc cct gta caa cta agt gaa gtg gga cag caa gtg gaa gtt gaa cta      2220
Val Pro Val Gln Leu Ser Glu Val Gly Gln Gln Val Glu Val Glu Leu
            705                 710                 715

tta ggc aaa aat tac cca gca gtc atc ata caa gaa cct ttg gta ttg      2268
Leu Gly Lys Asn Tyr Pro Ala Val Ile Ile Gln Glu Pro Leu Val Leu
        720                 725                 730

acc gaa cca acc aga aac cgg ctt cag aaa aaa ggt gga aag gac aaa      2316
Thr Glu Pro Thr Arg Asn Arg Leu Gln Lys Lys Gly Gly Lys Asp Lys
    735                 740                 745

act tga aaaaagacct tcagcagtca actgaattag agttgctaat gactgtcctt       2372
Thr  *
750

gaaattatta taactggctc ccaggggaat agaggaaacc aggaattcat ttcaaaatca   2432

tcaaagtcta aatttagaat cttaatgaaa cctttctgtt aagtgttttc taagcaagac   2492

agaataatag ataaatgatt tacattgttc ttttaaatga agaaatttga aatgaatgtt   2552

tttttattta ccccacatta cccaatcagt aaaacattta ggtgtttgct aatatacaca   2612

atcattacta taacctaatt aagggacatt ttataatttt agtaacaaat gcattcggtt   2672

cttgacagct gaaaacaaat taataaatta tcttttacat aaaaacatgt acaatattgt   2732

ttatggattt acttctttga gaaatctttc cttagatgaa taaatgaaag ttttaatttt   2792

tcatgatata tctgtgatga aaatagtaaa acttaacatt gacatataaa aaaaaaaaa    2851


    <210> 25
    <211> 2426
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (630)..(2360)

    <400> 25
tttcgtgcgg gggtgggctc tgcgcgtaat ggcagcgccg tggcctcgcg tccatctttg     60
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ccgttctctc ggacctgtca caaaggagtc gcgccgccgc cgccgccccc tccctccggt      120

gggcccggga ggtagagaaa gtcagtgcca cagcccgacc gcgctgctct gagccctggg      180

cacgcggaac gggagggagt ctgagggttg gggacgtctg tgagggaggg gaacagccgc      240

tcgagcctgg ggcgggcgga ccggactggg gccggggtag gctctggaaa gggcccggga      300

gagaggtggc gttggtcaga acctgagaaa cagccgagag gttttccacc gaggcccgcg      360

cttgagggat ctgaagaggt tcctagaaga gggtgttccc tctttcgggg gtcctcacca      420

gaagaggttc ttgggggtcg cccttctgag gaggctgcgg ctaacagggc ccagaactgc      480

cattggatgt ccagaatccc ctgtagttga taatgttggg aataagctct gcaactttct      540

ttggcattca gttgttaaaa acaaatagga tgcaaattcc tcaactccag gttatgaaaa      600

cagtacttgg aaaactgaaa actacctaa  atg atc gtc ttt ggt tgg gcc gtg       653
                                 Met Ile Val Phe Gly Trp Ala Val
                                   1               5

ttc tta gcg agc aga agc ctt ggc cag ggt ctg ttg ttg act ctc gaa        701
Phe Leu Ala Ser Arg Ser Leu Gly Gln Gly Leu Leu Leu Thr Leu Glu
     10                  15                  20

gag cac ata gcc cac ttc cta ggg act gga ggt gcc gct act acc atg        749
Glu His Ile Ala His Phe Leu Gly Thr Gly Gly Ala Ala Thr Thr Met
 25                  30                  35                  40

ggt aat tcc tgt atc tgc cga gat gac agt gga aca gat gac agt gtt        797
Gly Asn Ser Cys Ile Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val
                 45                  50                  55

gac acc caa cag caa cag gcc gag aac agt gca gta ccc act gct gac        845
Asp Thr Gln Gln Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp
             60                  65                  70

aca agg agc caa cca cgg gac cct gtt cgg cca cca agg agg ggc cga        893
Thr Arg Ser Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg
         75                  80                  85

gga cct cat gag cca agg aga aag aaa caa aat gtg gat ggg cta gtg        941
Gly Pro His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val
     90                  95                 100

ttg gac aca ctg gca gta ata cgg act ctt gta gat aat gat cag gaa        989
Leu Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Asn Asp Gln Glu
105                 110                 115                 120

cct ccc tat tca atg ata aca tta cac gaa atg gca gaa aca gat gaa       1037
Pro Pro Tyr Ser Met Ile Thr Leu His Glu Met Ala Glu Thr Asp Glu
                125                 130                 135

gga tgg ttg gat gtt gtc cag tct tta att aga gtt att cca ctg gaa       1085
Gly Trp Leu Asp Val Val Gln Ser Leu Ile Arg Val Ile Pro Leu Glu
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            140                 145                 150

gat cca ctg gga cca gct gtt ata aca ttg tta cta gat gaa tgt cca      1133
Asp Pro Leu Gly Pro Ala Val Ile Thr Leu Leu Leu Asp Glu Cys Pro
        155                 160                 165

ttg ccc act aaa gat gca ctc cag aaa ttg act gaa att ctc aat tta      1181
Leu Pro Thr Lys Asp Ala Leu Gln Lys Leu Thr Glu Ile Leu Asn Leu
    170                 175                 180

aat gga gaa gta gct tgc cag gac tca agc cat cct gcc aaa cac agg      1229
Asn Gly Glu Val Ala Cys Gln Asp Ser Ser His Pro Ala Lys His Arg
185                 190                 195                 200

aac aca tct gca gtc cta ggc tgc ttg gcc gag aaa cta gca ggt cct      1277
Asn Thr Ser Ala Val Leu Gly Cys Leu Ala Glu Lys Leu Ala Gly Pro
                205                 210                 215

gca agt ata ggt tta ctt agc cca gga ata ctg gaa tac ttg cta cag      1325
Ala Ser Ile Gly Leu Leu Ser Pro Gly Ile Leu Glu Tyr Leu Leu Gln
            220                 225                 230

tgt ctg aag tta cag tcc cac ccc aca gtc atg ctt ttt gca ctt atc      1373
Cys Leu Lys Leu Gln Ser His Pro Thr Val Met Leu Phe Ala Leu Ile
        235                 240                 245

gca ctg gaa aag ttt gca cag aca agt gaa aat aaa ttg act att tct      1421
Ala Leu Glu Lys Phe Ala Gln Thr Ser Glu Asn Lys Leu Thr Ile Ser
    250                 255                 260

gaa tcc agt att agt gac cgg ctt gtc aca ttg gag tcc tgg gct aat      1469
Glu Ser Ser Ile Ser Asp Arg Leu Val Thr Leu Glu Ser Trp Ala Asn
265                 270                 275                 280

gat cct gat tat ctg aaa cgt caa gtt ggt ttc tgt gcc cag tgg agc      1517
Asp Pro Asp Tyr Leu Lys Arg Gln Val Gly Phe Cys Ala Gln Trp Ser
                285                 290                 295

tta gac aat ctc ttt tta aaa gaa ggt aga cag ctg acc tat gag aaa      1565
Leu Asp Asn Leu Phe Leu Lys Glu Gly Arg Gln Leu Thr Tyr Glu Lys
            300                 305                 310

gtg aac ttg agt agc att agg gcc atg ctg aat agc aat gat gtc agc      1613
Val Asn Leu Ser Ser Ile Arg Ala Met Leu Asn Ser Asn Asp Val Ser
        315                 320                 325

gag tac ctg aag atc tca cct cat ggc tta gag gct cgc tgt gat gcc      1661
Glu Tyr Leu Lys Ile Ser Pro His Gly Leu Glu Ala Arg Cys Asp Ala
    330                 335                 340

tcc tct ttt gaa agt gtg cgt tgc acc ttt tgt gtg gat gcc ggg gta      1709
Ser Ser Phe Glu Ser Val Arg Cys Thr Phe Cys Val Asp Ala Gly Val
345                 350                 355                 360

tgg tac tat gaa gta aca gtg gtc act tct ggc gtc atg cag att ggc      1757
Trp Tyr Tyr Glu Val Thr Val Val Thr Ser Gly Val Met Gln Ile Gly
                365                 370                 375
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tgg gcc act cga gac agc aaa ttc ctc aat cat gaa ggc tac ggc att      1805
Trp Ala Thr Arg Asp Ser Lys Phe Leu Asn His Glu Gly Tyr Gly Ile
            380                 385                 390

ggg gat gat gaa tac tcc tgt gcg tat gat ggc tgc cgg cag ctg att      1853
Gly Asp Asp Glu Tyr Ser Cys Ala Tyr Asp Gly Cys Arg Gln Leu Ile
        395                 400                 405

tgg tac aat gcc aga agt aag cct cac ata cac cca tgc tgg aaa gaa      1901
Trp Tyr Asn Ala Arg Ser Lys Pro His Ile His Pro Cys Trp Lys Glu
    410                 415                 420

gga gat aca gta gga ttt ctg tta gac ttg aat gaa aag caa atg atc      1949
Gly Asp Thr Val Gly Phe Leu Leu Asp Leu Asn Glu Lys Gln Met Ile
425                 430                 435                 440

ttc ttt tta aat ggc aac cag ctg cct cct gaa aag caa gtc ttt tca      1997
Phe Phe Leu Asn Gly Asn Gln Leu Pro Pro Glu Lys Gln Val Phe Ser
                445                 450                 455

tct act gta tct gga ttt ttt gct gca gct agt ttc atg tca tat caa      2045
Ser Thr Val Ser Gly Phe Phe Ala Ala Ala Ser Phe Met Ser Tyr Gln
            460                 465                 470

caa tgt gag ttc aat ttt gga gca aaa cca ttc aaa tac cca cca tct      2093
Gln Cys Glu Phe Asn Phe Gly Ala Lys Pro Phe Lys Tyr Pro Pro Ser
        475                 480                 485

atg aaa ttt agc act ttt aat gac tac gcc ttc cta aca gct gaa gaa      2141
Met Lys Phe Ser Thr Phe Asn Asp Tyr Ala Phe Leu Thr Ala Glu Glu
    490                 495                 500

aaa atc att ttg cca agg cac agg cgt ctt gct ctg ttg aag caa gtc      2189
Lys Ile Ile Leu Pro Arg His Arg Arg Leu Ala Leu Leu Lys Gln Val
505                 510                 515                 520

agt atc cga gaa aac tgc tgt tcc ctt tgt tgt gat gag gta gca gac      2237
Ser Ile Arg Glu Asn Cys Cys Ser Leu Cys Cys Asp Glu Val Ala Asp
                525                 530                 535

aca caa ttg aag cca tgt gga cac agt gac ctg tgc atg gat tgt gcc      2285
Thr Gln Leu Lys Pro Cys Gly His Ser Asp Leu Cys Met Asp Cys Ala
            540                 545                 550

ttg cag ctg gag acc tgc cca ttg tgt cgt aaa gaa ata gta tct aga      2333
Leu Gln Leu Glu Thr Cys Pro Leu Cys Arg Lys Glu Ile Val Ser Arg
        555                 560                 565

atc aga cag att tct cat att tca tga cacat gtgaagaggc atcgtggact      2385
Ile Arg Gln Ile Ser His Ile Ser  *
    570                 575

tttttctact caattccagc caatgttgaa aaaaaaaaaa a                        2426
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<210> 26
<211> 564
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (14)..(475)

<400> 26
ttttgaaccc tag   atg gcg tcc tat ttc gat gaa cac gac tgc gag ccg        49
                 Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu Pro
                  1               5                  10

tcg gac cct gag cag gag acg cga acc aac atg ctg ctg gag ctc gca         97
Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu Ala
        15                  20                  25

agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta gta        145
Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val
    30                  35                  40

gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt gag        193
Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu
45                  50                  55                  60

aac ctc ccc agg aca gtc atc aga ggc tct cag gct gag ctc aag tgc        241
Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys
                65                  70                  75

ccc gtg tgt ctt ttg gaa ttt gag gag gag gag act gcc att gag atg        289
Pro Val Cys Leu Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met
            80                  85                  90

cct tgc cat cac ctt ttc cat tcc agc tgc att ctg ccc tgg cta agc        337
Pro Cys His His Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser
        95                  100                 105

aag aca aat tcc tgt ccc ttg tgc cgc cat gag ctg ccc act gat gac        385
Lys Thr Asn Ser Cys Pro Leu Cys Arg His Glu Leu Pro Thr Asp Asp
    110                 115                 120

gac act tat gag gag cac aga cga gat aag gct cga aaa cag cag cag        433
Asp Thr Tyr Glu Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln
125                 130                 135                 140

caa cac cga ctg gag aac ctc cat gga gcc atg tac acg tga ggaggtt        482
Gln His Arg Leu Glu Asn Leu His Gly Ala Met Tyr Thr  *
                145                 150

ggggctgagt gctggccctc tgcgtcttcc ttattaacct tgaatcctca ttaaaggttt      542

ctttacccac aaaaaaaaaa aa                                               564
```

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<210> 27
<211> 609
<212> DNA
<213> Homo sapiens

<220>
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<222> (18)..(581)

<400> 27
gcagaaggct ggcagcc  atg gcg tcc tat ttc gat gaa cac gac tgc gag       50
                    Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu
                     1               5                  10

ccg tcg gac cct gag cag gag acg cga acc aac atg ctg ctg gag ctc       98
Pro Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu
            15                  20                  25

gca agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta      146
Ala Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val
        30                  35                  40

gta gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt      194
Val Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val
    45                  50                  55

gag aac ctc ccc agg aca gtc atc aga ggc tct cag gct gct ctc acc      242
Glu Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Ala Leu Thr
60                  65                  70                  75

gtg ccc tgg gcc cag tac tca agc ttc ttt ctg ttc atg gac tgc tgg      290
Val Pro Trp Ala Gln Tyr Ser Ser Phe Phe Leu Phe Met Asp Cys Trp
                80                  85                  90

ggg atg gaa gaa gag tgg cag ttg gga gca ggg gag ggt ggt tat cag      338
Gly Met Glu Glu Glu Trp Gln Leu Gly Ala Gly Glu Gly Gly Tyr Gln
            95                  100                 105

ctt atg aag atc aga cca agg cta gaa cac tac tct act ttt ctc aga      386
Leu Met Lys Ile Arg Pro Arg Leu Glu His Tyr Ser Thr Phe Leu Arg
        110                 115                 120

caa att cct gtc cct tgt gcc gct atg agc tgc cca ctg atg acg aca      434
Gln Ile Pro Val Pro Cys Ala Ala Met Ser Cys Pro Leu Met Thr Thr
    125                 130                 135

ctt atg agg agc aca gac gag ata agg ctc gaa aac agc agc agc aac      482
Leu Met Arg Ser Thr Asp Glu Ile Arg Leu Glu Asn Ser Ser Ser Asn
140                 145                 150                 155

acc gac tgg aga acc tcc atg gag cca tgt aca cgt gag gag gtt ggg      530
Thr Asp Trp Arg Thr Ser Met Glu Pro Cys Thr Arg Glu Glu Val Gly
                160                 165                 170

gct gag tgc tgg ccc tct gcg tct tcc tta tta acc ttg aat cct cat      578
Ala Glu Cys Trp Pro Ser Ala Ser Ser Leu Leu Thr Leu Asn Pro His
```

```
            175                 180                 185

taa aggtttcttt acccacaaaa aaaaaaaa                                    609
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     <210> 28
     <211> 1291
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (26)..(1057)

     <400> 28
tgctggaatt ccccggcgcc gcgcc  atg tgg gct gcg gcg ggc ggg ctg tgg       52
                             Met Trp Ala Ala Ala Gly Gly Leu Trp
                              1               5

cgc tcc cgc gcg ggt ctc cgg gcc ctg ttc cgt agc cgc gat gct gcg       100
Arg Ser Arg Ala Gly Leu Arg Ala Leu Phe Arg Ser Arg Asp Ala Ala
 10                  15                  20                  25

cta ttt cca ggc tgc gag cgg gga ctt cac tgc tct gct gtc tcc tgc       148
Leu Phe Pro Gly Cys Glu Arg Gly Leu His Cys Ser Ala Val Ser Cys
                 30                  35                  40

aag aac tgg ctc aag aaa ttt gcc tcg aaa acc aaa aaa aag gtt tgg       196
Lys Asn Trp Leu Lys Lys Phe Ala Ser Lys Thr Lys Lys Lys Val Trp
             45                  50                  55

tat gaa agt cct tcc ttg ggt tct cac tcg act tac aaa cca tcc aag       244
Tyr Glu Ser Pro Ser Leu Gly Ser His Ser Thr Tyr Lys Pro Ser Lys
         60                  65                  70

ttg gaa ttc ctc atg agg agc acc tca aag aaa acc agg aag gaa gac       292
Leu Glu Phe Leu Met Arg Ser Thr Ser Lys Lys Thr Arg Lys Glu Asp
     75                  80                  85

cat gcg cgc ctg agg gcc ctg aac ggc ctc ctc tat aag gca ctg aca       340
His Ala Arg Leu Arg Ala Leu Asn Gly Leu Leu Tyr Lys Ala Leu Thr
 90                  95                  100                 105

gac ctg ctg tgt acc cct gaa gtg agt cag gag ctg tat gac ctt aac       388
Asp Leu Leu Cys Thr Pro Glu Val Ser Gln Glu Leu Tyr Asp Leu Asn
                110                 115                 120

gtg gag ctc tcc aag gtt tcc ctg act cca gac ttc tca gcc tgc cga       436
Val Glu Leu Ser Lys Val Ser Leu Thr Pro Asp Phe Ser Ala Cys Arg
            125                 130                 135

gcg tac tgg aag aca acg ctc tct gct gag cag aac gca cac atg gag       484
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Ala Tyr Trp Lys Thr Thr Leu Ser Ala Glu Gln Asn Ala His Met Glu
        140                 145                 150

gct gtc ctg cag aga agt gcc gcg cac atg agg cac ctt ttg atg tcc       532
Ala Val Leu Gln Arg Ser Ala Ala His Met Arg His Leu Leu Met Ser
    155                 160                 165

cag cag acc ctg agg aat gtg cca ccg ata gtg ttt gtt caa gac aag       580
Gln Gln Thr Leu Arg Asn Val Pro Pro Ile Val Phe Val Gln Asp Lys
170                 175                 180                 185

gga aat gca gct cta gct gag ctt gat cag tta ctg gca gtc gca gac       628
Gly Asn Ala Ala Leu Ala Glu Leu Asp Gln Leu Leu Ala Val Ala Asp
                190                 195                 200

ttt gga ccc cgg gat gaa aga gac aac ttt gta caa aat gat ttc agg       676
Phe Gly Pro Arg Asp Glu Arg Asp Asn Phe Val Gln Asn Asp Phe Arg
            205                 210                 215

gac cct gat gcc cca caa ccc tgc ggc acc aca gag ccg acc aca agc       724
Asp Pro Asp Ala Pro Gln Pro Cys Gly Thr Thr Glu Pro Thr Thr Ser
        220                 225                 230

tcc agt ctg tgt ggg atc gat cat gag gcg ctc cac aag cag att atg       772
Ser Ser Leu Cys Gly Ile Asp His Glu Ala Leu His Lys Gln Ile Met
    235                 240                 245

gag tac aaa agg agg aaa gat aaa ggg ctc ggg ggc ctg gtg tgg cag       820
Glu Tyr Lys Arg Arg Lys Asp Lys Gly Leu Gly Gly Leu Val Trp Gln
250                 255                 260                 265

ggg cag gtg gct gag ctg aca acg cag atg aaa aag gga agg aag agg       868
Gly Gln Val Ala Glu Leu Thr Thr Gln Met Lys Lys Gly Arg Lys Arg
                270                 275                 280

gcc aag ccc cgc ctg gag cag gac agc tcc ctc aag agt tac ctg tca       916
Ala Lys Pro Arg Leu Glu Gln Asp Ser Ser Leu Lys Ser Tyr Leu Ser
            285                 290                 295

ggc gag gag gtt gaa gat gac ctg gac ctg gtt ggt gcc ccg gag tac       964
Gly Glu Glu Val Glu Asp Asp Leu Asp Leu Val Gly Ala Pro Glu Tyr
        300                 305                 310

gaa tgc tat gcc ccg gac aca gag gag ttg gag gca gag aga gga ggt      1012
Glu Cys Tyr Ala Pro Asp Thr Glu Glu Leu Glu Ala Glu Arg Gly Gly
    315                 320                 325

ggc aga aca gag gat ggc cac agc tgc gga gca agc agg gag tag atg      1060
Gly Arg Thr Glu Asp Gly His Ser Cys Gly Ala Ser Arg Glu  *
330                 335                 340

gagaggctct gcccatccca catttgcagg gaaaagcatt ggcacgcaac gcagcatgtg   1120

gcttcattga ggcagttgat ggagttaaac catctgctct tctgctactt caacattttc   1180

tagcttttcc gtgtatctaa acacaatttg ctacacaagt cactgttttt ttttccatgc   1240
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                                                 Met Ser Glu Lys
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gag aac aac ttc ccg cca ctg ccc aag ttc atc cct gtg aag ccc tgc       162
Glu Asn Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro Val Lys Pro Cys
  5                  10                  15                  20

ttc tac cag aac ttc tcc gac gag atc cca gtg gag cac cag gtc ctg       210
Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu His Gln Val Leu
                 25                  30                  35

gtg aag agg atc tac cgg ctg tgg atg ttt tac tgc gcc acc ctc ggc       258
Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly
             40                  45                  50

gtc aac ctc att gcc tgc ctg gcc tgg tgg atc ggc gga ggc tcg ggg       306
Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly
         55                  60                  65

acc aac ttc ggc ctg gcc ttc gtg tgg ctg ctc ctg ttc acg cct tgc       354
Thr Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Leu Phe Thr Pro Cys
     70                  75                  80

ggc tac gtg tgc tgg ttc cgg cct gtc tac aag gcc ttc cga gcc gac       402
Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp
 85                  90                  95                 100

agc tcc ttt aat ttc atg gcg ttt ttc ttc atc ttc gga gcc cag ttt       450
Ser Ser Phe Asn Phe Met Ala Phe Phe Phe Ile Phe Gly Ala Gln Phe
                105                 110                 115

gtc ctg acc gtc atc cag gcg att ggc ttc tcc ggc tgg ggc gcg tgc       498
Val Leu Thr Val Ile Gln Ala Ile Gly Phe Ser Gly Trp Gly Ala Cys
            120                 125                 130

ggc tgg ctg tcg gca att gga ttc ttc cag tac agc ccg ggc gct gcc       546
Gly Trp Leu Ser Ala Ile Gly Phe Phe Gln Tyr Ser Pro Gly Ala Ala
        135                 140                 145
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gtg gtc atg ctg ctt cca gcc atc atg ttc tcc gtg tcg gct gcc atg       594
Val Val Met Leu Leu Pro Ala Ile Met Phe Ser Val Ser Ala Ala Met
    150                 155                 160

atg gcc atc gcg atc atg aag gtg cac agg atc tac cga ggg ggc tgg       642
Met Ala Ile Ala Ile Met Lys Val His Arg Ile Tyr Arg Gly Gly Trp
165                 170                 175                 180

cgg aag ctt cca gaa ggc cag acg gag tgg cac acg ggc ctt ggc gga       690
Arg Lys Leu Pro Glu Gly Gln Thr Glu Trp His Thr Gly Leu Gly Gly
                185                 190                 195

acc ccc cgc gac ggg ggc ccc gtc aac atc ttt cgg cga agc ttg ccc       738
Thr Pro Arg Asp Gly Gly Pro Val Asn Ile Phe Arg Arg Ser Leu Pro
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agt acc ccc ttg tgc ccg taa ccggcgg                                   766
Ser Thr Pro Leu Cys Pro  *
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gaggtacggc ctgtggtc  atg gcg ctg ttc cca gcc ttt gcg ggg ctt agt      171
                     Met Ala Leu Phe Pro Ala Phe Ala Gly Leu Ser
                       1               5                  10

gag gct ccc gat ggc ggg agc tcc agg aaa gag tta gac tgg ctg agc       219
Glu Ala Pro Asp Gly Gly Ser Ser Arg Lys Glu Leu Asp Trp Leu Ser
             15                  20                  25

aac cca agc ttt tgt gtt gga tcc ata acg tcc ctg agc caa caa act       267
Asn Pro Ser Phe Cys Val Gly Ser Ile Thr Ser Leu Ser Gln Gln Thr
         30                  35                  40

gaa gca gct cca gcc cat gtt tct gaa ggg tta ccg ctg aca agg agt       315
Glu Ala Ala Pro Ala His Val Ser Glu Gly Leu Pro Leu Thr Arg Ser
     45                  50                  55

cat ctg aaa tca gag tct tca gat gaa agt gac act aac aaa aag ctc       363
His Leu Lys Ser Glu Ser Ser Asp Glu Ser Asp Thr Asn Lys Lys Leu
 60                  65                  70                  75
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aaa caa aca agt aga aaa aag aag aaa gag aaa aag aaa aaa agg aag        411
Lys Gln Thr Ser Arg Lys Lys Lys Lys Glu Lys Lys Lys Lys Arg Lys
                 80                  85                  90

cat cag cat cat aag aaa aca aag agg aag cat ggg ccg tcg agt agc        459
His Gln His His Lys Lys Thr Lys Arg Lys His Gly Pro Ser Ser Ser
             95                 100                 105

agc agg tct gag aca gac acc gat tct gaa aag gac aaa cct tcc aga        507
Ser Arg Ser Glu Thr Asp Thr Asp Ser Glu Lys Asp Lys Pro Ser Arg
        110                 115                 120

ggc gtt gga ggc agt aaa aag gaa tct gag gaa ccg aat caa gga aat        555
Gly Val Gly Gly Ser Lys Lys Glu Ser Glu Glu Pro Asn Gln Gly Asn
    125                 130                 135

aat gct gca gct gat act gga cat cgc ttt gtt tgg ctt gag gac att        603
Asn Ala Ala Ala Asp Thr Gly His Arg Phe Val Trp Leu Glu Asp Ile
140                 145                 150                 155

cag gct gtg acg gga gaa acc ttc aga aca gat aag aaa cca gat cct        651
Gln Ala Val Thr Gly Glu Thr Phe Arg Thr Asp Lys Lys Pro Asp Pro
                160                 165                 170

gcg aac tgg gag tac aag tct ctc tac cga ggg gat ata gca aga tac        699
Ala Asn Trp Glu Tyr Lys Ser Leu Tyr Arg Gly Asp Ile Ala Arg Tyr
            175                 180                 185

aag agg aaa gga gac tcc tgc ctt ggc att aac cct aag aag cag tgc        747
Lys Arg Lys Gly Asp Ser Cys Leu Gly Ile Asn Pro Lys Lys Gln Cys
        190                 195                 200

ata tct tgg gaa ggg act tcc aca gag aag aag cat tca cgc aag cag        795
Ile Ser Trp Glu Gly Thr Ser Thr Glu Lys Lys His Ser Arg Lys Gln
    205                 210                 215

gtt gaa cgc tat ttt act aag aag agt gtg gga tta atg aac atc gat        843
Val Glu Arg Tyr Phe Thr Lys Lys Ser Val Gly Leu Met Asn Ile Asp
220                 225                 230                 235

gga gtt gcc att agc agt aaa act gaa cct ccc tca tct gag ccc atc        891
Gly Val Ala Ile Ser Ser Lys Thr Glu Pro Pro Ser Ser Glu Pro Ile
                240                 245                 250

tcc ttt ata cca gtg aag gac ttg gaa gat gcg gct cct gtt aca acc        939
Ser Phe Ile Pro Val Lys Asp Leu Glu Asp Ala Ala Pro Val Thr Thr
            255                 260                 265

tgg ttg aat cct ctg ggg att tat gat cag tca acc aca cat tgg cta        987
Trp Leu Asn Pro Leu Gly Ile Tyr Asp Gln Ser Thr Thr His Trp Leu
        270                 275                 280

caa gga cag ggt cct cca gag cag gaa tca aag cag cca gac gca cag       1035
Gln Gly Gln Gly Pro Pro Glu Gln Glu Ser Lys Gln Pro Asp Ala Gln
    285                 290                 295
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cca gac agc gag agt gcg gct ctc aag gcc aag gtg gag gag ttt aac      1083
Pro Asp Ser Glu Ser Ala Ala Leu Lys Ala Lys Val Glu Glu Phe Asn
300                 305                 310                 315

agg agg gtg cgg gag aat cct cgg gat acg cag ctg tgg atg gca ttt      1131
Arg Arg Val Arg Glu Asn Pro Arg Asp Thr Gln Leu Trp Met Ala Phe
                320                 325                 330

gtt gct ttt cag gac gag gtc atg aaa agt cct ggc ctg tat gcc atc      1179
Val Ala Phe Gln Asp Glu Val Met Lys Ser Pro Gly Leu Tyr Ala Ile
            335                 340                 345

gag gaa gga gag cag gaa aag cga aag agg tcc ctg aag ctc att ctg      1227
Glu Glu Gly Glu Gln Glu Lys Arg Lys Arg Ser Leu Lys Leu Ile Leu
        350                 355                 360

gag aag aag ctg gcc att ctg gag cgg gcc att gag agc aac cag agc      1275
Glu Lys Lys Leu Ala Ile Leu Glu Arg Ala Ile Glu Ser Asn Gln Ser
    365                 370                 375

agt gtg gat ctg aaa ctg gcc aag ctg aag ctc tgc aca gag ttc tgg      1323
Ser Val Asp Leu Lys Leu Ala Lys Leu Lys Leu Cys Thr Glu Phe Trp
380                 385                 390                 395

gag ccc tcc act ctg gtc aaa gag tgg cag aaa ctg ata ttt ttg cat      1371
Glu Pro Ser Thr Leu Val Lys Glu Trp Gln Lys Leu Ile Phe Leu His
                400                 405                 410

ccc aat aat aca gcc ctt tgg cag aaa tac ctt tta ttt tgc cag agc      1419
Pro Asn Asn Thr Ala Leu Trp Gln Lys Tyr Leu Leu Phe Cys Gln Ser
            415                 420                 425

cag ttt agt acc ttt tcg ata tca aaa att cac agt ctt tat gga aaa      1467
Gln Phe Ser Thr Phe Ser Ile Ser Lys Ile His Ser Leu Tyr Gly Lys
        430                 435                 440

tgc ttg agc act ttg tct gct gtt aag gac ggc agc atc tta tct cac      1515
Cys Leu Ser Thr Leu Ser Ala Val Lys Asp Gly Ser Ile Leu Ser His
    445                 450                 455

cct gcg ttg cct ggc acg gaa gag gcc atg ttt gca ctc ttt ctt cag      1563
Pro Ala Leu Pro Gly Thr Glu Glu Ala Met Phe Ala Leu Phe Leu Gln
460                 465                 470                 475

cag tgc cac ttt ctg cgg cag gct ggc cac tct gag aag gcc atc tca      1611
Gln Cys His Phe Leu Arg Gln Ala Gly His Ser Glu Lys Ala Ile Ser
                480                 485                 490

ttg ttc cag gcc atg gtg gac ttc acc ttc ttc aaa ccc gac agc gta      1659
Leu Phe Gln Ala Met Val Asp Phe Thr Phe Phe Lys Pro Asp Ser Val
            495                 500                 505

aaa gat ctg cct acc aaa gga cag gtg gaa ttc ttt gaa ccc ttt tgg      1707
Lys Asp Leu Pro Thr Lys Gly Gln Val Glu Phe Phe Glu Pro Phe Trp
        510                 515                 520

gac agt gga gag ccc cgg gct ggg gag aag gga gcc cga ggc tgg aag      1755
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Asp Ser Gly Glu Pro Arg Ala Gly Glu Lys Gly Ala Arg Gly Trp Lys
    525                 530                 535

gcg tgg atg cac cag cag gaa cga ggt ggc tgg gtg gtc atc aac cca      1803
Ala Trp Met His Gln Gln Glu Arg Gly Gly Trp Val Val Ile Asn Pro
540                 545                 550                 555

gat gag gat gac gat gaa cca gaa gag gat gac cag gaa ata aaa gat      1851
Asp Glu Asp Asp Asp Glu Pro Glu Glu Asp Asp Gln Glu Ile Lys Asp
                560                 565                 570

aag act ctg ccc agg tgg cag atc tgg ctt gct gct gag cgt tcc cgt      1899
Lys Thr Leu Pro Arg Trp Gln Ile Trp Leu Ala Ala Glu Arg Ser Arg
            575                 580                 585

gac cag agg cac tgg cgg ccc tgg cgc cct gat aag acc aag aag caa      1947
Asp Gln Arg His Trp Arg Pro Trp Arg Pro Asp Lys Thr Lys Lys Gln
        590                 595                 600

acc gag gaa gac tgt gag gat ccc gag aga cag ggg gtg ttt gat gat      1995
Thr Glu Glu Asp Cys Glu Asp Pro Glu Arg Gln Gly Val Phe Asp Asp
    605                 610                 615

att ggg caa tct ttg atc aga ctt tcc agc cat gat ctt cag ttc cag      2043
Ile Gly Gln Ser Leu Ile Arg Leu Ser Ser His Asp Leu Gln Phe Gln
620                 625                 630                 635

ctg gtg gag gcc ttc ctg cag ttc ttg ggt gtg cct tct ggc ttt act      2091
Leu Val Glu Ala Phe Leu Gln Phe Leu Gly Val Pro Ser Gly Phe Thr
                640                 645                 650

cct cca gcc tcc tgt ctt tat ctg gcc atg gat gag aac agc atc ttt      2139
Pro Pro Ala Ser Cys Leu Tyr Leu Ala Met Asp Glu Asn Ser Ile Phe
            655                 660                 665

gat aat gga ctt tat gat gaa aag ccc ttg act ttt ttc aac cct ttg      2187
Asp Asn Gly Leu Tyr Asp Glu Lys Pro Leu Thr Phe Phe Asn Pro Leu
        670                 675                 680

ttt tct ggg gct agc tgt gtt ggc cgc atg gat agg ttg ggc tat cct      2235
Phe Ser Gly Ala Ser Cys Val Gly Arg Met Asp Arg Leu Gly Tyr Pro
    685                 690                 695

cgc tgg acc agg ggt cag aac cga gag ggc gag gag ttc atc cgc aat      2283
Arg Trp Thr Arg Gly Gln Asn Arg Glu Gly Glu Glu Phe Ile Arg Asn
700                 705                 710                 715

gtc ttc cac ctt gtc atg cct tta ttt tca ggc aaa gag aag tcc cag      2331
Val Phe His Leu Val Met Pro Leu Phe Ser Gly Lys Glu Lys Ser Gln
                720                 725                 730

ctc tgc ttc tcc tgg tta cag tat gag att gca aag gtc att tgg tgc      2379
Leu Cys Phe Ser Trp Leu Gln Tyr Glu Ile Ala Lys Val Ile Trp Cys
            735                 740                 745

ctg cac act aaa aac aag aag aga tta aag tct caa ggg aag aac tgc      2427
Leu His Thr Lys Asn Lys Lys Arg Leu Lys Ser Gln Gly Lys Asn Cys
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        750                 755                 760

aaa aaa cta gcc aag aat ctc ctt aag gag cca gaa aac tgc aac aac     2475
Lys Lys Leu Ala Lys Asn Leu Leu Lys Glu Pro Glu Asn Cys Asn Asn
    765                 770                 775

ttt tgc ctg tgg aag cag tat gca cat ctg gag tgg ttg ctt ggc aac     2523
Phe Cys Leu Trp Lys Gln Tyr Ala His Leu Glu Trp Leu Leu Gly Asn
780                 785                 790                 795

acg gag gat gcc aga aaa gtt ttt gac aca gca ctt ggc atg gca gga     2571
Thr Glu Asp Ala Arg Lys Val Phe Asp Thr Ala Leu Gly Met Ala Gly
                800                 805                 810

agc aga gaa ctg aaa gac tct gac ctc tgt gag ctc agt ctg ctc tat     2619
Ser Arg Glu Leu Lys Asp Ser Asp Leu Cys Glu Leu Ser Leu Leu Tyr
            815                 820                 825

gct gag ctg gag gtg gag ctg tcg cca gaa gtg aga agg gct gcc aca     2667
Ala Glu Leu Glu Val Glu Leu Ser Pro Glu Val Arg Arg Ala Ala Thr
        830                 835                 840

gct cga gct gtt cac ata tta acc aag ctg act gag agc agc ccc tat     2715
Ala Arg Ala Val His Ile Leu Thr Lys Leu Thr Glu Ser Ser Pro Tyr
    845                 850                 855

ggg ccc tac act gga cag gtg ttg gct gtt cac att ttg aaa gcg cga     2763
Gly Pro Tyr Thr Gly Gln Val Leu Ala Val His Ile Leu Lys Ala Arg
860                 865                 870                 875

aag gct tat gag cac gca ctg cag gac tgt ttg ggt gac agc tgt gtc     2811
Lys Ala Tyr Glu His Ala Leu Gln Asp Cys Leu Gly Asp Ser Cys Val
                880                 885                 890

tcc aat cca gct ccc acc gat tcc tgt agc cgc cta att agc ctg gct     2859
Ser Asn Pro Ala Pro Thr Asp Ser Cys Ser Arg Leu Ile Ser Leu Ala
            895                 900                 905

aaa tgc ttc atg ctc ttc cag tat ttg acc ata ggg att gat gct gct     2907
Lys Cys Phe Met Leu Phe Gln Tyr Leu Thr Ile Gly Ile Asp Ala Ala
        910                 915                 920

gtg cag ata tac gaa cag gtg ttt gca aaa ctg aac agt tct gtt ttc     2955
Val Gln Ile Tyr Glu Gln Val Phe Ala Lys Leu Asn Ser Ser Val Phe
    925                 930                 935

cca gaa ggc tct ggc gag ggg gac agt gcc agc tcc cag agt tgg acc     3003
Pro Glu Gly Ser Gly Glu Gly Asp Ser Ala Ser Ser Gln Ser Trp Thr
940                 945                 950                 955

agt gtt ctc gaa gcc atc aca ctg atg cac acg agc ctg ctg aga ttc     3051
Ser Val Leu Glu Ala Ile Thr Leu Met His Thr Ser Leu Leu Arg Phe
                960                 965                 970

cac atg aaa gtg agt gtt tac ccg ctg gcc cct ctg cga gag gca ctc     3099
His Met Lys Val Ser Val Tyr Pro Leu Ala Pro Leu Arg Glu Ala Leu
            975                 980                 985
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 tca cag gct tta aag ttg tat cca ggc aac cag gtt ctt tgg agg tcc      3147
 Ser Gln Ala Leu Lys Leu Tyr Pro Gly Asn Gln Val Leu Trp Arg Ser
         990                 995                1000

 tat gta cag att cag aat aag tcc cac agt gcc agc aaa acc agg aga      3195
 Tyr Val Gln Ile Gln Asn Lys Ser His Ser Ala Ser Lys Thr Arg Arg
    1005                1010                1015

 ttt ttt gac aca atc acc agg tct gcc aaa ccc ttg gag cct tgg ttg      3243
 Phe Phe Asp Thr Ile Thr Arg Ser Ala Lys Pro Leu Glu Pro Trp Leu
1020                1025                1030                1035

 ttt gca att gaa gct gag aaa ctg agg aag aga ctg gtg gaa act gtc      3291
 Phe Ala Ile Glu Ala Glu Lys Leu Arg Lys Arg Leu Val Glu Thr Val
                1040                1045                1050

 cag agg tta gac ggt aga gag atc cac gcc aca att cct gag acc ggc      3339
 Gln Arg Leu Asp Gly Arg Glu Ile His Ala Thr Ile Pro Glu Thr Gly
            1055                1060                1065

 tta atg cat cgg atc caa gcc ctg ttt gaa aat gcc atg cgc agc gac      3387
 Leu Met His Arg Ile Gln Ala Leu Phe Glu Asn Ala Met Arg Ser Asp
        1070                1075                1080

 agt ggc agc cag tgc ccc ttg ctg tgg agg atg tat ttg aac ttt ctg      3435
 Ser Gly Ser Gln Cys Pro Leu Leu Trp Arg Met Tyr Leu Asn Phe Leu
    1085                1090                1095

 gtt tcc tta gga aat aaa gaa aga agc aaa ggt gta ttc tac aaa gca      3483
 Val Ser Leu Gly Asn Lys Glu Arg Ser Lys Gly Val Phe Tyr Lys Ala
1100                1105                1110                1115

 ctt cag aat tgc cct tgg gca aag gtg ttg tac ctg gac gcc gtg gag      3531
 Leu Gln Asn Cys Pro Trp Ala Lys Val Leu Tyr Leu Asp Ala Val Glu
                1120                1125                1130

 tat ttc ccc gat gag atg cag gag atc ctg gac ctg atg act gag aag      3579
 Tyr Phe Pro Asp Glu Met Gln Glu Ile Leu Asp Leu Met Thr Glu Lys
            1135                1140                1145

 gag ctc cgg gtg cgc ctg ccg ctg gag gag ctg gag ctg ctg ctg gag      3627
 Glu Leu Arg Val Arg Leu Pro Leu Glu Glu Leu Glu Leu Leu Leu Glu
        1150                1155                1160

 gat tag agagcagtgg gaaaacgggc tgtgcctgcg aggccaagtt gcccaccctg       3683
 Asp  *
    1165

 cggagctagg aggcgcgagc agagaacgtg tgtgttagga gaactcggct tttgaaatgt    3743

 tctttctcga tagtaataat gtgggctgcc agcctctcac atcttgcaca ctttttgggt    3803

 gtgtaaatga cacaaaagtt atttacatat tatatatgtg aatatgtgta tatatgtaca    3863

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                 1               5                  10

gcc gcg gcg gcg aat ctg aat gcg gtg cgg gag acc atg gac gtt ctg       97
Ala Ala Ala Ala Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu
         15                  20                  25

ctt gag att tca aga att ttg aat act ggc tta gat atg gaa act ctg      145
Leu Glu Ile Ser Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu
     30                  35                  40

tct att tgt gta cgg ctt tgt gaa caa gga att aac cca gaa gct tta      193
Ser Ile Cys Val Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu
 45                  50                  55                  60

tca tcg gtt att aag gag ctt cgc aag gct act gaa gca ctg aag gct      241
Ser Ser Val Ile Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala
                65                  70                  75

gct gaa aat atg aca agc tga ct ttctggagaa attctgatga gatatgtcaa      294
Ala Glu Asn Met Thr Ser  *
            80

gctctgcaag agggttagaa gattgcattg tagttgagaa tgtacaatga aattactgca    354

tgcagcagtg tagaaaaatt ttacttttta aaagaattat aaaaccatag ctttataaat    414

cagtggaaag tggcttacag agagaactat cagatgtgtt tacatcacat cttattcact    474

ttttttaaca gctctaatgc tttggcattg ctatgttcat atttatgtat tccttattta    534

tagctctgat agctttaatt ttctaagcag tctgtctatc agatgtgcac atctgctgtg    594

ccaggttgaa gtatagtgga acccatcagt agtaatgtgt agtagttatg acttgttgac    654

atttccatta taaactttaa ttttgaattg tttatgcatt ataactgtgg atttatattg    714

tattgggctg aaagttgaca ggatttcagc caccacttgt gaatttttat ttagattcat    774

tatgtatatc agaatcttgt tttttgaaat aagagcatgg aaaacatttc ttgtaatcta    834

ctcttgaaca aagaatattt agtttttcaa acagtttgtt gggcagctaa tagtgtgaac    894
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caggtcattt ttgtattgag taaaaaaatc aaactttgag aaacttggat tttaaaagta    954

atgacaatgc ttaggttagt attatttgta atttgaatca tttacatcta atgagaatgt   1014

tagttgagaa tgttttctta aagttttata tcctataaat aacggaataa aaaaatttgt   1074

aaaatgaaac aacaaaaaaa aaaaa                                         1099



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acacgaggct gtggagcggc gtgactcaaa cgtggcgcgc atcagctcgc acacttccaa    120

acctcgcgat agctactggc cctgggcgag ccgttgggat tgcgcttgcg cacagcgtgt    180

cttctggatc gccataccta ccctgtggtc ctcatcttcc tggcctcata gctcctcctc    240

tccaagc  atg tct tcc ccg ttg caa aga gct gtg gga gat acc aag agg    289
         Met Ser Ser Pro Leu Gln Arg Ala Val Gly Asp Thr Lys Arg
           1               5                  10

gcc ttt tct gca tct tct agt tcc tct gcc agt cta ccc ttt gat gac    337
Ala Phe Ser Ala Ser Ser Ser Ser Ser Ala Ser Leu Pro Phe Asp Asp
 15                  20                  25                  30

agg gac tca aac cat acc tca gag ggg aat ggc gac tct ttg tta gct    385
Arg Asp Ser Asn His Thr Ser Glu Gly Asn Gly Asp Ser Leu Leu Ala
                 35                  40                  45

gat gaa gac act gac ttt gaa gac agc ttg aat cgc aat gtg aag aag    433
Asp Glu Asp Thr Asp Phe Glu Asp Ser Leu Asn Arg Asn Val Lys Lys
             50                  55                  60

aga gca gca aaa cga cca ccg aaa aca aca ccg gtg gca aaa cat cca    481
Arg Ala Ala Lys Arg Pro Pro Lys Thr Thr Pro Val Ala Lys His Pro
         65                  70                  75

aag aaa ggg tcc cga gtg gta cat cgt cat agc cgg aaa cag tca gag    529
Lys Lys Gly Ser Arg Val Val His Arg His Ser Arg Lys Gln Ser Glu
     80                  85                  90

cca cca gcc aat gat ctt ttc aat gct gtg aaa gcc gcc aaa agt gac    577
Pro Pro Ala Asn Asp Leu Phe Asn Ala Val Lys Ala Ala Lys Ser Asp
 95                 100                 105                 110
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atg cag tct ttg gta gat gag tgg ctg gat agc tac aag caa gac cag       625
Met Gln Ser Leu Val Asp Glu Trp Leu Asp Ser Tyr Lys Gln Asp Gln
                115                 120                 125

gat gca gga ttt ctg gag ctt gtt aac ttt ttc atc caa tct tgc gga       673
Asp Ala Gly Phe Leu Glu Leu Val Asn Phe Phe Ile Gln Ser Cys Gly
            130                 135                 140

tgt aaa ggc att gtg acc cct gag atg ttc aag aag atg tcc aac tca       721
Cys Lys Gly Ile Val Thr Pro Glu Met Phe Lys Lys Met Ser Asn Ser
        145                 150                 155

gag atc atc cag cac cta aca gag cag ttt aat gag gac tcg ggg gac       769
Glu Ile Ile Gln His Leu Thr Glu Gln Phe Asn Glu Asp Ser Gly Asp
    160                 165                 170

tac cct ctc ata gct cca ggt cca tcc tgg aag aag ttc cag ggc agc       817
Tyr Pro Leu Ile Ala Pro Gly Pro Ser Trp Lys Lys Phe Gln Gly Ser
175                 180                 185                 190

ttc tgt gaa ttt gtg agg aca ttg gtc tgt cag tgc cag tac agc ctc       865
Phe Cys Glu Phe Val Arg Thr Leu Val Cys Gln Cys Gln Tyr Ser Leu
                195                 200                 205

ctc tat gat ggc ttc cct atg gac gac ctc atc tcc ctg ctc act ggc       913
Leu Tyr Asp Gly Phe Pro Met Asp Asp Leu Ile Ser Leu Leu Thr Gly
            210                 215                 220

ctc tca gac tca caa gtc cgc gcc ttc cgt cac act agc acc ctg gct       961
Leu Ser Asp Ser Gln Val Arg Ala Phe Arg His Thr Ser Thr Leu Ala
        225                 230                 235

gct atg aaa ctg atg acc tcc ctg gta aaa gtt gcc ctc caa ctg agt      1009
Ala Met Lys Leu Met Thr Ser Leu Val Lys Val Ala Leu Gln Leu Ser
    240                 245                 250

gtg cac caa gat aac aat cag cgt cag tat gag gct gaa aga aac aag      1057
Val His Gln Asp Asn Asn Gln Arg Gln Tyr Glu Ala Glu Arg Asn Lys
255                 260                 265                 270

ggg cca ggg cag agg gca cct gag cgg ctg gag agc ctg ttg gag aaa      1105
Gly Pro Gly Gln Arg Ala Pro Glu Arg Leu Glu Ser Leu Leu Glu Lys
                275                 280                 285

cgc aaa gag ctc caa gag cat caa gag gag att gag ggg atg atg aat      1153
Arg Lys Glu Leu Gln Glu His Gln Glu Glu Ile Glu Gly Met Met Asn
            290                 295                 300

gcc ctc ttc agg ggt gtc ttt gtt cat cgg tac agg gat gtc ctt cct      1201
Ala Leu Phe Arg Gly Val Phe Val His Arg Tyr Arg Asp Val Leu Pro
        305                 310                 315

gag atc cgt gct atc tgc att gag gaa att ggg tgt tgg atg caa agc      1249
Glu Ile Arg Ala Ile Cys Ile Glu Glu Ile Gly Cys Trp Met Gln Ser
    320                 325                 330

tac agc acg tct ttc ctc acc gac agc tat tta aaa tat att ggt tgg      1297
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Tyr Ser Thr Ser Phe Leu Thr Asp Ser Tyr Leu Lys Tyr Ile Gly Trp
335                 340                 345                 350

act ctg cat gat aag cac cga gaa gtc cgc gtg aag tgc gtg aag gct      1345
Thr Leu His Asp Lys His Arg Glu Val Arg Val Lys Cys Val Lys Ala
                355                 360                 365

ctg aaa ggg ctg tac ggt aac cgg gac ctg acc gca cgc ctg gag ctc      1393
Leu Lys Gly Leu Tyr Gly Asn Arg Asp Leu Thr Ala Arg Leu Glu Leu
            370                 375                 380

ttc acc agc cgc ttc aag gac cgg atg gtt tcc atg atc atg gac aga      1441
Phe Thr Ser Arg Phe Lys Asp Arg Met Val Ser Met Ile Met Asp Arg
        385                 390                 395

gag tac agt gtg gca gtg gag gcc gtc aga tta ctg ata ctt ata ctt      1489
Glu Tyr Ser Val Ala Val Glu Ala Val Arg Leu Leu Ile Leu Ile Leu
    400                 405                 410

aag aac atg gaa ggg ttg ctg acg gac gcg gat tgt gag agc gtc tac      1537
Lys Asn Met Glu Gly Leu Leu Thr Asp Ala Asp Cys Glu Ser Val Tyr
415                 420                 425                 430

ccc gtt gtg tat cct tct aat cga ggc ctg gct tct gcc gca ggc gaa      1585
Pro Val Val Tyr Pro Ser Asn Arg Gly Leu Ala Ser Ala Ala Gly Glu
                435                 440                 445

ttt ctg tac tgg aaa ctt ttc tac cct gag tgc gag ata aga acg atg      1633
Phe Leu Tyr Trp Lys Leu Phe Tyr Pro Glu Cys Glu Ile Arg Thr Met
            450                 455                 460

ggt gga aga gag caa cgc cag agc cca ggc gcc cag agg act ttc ttc      1681
Gly Gly Arg Glu Gln Arg Gln Ser Pro Gly Ala Gln Arg Thr Phe Phe
        465                 470                 475

cag ctt ctg ctg tcc ttc ttt gtg gag agc gag ctc cat gac cac gct      1729
Gln Leu Leu Leu Ser Phe Phe Val Glu Ser Glu Leu His Asp His Ala
    480                 485                 490

gct tac tta gta gac agt ctg tgg gac tgt gca ggg gct cgg ctg aag      1777
Ala Tyr Leu Val Asp Ser Leu Trp Asp Cys Ala Gly Ala Arg Leu Lys
495                 500                 505                 510

gac tgg gag ggt ctg aca agc ctg ctg ctg gag aag gac cag aac ctg      1825
Asp Trp Glu Gly Leu Thr Ser Leu Leu Leu Glu Lys Asp Gln Asn Leu
                515                 520                 525

ggt gat gtg cag gag agc aca ctg ata gaa atc ctt gtg tcc agt gcc      1873
Gly Asp Val Gln Glu Ser Thr Leu Ile Glu Ile Leu Val Ser Ser Ala
            530                 535                 540

cgg caa gct tca gag ggg cac ccg cct gtg ggc cgg gtc act ggg agg      1921
Arg Gln Ala Ser Glu Gly His Pro Pro Val Gly Arg Val Thr Gly Arg
        545                 550                 555

aag ggc tta acc tct aag gag cgc aag acc caa gcc gat gac agg gtg      1969
Lys Gly Leu Thr Ser Lys Glu Arg Lys Thr Gln Ala Asp Asp Arg Val
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    560                 565                 570

aag ttg act gag cac ctc atc ccc ctg ctg ccc cag ctc ctg gcc aag      2017
Lys Leu Thr Glu His Leu Ile Pro Leu Leu Pro Gln Leu Leu Ala Lys
575                 580                 585                 590

ttc tca gct gat gca gag aag gtc act ccc ctg ctc cag ctt ctc agc      2065
Phe Ser Ala Asp Ala Glu Lys Val Thr Pro Leu Leu Gln Leu Leu Ser
                595                 600                 605

tgc ttt gac ctc cac atc tac tgc act ggg cgc ttg gag aag cac ctg      2113
Cys Phe Asp Leu His Ile Tyr Cys Thr Gly Arg Leu Glu Lys His Leu
            610                 615                 620

gag ctg ttc ctg cag caa ctc cag gag gtg gtg gtg aag cat gca gag      2161
Glu Leu Phe Leu Gln Gln Leu Gln Glu Val Val Val Lys His Ala Glu
        625                 630                 635

cca gcg gtg ctt gag gct ggg gcg cat gcc ctc tac ctg ctc tgt aat      2209
Pro Ala Val Leu Glu Ala Gly Ala His Ala Leu Tyr Leu Leu Cys Asn
    640                 645                 650

ccc gaa ttc act ttc ttc agc cgg gcg gac ttt gcc cgc agc cag cta      2257
Pro Glu Phe Thr Phe Phe Ser Arg Ala Asp Phe Ala Arg Ser Gln Leu
655                 660                 665                 670

gta gat ttg ctg act gac cgc ttc cag cag gag ctt gaa gag ctg tta      2305
Val Asp Leu Leu Thr Asp Arg Phe Gln Gln Glu Leu Glu Glu Leu Leu
                675                 680                 685

cag tcg tcc ttc cta gat gag gat gag gta tat aat ctg gca gcc act      2353
Gln Ser Ser Phe Leu Asp Glu Asp Glu Val Tyr Asn Leu Ala Ala Thr
            690                 695                 700

ctg aaa cgc ctc tct gcc ttc tac aac act cat gac ctg act cgc tgg      2401
Leu Lys Arg Leu Ser Ala Phe Tyr Asn Thr His Asp Leu Thr Arg Trp
        705                 710                 715

gag ctc tat gag cca tgt tgc caa ctc ctg cag aag gct gtg gac aca      2449
Glu Leu Tyr Glu Pro Cys Cys Gln Leu Leu Gln Lys Ala Val Asp Thr
    720                 725                 730

gga gag gtt cct cac cag gtt atc ctg cca gcc ttg act ctt gtc tat      2497
Gly Glu Val Pro His Gln Val Ile Leu Pro Ala Leu Thr Leu Val Tyr
735                 740                 745                 750

ttt tcc att ctc tgg aca cta acc cac att tct aaa tca gat gct tcc      2545
Phe Ser Ile Leu Trp Thr Leu Thr His Ile Ser Lys Ser Asp Ala Ser
                755                 760                 765

cag aag cag ctg tcg agt ttg agg gac aga atg gtg gcc ttc tgt gaa      2593
Gln Lys Gln Leu Ser Ser Leu Arg Asp Arg Met Val Ala Phe Cys Glu
            770                 775                 780

ctc tgc cag agt tgc ctc tca gat gtg gat act gag atc cag gag cag      2641
Leu Cys Gln Ser Cys Leu Ser Asp Val Asp Thr Glu Ile Gln Glu Gln
        785                 790                 795
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gct ttt gtc tta tta agt gat cta ctt ctc atc ttt agc cct cag atg      2689
Ala Phe Val Leu Leu Ser Asp Leu Leu Leu Ile Phe Ser Pro Gln Met
    800                 805                 810

att gtt ggg ggc cgt gat ttc ctt agg cca ctt gtc ttt ttt cct gaa      2737
Ile Val Gly Gly Arg Asp Phe Leu Arg Pro Leu Val Phe Phe Pro Glu
815                 820                 825                 830

gct act ctc cag tct gag cta gcc agc ttc ctc atg gac cac gtc ttc      2785
Ala Thr Leu Gln Ser Glu Leu Ala Ser Phe Leu Met Asp His Val Phe
                835                 840                 845

atc cag ccg gga gac ctg ggc agt ggt gat tcc cag gag gat cat tta      2833
Ile Gln Pro Gly Asp Leu Gly Ser Gly Asp Ser Gln Glu Asp His Leu
            850                 855                 860

cag ata gag cgg cta cac cag cgg cgc cgc ctc cta gcc ggg ttc tgc      2881
Gln Ile Glu Arg Leu His Gln Arg Arg Arg Leu Leu Ala Gly Phe Cys
        865                 870                 875

aag ctg ttg ctt tat ggg gtg ctg gag atg gat gca gcc tca gat gtt      2929
Lys Leu Leu Leu Tyr Gly Val Leu Glu Met Asp Ala Ala Ser Asp Val
    880                 885                 890

ttc aaa cac tac aac aag ttc tac aat gac tat ggt gac att atc aag      2977
Phe Lys His Tyr Asn Lys Phe Tyr Asn Asp Tyr Gly Asp Ile Ile Lys
895                 900                 905                 910

gaa aca tta act aga gca agg cag att gac cga agt cat tgt tcc cga      3025
Glu Thr Leu Thr Arg Ala Arg Gln Ile Asp Arg Ser His Cys Ser Arg
                915                 920                 925

atc ctg ctg ctg agc ctc aag cag ctg tac aca gaa ctg ctg cag gag      3073
Ile Leu Leu Leu Ser Leu Lys Gln Leu Tyr Thr Glu Leu Leu Gln Glu
            930                 935                 940

cat ggg ccc cag ggc ctg aat gag ctt cct gcc ttc atc gag atg agg      3121
His Gly Pro Gln Gly Leu Asn Glu Leu Pro Ala Phe Ile Glu Met Arg
        945                 950                 955

gac ctg gcc cgg agg ttt gcc ttg agt ttt gga ccc cag cag ctg cag      3169
Asp Leu Ala Arg Arg Phe Ala Leu Ser Phe Gly Pro Gln Gln Leu Gln
    960                 965                 970

aac cgt gac ctc gtg gtc atg cta cac aag gaa ggc atc cag ttc tcc      3217
Asn Arg Asp Leu Val Val Met Leu His Lys Glu Gly Ile Gln Phe Ser
975                 980                 985                 990

ttg tct gag ctt cct cca gct ggc tcc tcc aat cag cct cca aat ctg      3265
Leu Ser Glu Leu Pro Pro Ala Gly Ser Ser Asn Gln Pro Pro Asn Leu
                995                1000                1005

gca ttc ctg gag ctc ctt tca gag ttt tcc ccc cga ctc ttc cat cag      3313
Ala Phe Leu Glu Leu Leu Ser Glu Phe Ser Pro Arg Leu Phe His Gln
           1010                1015                1020
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gac aag cag ctt tta ctg tcc tat cta gaa aag tgc ctg cag cat gtc      3361
Asp Lys Gln Leu Leu Leu Ser Tyr Leu Glu Lys Cys Leu Gln His Val
        1025                1030                1035

tcc cag gca cct ggc cat ccc tgg ggc cca gtc acc acc tac tgc cac      3409
Ser Gln Ala Pro Gly His Pro Trp Gly Pro Val Thr Thr Tyr Cys His
    1040                1045                1050

tcc ctc agc cct gtg gag aac aca gca gag acc agc cct cag gtc ctc      3457
Ser Leu Ser Pro Val Glu Asn Thr Ala Glu Thr Ser Pro Gln Val Leu
1055                1060                1065                1070

ccc agc tcc aag agg agg cgc gtt gaa ggg cct gcc aag cct aac aga      3505
Pro Ser Ser Lys Arg Arg Arg Val Glu Gly Pro Ala Lys Pro Asn Arg
                1075                1080                1085

gag gac gtc tcc tcg tcc cag gaa gaa agt ctg cag ctg aac agc atc      3553
Glu Asp Val Ser Ser Ser Gln Glu Glu Ser Leu Gln Leu Asn Ser Ile
            1090                1095                1100

ccg ccc acg ccc acc ctc acc tcc aca gct gtg aag agc agg cag ccc      3601
Pro Pro Thr Pro Thr Leu Thr Ser Thr Ala Val Lys Ser Arg Gln Pro
        1105                1110                1115

ctg tgg ggg ttg aaa gag atg gag gaa gaa gat ggc tca gag ttg gat      3649
Leu Trp Gly Leu Lys Glu Met Glu Glu Glu Asp Gly Ser Glu Leu Asp
    1120                1125                1130

ttt gcc cag ggc agt cag ccc gtc gca ggc acc gag agg tca agg ttc      3697
Phe Ala Gln Gly Ser Gln Pro Val Ala Gly Thr Glu Arg Ser Arg Phe
1135                1140                1145                1150

ttg ggt cca caa tat ttc cag act cca cac aac cct tca ggt cct ggc      3745
Leu Gly Pro Gln Tyr Phe Gln Thr Pro His Asn Pro Ser Gly Pro Gly
                1155                1160                1165

ctg ggc aac cag ctg atg cga ctc agc ctt atg gaa gag gac gag gaa      3793
Leu Gly Asn Gln Leu Met Arg Leu Ser Leu Met Glu Glu Asp Glu Glu
            1170                1175                1180

gaa gag tta gaa atc cag gat gag tca aat gaa gaa cgg cag gat aca      3841
Glu Glu Leu Glu Ile Gln Asp Glu Ser Asn Glu Glu Arg Gln Asp Thr
        1185                1190                1195

gac atg caa gca agt agc tac tct tcc acc agt gag cgc ggg ctg gac      3889
Asp Met Gln Ala Ser Ser Tyr Ser Ser Thr Ser Glu Arg Gly Leu Asp
    1200                1205                1210

ctc tta gat tct aca gag ctg gat att gag gat ttc tga caggactctg       3938
Leu Leu Asp Ser Thr Glu Leu Asp Ile Glu Asp Phe  *
1215                1220                1225

ggcccctccc cagctccact ccctacctca agaatgtgac catttggaaa aggcaaagag    3998

aaaaggagca aaatgaagca ttcccccagg cttcagccct gggctctgag gggaaagagt    4058

tgggcattgt ttttctaacc taacctttcc ctctggggta gagaagccga gagaccctgt    4118
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cctccctaat gcactgtggc ccagtcccct tgcctttttc ctgttctgtt tggagtggag   4178

aagggcagca cctctgtgtt taatggaaat agcccatagt ctcctggatt tttggaacat   4238

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aaaaaaaaaa a                                                        4309



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                                 Met Ala Gly Gly His Ser Leu Leu
                                   1               5

ctg gag aac gcg cag cat gtg gcg ttg gtg tgc gcc cgc ggc gag cgc      100
Leu Glu Asn Ala Gln His Val Ala Leu Val Cys Ala Arg Gly Glu Arg
     10                  15                  20

ttc ctg gcg cgg gat gcg ctg cgc agc ctg gcg gtg ctg gaa ggc gcc      148
Phe Leu Ala Arg Asp Ala Leu Arg Ser Leu Ala Val Leu Glu Gly Ala
 25                  30                  35                  40

agc ctg gtg gtg ggc aaa gat gga ttt ata aaa gct att ggt cct gct      196
Ser Leu Val Val Gly Lys Asp Gly Phe Ile Lys Ala Ile Gly Pro Ala
                 45                  50                  55

gat gtt att caa aga cag ttt tct gga gaa act ttt gaa gaa tta att      244
Asp Val Ile Gln Arg Gln Phe Ser Gly Glu Thr Phe Glu Glu Leu Ile
             60                  65                  70

gac tgc tct ggg aaa tgt atc cta cca ggt ttg gtg gat gca cac aca      292
Asp Cys Ser Gly Lys Cys Ile Leu Pro Gly Leu Val Asp Ala His Thr
         75                  80                  85

cat cca gta tgg gct ggt gaa aga gtt cac gaa ttt gca atg aag ttg      340
His Pro Val Trp Ala Gly Glu Arg Val His Glu Phe Ala Met Lys Leu
     90                  95                 100

gca gga gcc acc tac atg gaa att cac cag gcc gga gga ggg atc cac      388
Ala Gly Ala Thr Tyr Met Glu Ile His Gln Ala Gly Gly Gly Ile His
105                 110                 115                 120

ttt acc gtg gag cgc acg cgc caa gcc aca gag gag gag ctg ttc cgc      436
Phe Thr Val Glu Arg Thr Arg Gln Ala Thr Glu Glu Glu Leu Phe Arg
                125                 130                 135
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tcc ttg cag caa cgg ctc cag tgc atg atg agg gct ggc acc acg ctg       484
Ser Leu Gln Gln Arg Leu Gln Cys Met Met Arg Ala Gly Thr Thr Leu
            140                 145                 150

gtg gag tgc aag agt gga tat ggc ctc gac ctg gag acc gag ctc aag       532
Val Glu Cys Lys Ser Gly Tyr Gly Leu Asp Leu Glu Thr Glu Leu Lys
        155                 160                 165

atg ctg cgc gtg att gag cgc gcc cgg cgg gag ctg gac atc ggc atc       580
Met Leu Arg Val Ile Glu Arg Ala Arg Arg Glu Leu Asp Ile Gly Ile
    170                 175                 180

tcg gct acc tac tgc ggg gct cat tca gtg cct aaa gga aaa act gct       628
Ser Ala Thr Tyr Cys Gly Ala His Ser Val Pro Lys Gly Lys Thr Ala
185                 190                 195                 200

act gaa gct gct gat gac atc atc aat aac cac ctc cca aag ctg aag       676
Thr Glu Ala Ala Asp Asp Ile Ile Asn Asn His Leu Pro Lys Leu Lys
                205                 210                 215

gaa ctt ggc aga aat ggg gaa ata cac gtg gac aat ata gac gta ttt       724
Glu Leu Gly Arg Asn Gly Glu Ile His Val Asp Asn Ile Asp Val Phe
            220                 225                 230

tgt gag aaa ggt gtc ttt gat ctc gat tcc acc aga agg att ctt caa       772
Cys Glu Lys Gly Val Phe Asp Leu Asp Ser Thr Arg Arg Ile Leu Gln
        235                 240                 245

cgt gga aaa gat ata ggg tta cag att aac ttc cat ggg gat gaa ctc       820
Arg Gly Lys Asp Ile Gly Leu Gln Ile Asn Phe His Gly Asp Glu Leu
    250                 255                 260

cac ccg atg aag gct gct gag ctt ggg gct gaa ctg gga gcg cag gca       868
His Pro Met Lys Ala Ala Glu Leu Gly Ala Glu Leu Gly Ala Gln Ala
265                 270                 275                 280

atc agc cac ctg gaa gaa gtg agt gat gaa ggc atc gtt gcc atg gca       916
Ile Ser His Leu Glu Glu Val Ser Asp Glu Gly Ile Val Ala Met Ala
                285                 290                 295

acg gcc agg tgc tct gcc atc ctt ctg ccc acc aca gcc tac atg ctg       964
Thr Ala Arg Cys Ser Ala Ile Leu Leu Pro Thr Thr Ala Tyr Met Leu
            300                 305                 310

aga ctg aaa caa cct cga gcc agg aag atg tta gat gaa gga gta ata      1012
Arg Leu Lys Gln Pro Arg Ala Arg Lys Met Leu Asp Glu Gly Val Ile
        315                 320                 325

gtt gct ctg gga agt gat ttc aac ccc aat gca tat tgc ttt tca atg      1060
Val Ala Leu Gly Ser Asp Phe Asn Pro Asn Ala Tyr Cys Phe Ser Met
    330                 335                 340

cca atg gtc atg cat ctg gcc tgt gta aac atg aga atg tcc atg cct      1108
Pro Met Val Met His Leu Ala Cys Val Asn Met Arg Met Ser Met Pro
345                 350                 355                 360
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gag gcc ttg gcc gct gcc acc atc aat gca gct tat gca ctg gga aag     1156
Glu Ala Leu Ala Ala Ala Thr Ile Asn Ala Ala Tyr Ala Leu Gly Lys
                365                 370                 375

tct cac aca cac gga tcg ttg gaa gtt ggc aaa cag gga gat ctc att     1204
Ser His Thr His Gly Ser Leu Glu Val Gly Lys Gln Gly Asp Leu Ile
            380                 385                 390

atc atc aat tca tcc cga tgg gag cat ttg att tac cag ttc gga ggc     1252
Ile Ile Asn Ser Ser Arg Trp Glu His Leu Ile Tyr Gln Phe Gly Gly
        395                 400                 405

cat cat gaa tta att gaa tat gtt ata gct aaa gga aaa ctc atc tat     1300
His His Glu Leu Ile Glu Tyr Val Ile Ala Lys Gly Lys Leu Ile Tyr
    410                 415                 420

aaa aca tga tagattt gaaaagagaa gactttttga ctatatgaaa taagtcaata     1356
Lys Thr  *
425

tagttatatt aaaagttaaa acaccttaat atttacaaga attatatcac ttaaacctga   1416

atgtacttca atgtcttttt aagtcactca aaaaacccaa gggatagatt tattttcatt   1476

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gttgcagcct taaatattca agtggggaat ctttgccagt ttctccctca ggacaaagtt    180

ggagaatttg ctaaactcag caaaattgaa ctcctcgaag ccactgaaaa gtcaattggt    240

cccccagaa    atg cac aaa tat cac tgt gaa ctc aaa aac tta agg gag      288
             Met His Lys Tyr His Cys Glu Leu Lys Asn Leu Arg Glu
               1               5                  10

aaa gaa aaa cag ctc gag acc tca tgc aaa gag aaa act gag tat cta      336
Lys Glu Lys Gln Leu Glu Thr Ser Cys Lys Glu Lys Thr Glu Tyr Leu
     15                  20                  25
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cag aaa atg gtt cag agg aat gaa aga tat aaa caa gat gtg gag agg      384
Gln Lys Met Val Gln Arg Asn Glu Arg Tyr Lys Gln Asp Val Glu Arg
 30                  35                  40                  45

ttc tat gaa cgg aag cga cat tta gat tta att gag atg ctt gaa gca      432
Phe Tyr Glu Arg Lys Arg His Leu Asp Leu Ile Glu Met Leu Glu Ala
                 50                  55                  60

aaa agg cca tgg gtg gaa tat gaa aat gtt cgt cag gaa tat gaa gaa      480
Lys Arg Pro Trp Val Glu Tyr Glu Asn Val Arg Gln Glu Tyr Glu Glu
             65                  70                  75

gta aaa cta gtt cgt gac cga gtg aag gaa gag gtc aga aaa ctt aaa      528
Val Lys Leu Val Arg Asp Arg Val Lys Glu Glu Val Arg Lys Leu Lys
         80                  85                  90

gaa ggg cag att cct ata aca cgt cga att gaa gaa atg gaa aac gag      576
Glu Gly Gln Ile Pro Ile Thr Arg Arg Ile Glu Glu Met Glu Asn Glu
     95                 100                 105

cgt cac aat ttg gag gct cga atc aaa gaa aag gca aca gat att aag      624
Arg His Asn Leu Glu Ala Arg Ile Lys Glu Lys Ala Thr Asp Ile Lys
110                 115                 120                 125

gag gca tct caa aaa tgc aaa cag aag caa gat gtt ata gaa agg aaa      672
Glu Ala Ser Gln Lys Cys Lys Gln Lys Gln Asp Val Ile Glu Arg Lys
                130                 135                 140

gat aaa cat att gag gaa ctt cag cag gct tta ata gta aag caa aat      720
Asp Lys His Ile Glu Glu Leu Gln Gln Ala Leu Ile Val Lys Gln Asn
            145                 150                 155

gaa gag ctt gac cga cag agg aga ata ggt aat acc cgc aaa atg ata      768
Glu Glu Leu Asp Arg Gln Arg Arg Ile Gly Asn Thr Arg Lys Met Ile
        160                 165                 170

gag gat ttg caa aat gaa cta aag acc acg gaa aac tgc gag aat ctt      816
Glu Asp Leu Gln Asn Glu Leu Lys Thr Thr Glu Asn Cys Glu Asn Leu
    175                 180                 185

cag ccc cag att gat gcc att aca aat gat ctg aga cgg att cag gat      864
Gln Pro Gln Ile Asp Ala Ile Thr Asn Asp Leu Arg Arg Ile Gln Asp
190                 195                 200                 205

gaa aag gca tta tgt gaa ggc gaa ata att gat aag cga aga gag agg      912
Glu Lys Ala Leu Cys Glu Gly Glu Ile Ile Asp Lys Arg Arg Glu Arg
                210                 215                 220

gaa act cta gag aag gag aaa aag agt gtg gac gat cat att gta cgt      960
Glu Thr Leu Glu Lys Glu Lys Lys Ser Val Asp Asp His Ile Val Arg
            225                 230                 235

ttt gac aat ctt atg aat cag aag gaa gat aag cta aga cag aga ttc     1008
Phe Asp Asn Leu Met Asn Gln Lys Glu Asp Lys Leu Arg Gln Arg Phe
        240                 245                 250

cgt gac acg tat gat gct gtt tta tgg cta aga aat aac aga gac aaa     1056
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Arg Asp Thr Tyr Asp Ala Val Leu Trp Leu Arg Asn Asn Arg Asp Lys
    255                 260                 265

ttt aaa caa aga gtc tgt gag ccc ata atg ctc acg atc aat atg aaa      1104
Phe Lys Gln Arg Val Cys Glu Pro Ile Met Leu Thr Ile Asn Met Lys
270                 275                 280                 285

gat aat aaa aat gcc aaa tat att gaa aat cat att cca tca aat gac      1152
Asp Asn Lys Asn Ala Lys Tyr Ile Glu Asn His Ile Pro Ser Asn Asp
                290                 295                 300

tta aga gcc ttt gta ttt gaa agt caa gaa gat atg gag gtt ttc ctc      1200
Leu Arg Ala Phe Val Phe Glu Ser Gln Glu Asp Met Glu Val Phe Leu
            305                 310                 315

aaa gag gtt cgt gac aat aaa aaa tta aga gta aat gct gtt att gct      1248
Lys Glu Val Arg Asp Asn Lys Lys Leu Arg Val Asn Ala Val Ile Ala
        320                 325                 330

ccc aag agt tca tat gca gac aaa gca cct tca aga tct ttg aat gaa      1296
Pro Lys Ser Ser Tyr Ala Asp Lys Ala Pro Ser Arg Ser Leu Asn Glu
    335                 340                 345

ctt aaa caa tac gga ttt ttc tct tat ttg aga gaa tta ttt gat gca      1344
Leu Lys Gln Tyr Gly Phe Phe Ser Tyr Leu Arg Glu Leu Phe Asp Ala
350                 355                 360                 365

cct gat cct gta atg agt tac ctt tgc tgt cag tat cat att cat gaa      1392
Pro Asp Pro Val Met Ser Tyr Leu Cys Cys Gln Tyr His Ile His Glu
                370                 375                 380

gtt cct gta gga act gaa aag acc aga gaa aga att gaa cgg gta ata      1440
Val Pro Val Gly Thr Glu Lys Thr Arg Glu Arg Ile Glu Arg Val Ile
            385                 390                 395

caa gaa acc cga tta aaa cag att tat aca gca gaa gaa aag tat gtg      1488
Gln Glu Thr Arg Leu Lys Gln Ile Tyr Thr Ala Glu Glu Lys Tyr Val
        400                 405                 410

gtg aaa act tct ttt tat tca aac aaa gtt att tct agt aac aca tct      1536
Val Lys Thr Ser Phe Tyr Ser Asn Lys Val Ile Ser Ser Asn Thr Ser
    415                 420                 425

cta aaa gta gcg cag ttt ctc act gtc act gtg gac cta gag cag aga      1584
Leu Lys Val Ala Gln Phe Leu Thr Val Thr Val Asp Leu Glu Gln Arg
430                 435                 440                 445

aga cac tta gaa gaa cag cta aag gaa att cat aga aaa ttg caa gca      1632
Arg His Leu Glu Glu Gln Leu Lys Glu Ile His Arg Lys Leu Gln Ala
                450                 455                 460

gtg gat tca ggg ttg att gcc tta cgt gaa aca agc aaa cat ctg gag      1680
Val Asp Ser Gly Leu Ile Ala Leu Arg Glu Thr Ser Lys His Leu Glu
            465                 470                 475

cac aaa gac aat gaa ctt aga caa aag aag aag gag ctt ctt gag aga      1728
His Lys Asp Asn Glu Leu Arg Gln Lys Lys Lys Glu Leu Leu Glu Arg
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        480                 485                 490

aaa acc aag aaa aga caa ctg gaa caa aaa atc agt tcc aaa cta gga     1776
Lys Thr Lys Lys Arg Gln Leu Glu Gln Lys Ile Ser Ser Lys Leu Gly
    495                 500                 505

agt tta aag ctg atg gaa cag gat act tgc aat ctt gaa gag gaa gag     1824
Ser Leu Lys Leu Met Glu Gln Asp Thr Cys Asn Leu Glu Glu Glu Glu
510                 515                 520                 525

cga aaa gca agt acc aaa atc aaa gaa ata aat gtt caa aaa gcg aaa     1872
Arg Lys Ala Ser Thr Lys Ile Lys Glu Ile Asn Val Gln Lys Ala Lys
                530                 535                 540

ctt gtt acc gaa tta aca aac cta ata aag att tgt act tct ttg cat     1920
Leu Val Thr Glu Leu Thr Asn Leu Ile Lys Ile Cys Thr Ser Leu His
            545                 550                 555

ata caa aaa gta gat tta att ctc caa aat act aca gtg atc tct gag     1968
Ile Gln Lys Val Asp Leu Ile Leu Gln Asn Thr Thr Val Ile Ser Glu
        560                 565                 570

aag aac aaa tta gaa tca gat tat atg gcc gca tct tca caa ctc cgt     2016
Lys Asn Lys Leu Glu Ser Asp Tyr Met Ala Ala Ser Ser Gln Leu Arg
    575                 580                 585

ctt aca gag caa cat ttc att gaa ttg gat gaa aat aga cag aga tta     2064
Leu Thr Glu Gln His Phe Ile Glu Leu Asp Glu Asn Arg Gln Arg Leu
590                 595                 600                 605

ttg cag aaa tgc aag gaa ctt atg aaa aga gct agg caa gta tgt aac     2112
Leu Gln Lys Cys Lys Glu Leu Met Lys Arg Ala Arg Gln Val Cys Asn
                610                 615                 620

ctg ggt gca gag cag act ctt cct caa gaa tac cag aca caa gta ccc     2160
Leu Gly Ala Glu Gln Thr Leu Pro Gln Glu Tyr Gln Thr Gln Val Pro
            625                 630                 635

acc att cca aat gga cac aac tcc tca ctc ccc atg gtt ttc caa gac     2208
Thr Ile Pro Asn Gly His Asn Ser Ser Leu Pro Met Val Phe Gln Asp
        640                 645                 650

ctt cca aac aca ttg gat gaa att gat gct tta tta act gaa gaa aga     2256
Leu Pro Asn Thr Leu Asp Glu Ile Asp Ala Leu Leu Thr Glu Glu Arg
    655                 660                 665

tca aga gct tcc tgc ttc acg gga ctg aat cct aca att gtt cag gaa     2304
Ser Arg Ala Ser Cys Phe Thr Gly Leu Asn Pro Thr Ile Val Gln Glu
670                 675                 680                 685

tat aca aaa aaa aag aaa aaa tag aacagttaac tgaggaacta aagggaaaga    2358
Tyr Thr Lys Lys Lys Lys Lys  *
                690

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                                                Met Pro His Leu
                                                  1

cct ctc gct tct ttt cga cca cca ttt tgg ggg ctg agg cac tca cgg     162
Pro Leu Ala Ser Phe Arg Pro Pro Phe Trp Gly Leu Arg His Ser Arg
 5                   10                  15                  20

ggc ctc ccc agg ttt cac tcc gtt tct aca cag tcg gag ccc cat gga     210
Gly Leu Pro Arg Phe His Ser Val Ser Thr Gln Ser Glu Pro His Gly
                 25                  30                  35

tct ccc atc tcc cgg agg aac cgt gaa gcc aaa cag aag cgc ctg cga     258
Ser Pro Ile Ser Arg Arg Asn Arg Glu Ala Lys Gln Lys Arg Leu Arg
             40                  45                  50

gag aag cag gct act ctg gag gct gag ata gca ggg gag agc aag tca     306
Glu Lys Gln Ala Thr Leu Glu Ala Glu Ile Ala Gly Glu Ser Lys Ser
         55                  60                  65

cct gca gaa tcc att aag gcc tgg agg cct aag gag tta gta ttg tat     354
Pro Ala Glu Ser Ile Lys Ala Trp Arg Pro Lys Glu Leu Val Leu Tyr
     70                  75                  80

gaa atc cct acg aaa ccc ggt gaa aag aaa gat gtc tct ggg ccc ctg     402
Glu Ile Pro Thr Lys Pro Gly Glu Lys Lys Asp Val Ser Gly Pro Leu
 85                  90                  95                 100

cct cct gca tac agc ccc cga tat gtt gag gct gcc tgg tac ccg tgg     450
Pro Pro Ala Tyr Ser Pro Arg Tyr Val Glu Ala Ala Trp Tyr Pro Trp
                105                 110                 115

tgg gta cga gag ggc ttc ttc aaa cca gaa tat cag gcc cgg ctg ccc     498
Trp Val Arg Glu Gly Phe Phe Lys Pro Glu Tyr Gln Ala Arg Leu Pro
            120                 125                 130

caa gct aca ggg gag acc ttt tcc atg tgt atc cca cct ccc aat gtc     546
Gln Ala Thr Gly Glu Thr Phe Ser Met Cys Ile Pro Pro Pro Asn Val
        135                 140                 145

act ggc tcc ctg cac att ggc cac gca ctc acg gtg gcc ata cag gat     594
Thr Gly Ser Leu His Ile Gly His Ala Leu Thr Val Ala Ile Gln Asp
    150                 155                 160

gcc ctc gtg cgc tgg cac cgg atg cgt ggg gat caa gtg ctg tgg gtc     642
Ala Leu Val Arg Trp His Arg Met Arg Gly Asp Gln Val Leu Trp Val
165                 170                 175                 180

cct ggt tca gat cat gca gga att gct aca caa gct gtg gtg gag aaa     690
Pro Gly Ser Asp His Ala Gly Ile Ala Thr Gln Ala Val Val Glu Lys
                185                 190                 195

caa ctg tgg aag gaa cgg gga gtg agg aga cat gag ctg agc cgg gag     738
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Gln Leu Trp Lys Glu Arg Gly Val Arg Arg His Glu Leu Ser Arg Glu
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gcc ttc ctt agg gag gtg tgg cag tgg aag gag gcg aaa ggt gga gag       786
Ala Phe Leu Arg Glu Val Trp Gln Trp Lys Glu Ala Lys Gly Gly Glu
        215                 220                 225

atc tgt gag cag ctg cga gct ctg ggt gcc tcc ctg gac tgg gat cga       834
Ile Cys Glu Gln Leu Arg Ala Leu Gly Ala Ser Leu Asp Trp Asp Arg
    230                 235                 240

gag tgt ttt acc atg gat gtt ggc tcc tca gtg gct gtg act gaa gct       882
Glu Cys Phe Thr Met Asp Val Gly Ser Ser Val Ala Val Thr Glu Ala
245                 250                 255                 260

ttt gtg cgg ctc tac aag gcg ggg ttg ctg tac cgg aac cat cag ctt       930
Phe Val Arg Leu Tyr Lys Ala Gly Leu Leu Tyr Arg Asn His Gln Leu
                265                 270                 275

gtc aac tgg tca tgt gct tta aga tca gcc atc tcg gac att gag gtg       978
Val Asn Trp Ser Cys Ala Leu Arg Ser Ala Ile Ser Asp Ile Glu Val
            280                 285                 290

gag aac cgg ccc ctg cct ggc cac aca cag cct ctt ccc ctc atc aca      1026
Glu Asn Arg Pro Leu Pro Gly His Thr Gln Pro Leu Pro Leu Ile Thr
        295                 300                 305

gac tat gct gtt cag cca cat gtg ggc acg ggg gca gtg aag gtg act      1074
Asp Tyr Ala Val Gln Pro His Val Gly Thr Gly Ala Val Lys Val Thr
    310                 315                 320

cca gct cac agt cct gcc gat gct gag atg ggg gcc cga cat ggc ttg      1122
Pro Ala His Ser Pro Ala Asp Ala Glu Met Gly Ala Arg His Gly Leu
325                 330                 335                 340

agc ccc ttg aat gtc att gcg gag gat ggg acc atg acc tct ctc tgc      1170
Ser Pro Leu Asn Val Ile Ala Glu Asp Gly Thr Met Thr Ser Leu Cys
                345                 350                 355

ggg gac tgg ctg cag ggt ctt cac cgg ttt gtg gcc cgg gaa aag ata      1218
Gly Asp Trp Leu Gln Gly Leu His Arg Phe Val Ala Arg Glu Lys Ile
            360                 365                 370

atg tct gtg ctg agt gaa cgg ggc ctg ttc cgg ggc ctc cag aac cac      1266
Met Ser Val Leu Ser Glu Arg Gly Leu Phe Arg Gly Leu Gln Asn His
        375                 380                 385

ccc atg gta ctg ccc atc tgc agc cgt tct ggg gat gtg ata gaa tac      1314
Pro Met Val Leu Pro Ile Cys Ser Arg Ser Gly Asp Val Ile Glu Tyr
    390                 395                 400

ctg ctg aag aac cag tgg ttt gtc cgc tgc cag gaa atg ggg gcc cga      1362
Leu Leu Lys Asn Gln Trp Phe Val Arg Cys Gln Glu Met Gly Ala Arg
405                 410                 415                 420

gct gcc aag gct gtg gag tcg ggg gcc ctg gag ctc agt ccc tcc ttc      1410
Ala Ala Lys Ala Val Glu Ser Gly Ala Leu Glu Leu Ser Pro Ser Phe
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                425                 430                 435

cac cag aag aac tgg cag cac tgg ttt tcc cat att ggg gac tgg tgt      1458
His Gln Lys Asn Trp Gln His Trp Phe Ser His Ile Gly Asp Trp Cys
            440                 445                 450

gtc tcc cgg cag ctg tgg tgg ggc cat cag att cca gcc tac ctg gtt      1506
Val Ser Arg Gln Leu Trp Trp Gly His Gln Ile Pro Ala Tyr Leu Val
        455                 460                 465

gta gag gac cat gcg cag gga gaa gag gac tgt tgg gtg gtc ggg cgg      1554
Val Glu Asp His Ala Gln Gly Glu Glu Asp Cys Trp Val Val Gly Arg
    470                 475                 480

tca gag gct gag gcc aga gag gta gca gcg gaa ctg aca ggg agg cca      1602
Ser Glu Ala Glu Ala Arg Glu Val Ala Ala Glu Leu Thr Gly Arg Pro
485                 490                 495                 500

ggg gca gag ctg acc ctg gag agg gat cct gat gtc cta gac aca tgg      1650
Gly Ala Glu Leu Thr Leu Glu Arg Asp Pro Asp Val Leu Asp Thr Trp
                505                 510                 515

ttt tct tct gcc ctg ttc ccc ttt tct gcc ctg ggc tgg ccc caa gag      1698
Phe Ser Ser Ala Leu Phe Pro Phe Ser Ala Leu Gly Trp Pro Gln Glu
            520                 525                 530

acc cca gac ctt gct cgt ttc tac ccc ctg tca ctt ttg gaa acg ggc      1746
Thr Pro Asp Leu Ala Arg Phe Tyr Pro Leu Ser Leu Leu Glu Thr Gly
        535                 540                 545

agc gac ctt ctg ctg ttc tgg gtg ggc cgc atg gtc atg ttg ggg acc      1794
Ser Asp Leu Leu Leu Phe Trp Val Gly Arg Met Val Met Leu Gly Thr
    550                 555                 560

cag ctc aca ggg cag ctg ccc ttc agc aag gtg ctt ctt cat ccc atg      1842
Gln Leu Thr Gly Gln Leu Pro Phe Ser Lys Val Leu Leu His Pro Met
565                 570                 575                 580

gtt cgg gac agg cag ggc cgg aag atg agc aag tcc ctg ggg aat gtg      1890
Val Arg Asp Arg Gln Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Val
                585                 590                 595

ctg gac cca aga gac atc atc agt ggg gtg gag atg cag gtg ctg cag      1938
Leu Asp Pro Arg Asp Ile Ile Ser Gly Val Glu Met Gln Val Leu Gln
            600                 605                 610

gaa aag ctg aga agc gga aat ttg gac cct gca gag ctg gcc att gtg      1986
Glu Lys Leu Arg Ser Gly Asn Leu Asp Pro Ala Glu Leu Ala Ile Val
        615                 620                 625

gct gca gca cag aaa aag gac ttt cct cac ggg atc cct gag tgt ggg      2034
Ala Ala Ala Gln Lys Lys Asp Phe Pro His Gly Ile Pro Glu Cys Gly
    630                 635                 640

aca gat gcc ctg aga ttc aca ctc tgc tcc cat gga gtt cag gcg ggc      2082
Thr Asp Ala Leu Arg Phe Thr Leu Cys Ser His Gly Val Gln Ala Gly
645                 650                 655                 660
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gac ttg cac ctg tca gtc tct gag gtc cag agc tgc cga cat ttc tgc        2130
Asp Leu His Leu Ser Val Ser Glu Val Gln Ser Cys Arg His Phe Cys
                665                 670                 675

aac aag atc tgg aat gct ctt cgc ttt atc ctc aat gct tta ggg gag        2178
Asn Lys Ile Trp Asn Ala Leu Arg Phe Ile Leu Asn Ala Leu Gly Glu
            680                 685                 690

aaa ttt gtg cca cag cct gct gag gag ctg tct ccc tcc tcc ccg atg        2226
Lys Phe Val Pro Gln Pro Ala Glu Glu Leu Ser Pro Ser Ser Pro Met
        695                 700                 705

gat gcc tgg atc ctg agc cgc ctt gcc ctg gct gcc cag gag tgt gag        2274
Asp Ala Trp Ile Leu Ser Arg Leu Ala Leu Ala Ala Gln Glu Cys Glu
    710                 715                 720

cgg ggc ttc ctc acc cga gag ctc tcg ctc gtc act cat gcc ctg cac        2322
Arg Gly Phe Leu Thr Arg Glu Leu Ser Leu Val Thr His Ala Leu His
725                 730                 735                 740

cac ttc tgg ctt cac aac ctc tgt gac gtc tac ctg gag gct gtg aag        2370
His Phe Trp Leu His Asn Leu Cys Asp Val Tyr Leu Glu Ala Val Lys
                745                 750                 755

ccc gtg ctg tgg cac tcg ccc cgc ccc ctg ggg ccc cct cag gtc ctg        2418
Pro Val Leu Trp His Ser Pro Arg Pro Leu Gly Pro Pro Gln Val Leu
            760                 765                 770

ttc tcc tgc gct gac ctc ggc ctc cgc ctc ctg gcc cca ctg atg ccc        2466
Phe Ser Cys Ala Asp Leu Gly Leu Arg Leu Leu Ala Pro Leu Met Pro
        775                 780                 785

ttc ctg gct gaa gag ctc tgg cag agg ctg ccc ccc agg cct ggt tgc        2514
Phe Leu Ala Glu Glu Leu Trp Gln Arg Leu Pro Pro Arg Pro Gly Cys
    790                 795                 800

ccc cct gcc ccc agc atc tcg gtt gcc ccc tac ccc agc gcc tgc agc        2562
Pro Pro Ala Pro Ser Ile Ser Val Ala Pro Tyr Pro Ser Ala Cys Ser
805                 810                 815                 820

ttg gag cac tgg cgc cag cca gag ctg gag cgg cgc ttc tcc cgg gtc        2610
Leu Glu His Trp Arg Gln Pro Glu Leu Glu Arg Arg Phe Ser Arg Val
                825                 830                 835

caa gag gtc gtg cag gtg cta agg gct ctc cga gcc acg tac cag ctc        2658
Gln Glu Val Val Gln Val Leu Arg Ala Leu Arg Ala Thr Tyr Gln Leu
            840                 845                 850

acc aaa gcc cgg ccc cga gtg ctg ctg cag agc tca gag cct ggg gac        2706
Thr Lys Ala Arg Pro Arg Val Leu Leu Gln Ser Ser Glu Pro Gly Asp
        855                 860                 865

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Gln Gly Leu Phe Glu Ala Phe Leu Glu Pro Leu Gly Thr Leu Gly Tyr
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tgg gcc cag gct cca ctc agt gac acg gct caa gtc tac atg gag ctg      2850
Trp Ala Gln Ala Pro Leu Ser Asp Thr Ala Gln Val Tyr Met Glu Leu
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cag ggc ctg gtg gac ccg cag atc cag cta cct ctg tta gcc gcc cga      2898
Gln Gly Leu Val Asp Pro Gln Ile Gln Leu Pro Leu Leu Ala Ala Arg
            920                 925                 930

agg tac aag ttg cag aag cag ctt gat agc ctc aca gcc agg acc cca      2946
Arg Tyr Lys Leu Gln Lys Gln Leu Asp Ser Leu Thr Ala Arg Thr Pro
        935                 940                 945

tca gaa ggg gag gca ggg act cag agg caa caa aag ctt tct tcc ctc      2994
Ser Glu Gly Glu Ala Gly Thr Gln Arg Gln Gln Lys Leu Ser Ser Leu
    950                 955                 960

cag ctg gaa ttg tca aaa ctg gac aag gca gcc tct cac ctc cag cag      3042
Gln Leu Glu Leu Ser Lys Leu Asp Lys Ala Ala Ser His Leu Gln Gln
965                 970                 975                 980

ctg atg gat gag cct cca gcc cca ggg agc ccg gag ctc taa ctcatca      3091
Leu Met Asp Glu Pro Pro Ala Pro Gly Ser Pro Glu Leu  *
                985                 990

tccccatcag ttttcctccc tctcagacct gtctttgagg acaaacagat ttgtcagctg    3151

tcagggtgca gtgggacgtc agagactatg tggtccatcg ccttcattgt gtaaatgagg    3211

acacagactg gcttggtcgc agtgactgtg gtgtccttga gatgctcaca ttactgcccg    3271

gcctgcctcc cacctggaag tctgggaatg aggagattga gataaacttt tgaaatccca    3331

aacatgtctg tttatggctc tttggtcccc tttgctccca gtggtgactt ttgtgcttct    3391

gagttgtccc ctgagagctt ggtctgggaa aagaggagga ggggtcctca ctggaggaag    3451

aggaaccttt tagtcatggg taaggggatg gggacagttg gttcccggtt ctacctccct    3511

ttctggactg acaattgccc tggctttttg cagggtcctt tctcccccac tttcactaaa    3571

ttggaagttc cccgctcctt gggtt                                          3596


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      <212> DNA
      <213> Homo sapiens

      <220>
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      <222> (555)..(1406)
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attagttggt agtaattact ctttatccca atattataat aatcctcgct ctacaatcat       120

aacctaggaa aaaccaggcc atacagagat aggagctgag gggacatagt gaggtgtgac       180

cagaagacaa gagtgcgagc cttctgttat gcctggcaac gggcgtcttc ccagatgctg       240

gcgtcaccgc tagaccaagg agccctctgg gcagggcgaa gccagaggaa actctggtgg       300

aggtccgtag cggtcctgac gtgcaaatcg gtcgtccgac ctgggtatag gggcgaaaga       360

ctaatcgaac catctagtag ctggttccct ccgaagtttc cctcaggata gctggcgctc       420

tcgcagaccc gacgcacccc cgccacgcag ttttatccgg taaagcgaat gattagaggt       480

cttggggtaa gaagcccgtc tcgcccgccg cgccggggag gtggagcacg agcgcacgtg       540

ttaggacccg aaag  atg gtg aac tat gcc tgg gca ggg cga agc cag agg        590
                 Met Val Asn Tyr Ala Trp Ala Gly Arg Ser Gln Arg
                  1               5                   10

aaa ctc tgg tgg agg tcc gta gcg gtc ctg acg tgc aaa tcg gtc gtc         638
Lys Leu Trp Trp Arg Ser Val Ala Val Leu Thr Cys Lys Ser Val Val
         15                  20                  25

cga cct ggg tat agg ggc ggg ctc cag gcg agg cgg tcg acg ctc ctg         686
Arg Pro Gly Tyr Arg Gly Gly Leu Gln Ala Arg Arg Ser Thr Leu Leu
     30                  35                  40

aaa act tgc gcg cgc gct cgc gcc act gcg ccc gga gcg atg aag atg         734
Lys Thr Cys Ala Arg Ala Arg Ala Thr Ala Pro Gly Ala Met Lys Met
 45                  50                  55                  60

gtc gcg ccc tgg acg cgg ttc tac tcc aac agc tgc tgc ttg tgc tgc         782
Val Ala Pro Trp Thr Arg Phe Tyr Ser Asn Ser Cys Cys Leu Cys Cys
                 65                  70                  75

cat gtc cgc acc ggc acc atc ctg ctc ggc gtc tgg tat ctg atc atc         830
His Val Arg Thr Gly Thr Ile Leu Leu Gly Val Trp Tyr Leu Ile Ile
             80                  85                  90

aat gct gtg gta ctg ttg att tta ttg agt gcc ctg gct gat ccg gat         878
Asn Ala Val Val Leu Leu Ile Leu Leu Ser Ala Leu Ala Asp Pro Asp
         95                 100                 105

cag tat aac ttt tca agt tct gaa ctg gga ggt gac ttt gag ttc atg         926
Gln Tyr Asn Phe Ser Ser Ser Glu Leu Gly Gly Asp Phe Glu Phe Met
    110                 115                 120

gat gat gcc aac atg tgc att gcc att gcg att tct ctt ctc atg atc         974
Asp Asp Ala Asn Met Cys Ile Ala Ile Ala Ile Ser Leu Leu Met Ile
125                 130                 135                 140

ctg ata tgt gct atg gct act tac gga gcg tac aag caa cgc gca gcc        1022
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Leu Ile Cys Ala Met Ala Thr Tyr Gly Ala Tyr Lys Gln Arg Ala Ala
                145                 150                 155

tgg atc atc cca ttc ttc tgt tac cag atc ttt gac ttt gcc ctg aac      1070
Trp Ile Ile Pro Phe Phe Cys Tyr Gln Ile Phe Asp Phe Ala Leu Asn
            160                 165                 170

atg ttg gtt gca atc act gtg ctt att tat cca aac tcc att cag gaa      1118
Met Leu Val Ala Ile Thr Val Leu Ile Tyr Pro Asn Ser Ile Gln Glu
        175                 180                 185

tac ata cgg caa ctg cct cct aat ttt ccc tac aga gat gat gtc atg      1166
Tyr Ile Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp Asp Val Met
    190                 195                 200

tca gtg aat cct acc tgt ttg gtc ctt att att ctt ctg ttt att agc      1214
Ser Val Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu Phe Ile Ser
205                 210                 215                 220

att atc ttg act ttt aag ggt tac ttg att agc tgt gtt tgg aac tgc      1262
Ile Ile Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val Trp Asn Cys
                225                 230                 235

tac cga tac atc aat ggt agg aac tcc tct gat gtc ctg gtt tat gtt      1310
Tyr Arg Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu Val Tyr Val
            240                 245                 250

acc agc aat gac act acg gtg ctg cta ccc ccg tat gat gat gcc act      1358
Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp Asp Ala Thr
        255                 260                 265

gtg aat ggt gct gcc aag gag cca ccg cca cct tac gtg tct gcc taa      1406
Val Asn Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val Ser Ala  *
    270                 275                 280



      <210> 37
      <211> 3003
      <212> DNA
      <213> Homo sapiens

      <220>
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      <222> (55)..(1692)

      <400> 37
gtaccggtcc ggaattcccg ggtcgacgat ttcgtccgct cggccctcac gaag  atg       57
                                                             Met
                                                               1

ctc cct gga gcc tgg ctg ctc tgg acc tcc ctc ctg ctc ctg gcc agg      105
Leu Pro Gly Ala Trp Leu Leu Trp Thr Ser Leu Leu Leu Leu Ala Arg
              5                  10                  15
```

```
cct gcc cag ccc tgt ccc atg ggt tgt gac tgc ttc gtc cag gag gtg       153
Pro Ala Gln Pro Cys Pro Met Gly Cys Asp Cys Phe Val Gln Glu Val
         20                  25                  30

ttc tgc tca gat gag gag ctt gcc acc gtc ccg ctg gac atc ccg cca       201
Phe Cys Ser Asp Glu Glu Leu Ala Thr Val Pro Leu Asp Ile Pro Pro
     35                  40                  45

tat acg aaa aac atc atc ttt gtg gag acc tcg ttc acc aca ttg gaa       249
Tyr Thr Lys Asn Ile Ile Phe Val Glu Thr Ser Phe Thr Thr Leu Glu
 50                  55                  60                  65

acc aga gct ttt ggc agt aac ccc aac ttg acc aag gtg gtc ttc ctc       297
Thr Arg Ala Phe Gly Ser Asn Pro Asn Leu Thr Lys Val Val Phe Leu
                 70                  75                  80

aac act cag ctc tgc cag ttt agg ccg gat gcc ttt ggg ggg ctg ccc       345
Asn Thr Gln Leu Cys Gln Phe Arg Pro Asp Ala Phe Gly Gly Leu Pro
             85                  90                  95

agg ctg gag gac ctg gag gtc aca ggc agt agc ttc ttg aac ctc agc       393
Arg Leu Glu Asp Leu Glu Val Thr Gly Ser Ser Phe Leu Asn Leu Ser
        100                 105                 110

acc aac atc ttc tcc aac ctg acc tcg ctg ggc aag ctc acc ctc aac       441
Thr Asn Ile Phe Ser Asn Leu Thr Ser Leu Gly Lys Leu Thr Leu Asn
    115                 120                 125

ttc aac atg ctg gag gct ctg ccc gag ggt ctt ttc cag cac ctg gct       489
Phe Asn Met Leu Glu Ala Leu Pro Glu Gly Leu Phe Gln His Leu Ala
130                 135                 140                 145

gcc ctg gag tcc ctc cac ctg cag ggg aac cag ctc cag gcc ctg ccc       537
Ala Leu Glu Ser Leu His Leu Gln Gly Asn Gln Leu Gln Ala Leu Pro
                150                 155                 160

agg agg ctc ttc cag cct ctg acc cat ctg aag aca ctc aac ctg gcc       585
Arg Arg Leu Phe Gln Pro Leu Thr His Leu Lys Thr Leu Asn Leu Ala
            165                 170                 175

cag aac ctc ctg gcc cag ctc ccg gag gag ctg ttc cac cca ctc acc       633
Gln Asn Leu Leu Ala Gln Leu Pro Glu Glu Leu Phe His Pro Leu Thr
        180                 185                 190

agc ctg cag acc ctg aag ctg agc aac aac gcg ctc tct ggt ctc ccc       681
Ser Leu Gln Thr Leu Lys Leu Ser Asn Asn Ala Leu Ser Gly Leu Pro
    195                 200                 205

cag ggt gtg ttt ggc aaa ctg ggc agc ctg cag gag ctc ttc ctg gac       729
Gln Gly Val Phe Gly Lys Leu Gly Ser Leu Gln Glu Leu Phe Leu Asp
210                 215                 220                 225

agc aac aac atc tcg gag ctg ccc cct cag gtg ttc tcc cag ctc ttc       777
Ser Asn Asn Ile Ser Glu Leu Pro Pro Gln Val Phe Ser Gln Leu Phe
                230                 235                 240

tgc cta gag agg ctg tgg ctg caa cgc aac gcc atc acg cac ctg ccg       825
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```
Cys Leu Glu Arg Leu Trp Leu Gln Arg Asn Ala Ile Thr His Leu Pro
            245                 250                 255

ctc tcc atc ttt gcc tcc ctg ggt aat ctg acc ttt ctg agc ttg cag      873
Leu Ser Ile Phe Ala Ser Leu Gly Asn Leu Thr Phe Leu Ser Leu Gln
        260                 265                 270

tgg aac atg ctt cgg gtc ctg cct gcc ggc ctc ttt gcc cac acc cca      921
Trp Asn Met Leu Arg Val Leu Pro Ala Gly Leu Phe Ala His Thr Pro
    275                 280                 285

tgc ctg gtt ggc ctg tct ctg acc cat aac cag ctg gag act gtc gct      969
Cys Leu Val Gly Leu Ser Leu Thr His Asn Gln Leu Glu Thr Val Ala
290                 295                 300                 305

gag ggc acc ttt gcc cac ctg tcc aac ctg cgt tcc ctc atg ctc tca     1017
Glu Gly Thr Phe Ala His Leu Ser Asn Leu Arg Ser Leu Met Leu Ser
                310                 315                 320

tac aat gcc att acc cac ctc cca gct ggc atc ttc aga gac ctg gag     1065
Tyr Asn Ala Ile Thr His Leu Pro Ala Gly Ile Phe Arg Asp Leu Glu
            325                 330                 335

gag ttg gtc aaa ctc tac ctg ggc agc aac aac ctt acg gcg ctg cac     1113
Glu Leu Val Lys Leu Tyr Leu Gly Ser Asn Asn Leu Thr Ala Leu His
        340                 345                 350

cca gcc ctc ttc cag aac ctg tcc aag ctg gag ctg ctc agc ctc tcc     1161
Pro Ala Leu Phe Gln Asn Leu Ser Lys Leu Glu Leu Leu Ser Leu Ser
    355                 360                 365

aag aac cag ctg acc aca ctt ccg gag ggc atc ttc gac acc aac tac     1209
Lys Asn Gln Leu Thr Thr Leu Pro Glu Gly Ile Phe Asp Thr Asn Tyr
370                 375                 380                 385

aac ctg ttc aac ctg gcc ctg cac ggt aac ccc tgg cag tgc gac tgc     1257
Asn Leu Phe Asn Leu Ala Leu His Gly Asn Pro Trp Gln Cys Asp Cys
                390                 395                 400

cac ctg gcc tac ctc ttc aac tgg ctg cag cag tac acc gat cgg ctc     1305
His Leu Ala Tyr Leu Phe Asn Trp Leu Gln Gln Tyr Thr Asp Arg Leu
            405                 410                 415

ctg aac atc cag acc tac tgc gct ggc cct gcc tac ctc aaa ggc cag     1353
Leu Asn Ile Gln Thr Tyr Cys Ala Gly Pro Ala Tyr Leu Lys Gly Gln
        420                 425                 430

gtg gtg ccc gcc ttg aat gag aag cag ctg gtg tgt ccc gtc acc cgg     1401
Val Val Pro Ala Leu Asn Glu Lys Gln Leu Val Cys Pro Val Thr Arg
    435                 440                 445

gac cac ttg ggc ttc cag gtc acg tgg ccg gac gaa agc aag gca ggg     1449
Asp His Leu Gly Phe Gln Val Thr Trp Pro Asp Glu Ser Lys Ala Gly
450                 455                 460                 465

ggc agc tgg gat ctg gct gtg cag gaa agg gca gcc cgg agc cag tgc     1497
Gly Ser Trp Asp Leu Ala Val Gln Glu Arg Ala Ala Arg Ser Gln Cys
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                470                 475                 480

acc tac agc aac ccc gag ggc acc gtg gtg ctc gcc tgt gac cag gcc      1545
Thr Tyr Ser Asn Pro Glu Gly Thr Val Val Leu Ala Cys Asp Gln Ala
            485                 490                 495

cag tgt cgc tgg ctg aac gtc cag ctc tct cct cgg cag ggc tcc ctg      1593
Gln Cys Arg Trp Leu Asn Val Gln Leu Ser Pro Arg Gln Gly Ser Leu
        500                 505                 510

gga ctg cag tac aat gct agt cag gag tgg gac ctg agg tcg agc tgc      1641
Gly Leu Gln Tyr Asn Ala Ser Gln Glu Trp Asp Leu Arg Ser Ser Cys
    515                 520                 525

ggt tct ctg cgg ctc acc gtg tct atc gag gct cgg gca gca ggg ccc      1689
Gly Ser Leu Arg Leu Thr Val Ser Ile Glu Ala Arg Ala Ala Gly Pro
530                 535                 540                 545

tag tagc agcgcataca ggagctgggg aaggggggcct ctggggcctg accaggcgac      1746
 *


aggtaggggc ggaggggagc tgagtctccg aagccttggc ttttcacatg caagggacag   1806

ggttacatcc ccaaggtgag ggggtggagt ctggtctgct ccactaacca gggtctcctc   1866

ctcctcttcc ttcatcgctt ctcctggagt gtgcggccta acaaggccat ccttatgctt   1926

tgcaaagcac cctcaaaagc tgcaccacag cctggagaat aaaatatcct cagccctgat   1986

gcctccccat tatgtaacac ccaaccgctc tcacctacac cctgaggtct attcactgca   2046

tcccagtgat acaaagtgga ggccactgcc ttctgacatc tggctcaaaa gcccagtgtc   2106

tgtttccatt tatttccctg gaatttcatt taaaattggt atagagaaaa aaaggatgtg   2166

acagaagcag agatgaccag aaagcacagg ggcagggttc tgactggcgt gtgggagacc   2226

ctgtggccgg cacccacctc cacacgagga ctaagctctg atttttttat cttgcccaaa   2286

ttcctaccta aggggtctag ggagtcgcgc cttacaaatc ataaattctc atcagatggg   2346

ttttatttga ccctgtatat catgacttat ttttaatctg actatggcat aacattacaa   2406

gacgaggcaa aaatatttaa cccccaaata tatttctttg ccctaccttg aacttgccct   2466

gcagagtctc ttgtgaggag aatccacatc ctataaagaa gcccctttcc cctttgtttt   2526

ccttcctttc tttccagtcc aggagatcat caactaagag ccaggcaccc cttttaagtc   2586

gataagaaac agtttacaac ctgctctctc tctctctgaa gtctgctgag agcttcccct   2646

gcacaataaa acttggcctc cacgatcctt tatcttaacc tgaacattcc tttccattga   2706

tcccaggtct tcagctaagc tcaaccaatt gtcaaccaga aaatgtttaa atttacctac   2766

agcctggaag cacccacccc cgctgcttcg agttgtcctg cctttctgaa ctcaaccaat   2826
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gtatttctta aatgtatttg attgatgcct cattcctccc taaaatgtat aaaaccaagc   2886

tgtacctcga ccaccttggg cacatgttcc caggccctcc tgaggtctgt gtcacgggcc   2946

atggccactc atatttggct cagaataaat ctcttcaaat attttaaaaa aaaaaaa      3003
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<212> DNA
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<220>
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<222> (68)..(466)

<400> 38

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ggtcacc  atg aac cac att gtg caa acc ttc tct cct gtc aac agc ggc      109
         Met Asn His Ile Val Gln Thr Phe Ser Pro Val Asn Ser Gly
           1               5                  10

cag cct ccc aac tac gag atg ctc aag gag gag cag gaa gtg gct atg      157
Gln Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met
 15                  20                  25                  30

ctg ggg gtg ccc cac aac cct gct ccc ccg atg tcc acc gtg atc cac      205
Leu Gly Val Pro His Asn Pro Ala Pro Pro Met Ser Thr Val Ile His
                 35                  40                  45

atc cgc agc gag acc tcc gtg cct gac cat gtg gtc tgg tcc ctg ttc      253
Ile Arg Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe
             50                  55                  60

aac acc ctc ttc atg aac acc tgc tgc ctg ggc ttc ata gca ttc gcg      301
Asn Thr Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala
         65                  70                  75

tac tcc gtg aag tct agg gac agg aag atg gtt ggc gac gtg acc ggg      349
Tyr Ser Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly
     80                  85                  90

gcc cag gcc tat gcc tcc acc gcc aag tgc ctg aac atc tgg gcc ctg      397
Ala Gln Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu
 95                 100                 105                 110

att ttg ggc atc ttc atg acc att ctg ctc atc atc atc cca gtg ttg      445
Ile Leu Gly Ile Phe Met Thr Ile Leu Leu Ile Ile Ile Pro Val Leu
                115                 120                 125

gtc gtc cag gcc cag cga tag at caggaggcat cattgaggcc aggagctctg      498
Val Val Gln Ala Gln Arg  *
            130
```

```
cccgtgagct gtatccacgt actctatctt ccattcttcg cctgccccca gaggccagag      558

ctctgccctt gactgtattc acttattcag ctccattctg cctgtccaaa gcgagtctga      618

ttagccttta caa                                                         631




      <210> 39
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      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (274)..(2271)

      <400> 39
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gtcgccccgg ggcagcagcg gcagcagcag cagaggcagc agcgggcggc gctgagccgc      120

cgccgccgcc actgaggaag aagccggccc agccgccgcc gcgtccggac cctcgcgcct      180

ggatcccagc gccccgatcc cggcgcccca acccccacgc ccgcctccgc caactttcac      240

gctgcctcgg cggcccggcc cggctcgacg cca atg gtg gag gcc ata gtg gag      294
                                     Met Val Glu Ala Ile Val Glu
                                     1               5

ttt gac tac cag gcc cag cac gat gat gag ctg acg atc agc gtg ggt        342
Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
        10                  15                  20

gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga        390
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
    25                  30                  35

cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa        438
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
40                  45                  50                  55

ata aag aaa gag atg aag aaa gac cct ctc acc aac aaa gct cca gaa        486
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
                60                  65                  70

aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa        534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
            75                  80                  85

acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc        582
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
        90                  95                  100

cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg        630
```

```
Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu
    105                 110                 115

aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg       678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp
120                 125                 130                 135

tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc       726
Trp Glu Gly Val Leu Asn Gly Lys Thr Gly Met Phe Pro Ser Asn Phe
                140                 145                 150

atc aag gag ctg tca ggg gag tcg gat gag ctt ggc att tcc cag gat       774
Ile Lys Glu Leu Ser Gly Glu Ser Asp Glu Leu Gly Ile Ser Gln Asp
            155                 160                 165

gag cag cta tcc aag tca agt tta agg gaa acc aca ggc tcc gag agt       822
Glu Gln Leu Ser Lys Ser Ser Leu Arg Glu Thr Thr Gly Ser Glu Ser
        170                 175                 180

gat ggg ggt gac tca agc agc acc aag tct gaa ggt gcc aac ggg aca       870
Asp Gly Gly Asp Ser Ser Ser Thr Lys Ser Glu Gly Ala Asn Gly Thr
    185                 190                 195

gtg gca act gca gca atc cag ccc aag aaa gtt aag gga gtg ggc ttt       918
Val Ala Thr Ala Ala Ile Gln Pro Lys Lys Val Lys Gly Val Gly Phe
200                 205                 210                 215

gga gac att ttc aaa gac aag cca atc aaa cta aga cca agg tca att       966
Gly Asp Ile Phe Lys Asp Lys Pro Ile Lys Leu Arg Pro Arg Ser Ile
                220                 225                 230

gaa gta gaa aat gac ttt ctg ccg gta gaa aag act att ggg aag aag      1014
Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys
            235                 240                 245

tta cct gca act aca gca act cca gac tca tca aaa aca gaa atg gac      1062
Leu Pro Ala Thr Thr Ala Thr Pro Asp Ser Ser Lys Thr Glu Met Asp
        250                 255                 260

agc agg aca aag agc aag gat tac tgc aaa gta ata ttt cca tat gag      1110
Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu
    265                 270                 275

gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act      1158
Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr
280                 285                 290                 295

ctc atc aat aag gac tgc atc gac gta ggc tgg tgg gaa gga gag ctg      1206
Leu Ile Asn Lys Asp Cys Ile Asp Val Gly Trp Trp Glu Gly Glu Leu
                300                 305                 310

aac ggc aga cga ggc gtg ttc ccc gat aac ttc gtg aag tta ctt cca      1254
Asn Gly Arg Arg Gly Val Phe Pro Asp Asn Phe Val Lys Leu Leu Pro
            315                 320                 325

ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca      1302
Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro
```

```
        330                 335                 340

tcc gct cct gtc atc aaa caa ggg gca ggc acc act gag aga aaa cat       1350
Ser Ala Pro Val Ile Lys Gln Gly Ala Gly Thr Thr Glu Arg Lys His
    345                 350                 355

gaa att aaa aag ata cct cct gaa aga cca gaa atg ctt cca aac aga       1398
Glu Ile Lys Lys Ile Pro Pro Glu Arg Pro Glu Met Leu Pro Asn Arg
360                 365                 370                 375

aca gaa gaa aaa gaa aga cca gag aga gag cca aaa ctg gat tta cag       1446
Thr Glu Glu Lys Glu Arg Pro Glu Arg Glu Pro Lys Leu Asp Leu Gln
                380                 385                 390

aag ccc tcc gtt cct gcc ata ccg cca aaa aag cct cgg cca cct aag       1494
Lys Pro Ser Val Pro Ala Ile Pro Pro Lys Lys Pro Arg Pro Pro Lys
            395                 400                 405

acc aat tct ctc agc aga cct ggc gca ctg ccc ccg aga agg ccg gag       1542
Thr Asn Ser Leu Ser Arg Pro Gly Ala Leu Pro Pro Arg Arg Pro Glu
        410                 415                 420

aga ccg gtg ggt ccg ctg aca cac acc agg ggt gac agt cca aag att       1590
Arg Pro Val Gly Pro Leu Thr His Thr Arg Gly Asp Ser Pro Lys Ile
    425                 430                 435

gac ttg gcc ggc agt tcg cta tct ggc atc ctg gac aaa gat ctc tcg       1638
Asp Leu Ala Gly Ser Ser Leu Ser Gly Ile Leu Asp Lys Asp Leu Ser
440                 445                 450                 455

gac cgc agc aat gac att gac tta gaa ggt ttt gac tcc gtg gta tca       1686
Asp Arg Ser Asn Asp Ile Asp Leu Glu Gly Phe Asp Ser Val Val Ser
                460                 465                 470

tct act gag aaa ctc agt cat ccg acc aca agc aga cca aaa gct aca       1734
Ser Thr Glu Lys Leu Ser His Pro Thr Thr Ser Arg Pro Lys Ala Thr
            475                 480                 485

ggg agg cgg cct ccg tcc cag tcc ctc aca tct tca tcc ctt tca agc       1782
Gly Arg Arg Pro Pro Ser Gln Ser Leu Thr Ser Ser Ser Leu Ser Ser
        490                 495                 500

cct gat atc ttc gac tcc cca agt ccc gaa gag gat aag gag gaa cac       1830
Pro Asp Ile Phe Asp Ser Pro Ser Pro Glu Glu Asp Lys Glu Glu His
    505                 510                 515

att tca ctt gcg cac aga gga gtg gac gcg tca aag aaa act tcc aag       1878
Ile Ser Leu Ala His Arg Gly Val Asp Ala Ser Lys Lys Thr Ser Lys
520                 525                 530                 535

act gtt acc ata tcc caa gtg tct gac aac aaa gca tcc ctg ccg ccc       1926
Thr Val Thr Ile Ser Gln Val Ser Asp Asn Lys Ala Ser Leu Pro Pro
                540                 545                 550

aag ccg ggg acc atg gca gca ggt ggc ggt ggg cca gcc cct ctg tcc       1974
Lys Pro Gly Thr Met Ala Ala Gly Gly Gly Gly Pro Ala Pro Leu Ser
            555                 560                 565
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tca gcg gcg ccc tcc ccc ctg tca tcc tct ttg gga aca gct gga cac       2022
Ser Ala Ala Pro Ser Pro Leu Ser Ser Ser Leu Gly Thr Ala Gly His
        570                 575                 580

aga gcc aac tcc ccg tct ctg ttc ggc acg gaa gga aaa cca aag atg       2070
Arg Ala Asn Ser Pro Ser Leu Phe Gly Thr Glu Gly Lys Pro Lys Met
    585                 590                 595

gag cct gcg gcc agc agc cag gcg gcc gtg gag gag cta agg aca cag       2118
Glu Pro Ala Ala Ser Ser Gln Ala Ala Val Glu Glu Leu Arg Thr Gln
600                 605                 610                 615

gtc cgc gag ctg agg agc atc atc gag acc atg aag gac cag cag aaa       2166
Val Arg Glu Leu Arg Ser Ile Ile Glu Thr Met Lys Asp Gln Gln Lys
                620                 625                 630

cga gag att aaa cag tta ttg tct gag ttg gat gaa gag aag aaa atc       2214
Arg Glu Ile Lys Gln Leu Leu Ser Glu Leu Asp Glu Glu Lys Lys Ile
            635                 640                 645

cgg ctt cgg ttg cag atg gaa gtg aac gac ata aag aaa gct cta caa       2262
Arg Leu Arg Leu Gln Met Glu Val Asn Asp Ile Lys Lys Ala Leu Gln
        650                 655                 660

tca aaa tga atacttg atcaatgaaa tgtcacatta ttcatcctga gtccgagact       2318
Ser Lys  *
    665

caaattttct gccccagcca aaataatctt gtgccaaaag attaaaggtt tgcctcaaaa     2378

tgtccctgtt tgaaagatta gcacaaaagt cttgatagca caacacaaat tccatccaag     2438

aggagaatct tccccagggt ttagtcctgg ggctggcact cgttgtgact tacacagagc     2498

aaaattgtgc taaaggcttt tctactctga gatctcaatg cgaaatgaaa actcaggcag     2558

tttagtccat agtggtacta ttttgatgat attttccatt aataaaatgt aatttcagat     2618

tattcgttta caagctttat aattttatga ttttttaatc gtgttttgtc acagacttcc     2678

ctagtgtttg tactacacgt agtcagaagc gagtgtcctt ttcttttgct tcaggctaag     2738

agctgcctcg ctctttgtcc ccccattagg attctattac atatgcaatt gtaggttcaa     2798

cctgtccctt tccctgccag caaaccccac caccctaaga gaaattttag cttatatatg     2858

acggtatatt tacaaaaaga gaaagagaaa atctggtatt tgcaatgatc tgtgccttct     2918

ttttaccacc ctcttgattg gagcttttgt gatgcagcta ccatgattca aaaaaattaa     2978

aaattaaaaa aaaaaaa                                                    2995
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<213> Homo sapiens

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<222> (274)..(2142)

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gtcgccccgg ggcagcagcg gcagcagcag cagaggcagc agcgggcggc gctgagccgc     120

cgccgccgcc actgaggaag aagccggccc agccgccgcc gcgtccggac cctcgcgcct     180

ggatcccagc gccccgatcc cggcgcccca acccccacgc ccgcctccgc caactttcac     240

gctgcctcgg cggcccggcc cggctcgacg cca atg gtg gag gcc ata gtg gag      294
                                     Met Val Glu Ala Ile Val Glu
                                      1               5

ttt gac tac cag gcc cag cac gat gat gag ctg acg atc agc gtg ggt       342
Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
         10                  15                  20

gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga       390
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
     25                  30                  35

cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa       438
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
 40                  45                  50                  55

ata aag aaa gag atg aag aaa gac cct ctc acc aac aaa gct cca gaa       486
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
                 60                  65                  70

aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa       534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
             75                  80                  85

acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc       582
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
         90                  95                 100

cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg       630
Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu
    105                 110                 115

aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg       678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp
120                 125                 130                 135

tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc       726
Trp Glu Gly Val Leu Asn Gly Lys Thr Gly Met Phe Pro Ser Asn Phe
                140                 145                 150
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atc aag gag ctg tca ggg gag tcg gat gag ctt ggc att tcc cag gat        774
Ile Lys Glu Leu Ser Gly Glu Ser Asp Glu Leu Gly Ile Ser Gln Asp
            155                 160                 165

gag cag cta tcc aag tca agt tta agg gaa acc aca ggc tcc gag agt        822
Glu Gln Leu Ser Lys Ser Ser Leu Arg Glu Thr Thr Gly Ser Glu Ser
        170                 175                 180

gat ggg ggt gac tca agc agc acc aag tct gaa ggt gcc aac ggg aca        870
Asp Gly Gly Asp Ser Ser Ser Thr Lys Ser Glu Gly Ala Asn Gly Thr
    185                 190                 195

gtg gca act gca gca atc cag ccc aag aaa gtt aag gga gtg ggc ttt        918
Val Ala Thr Ala Ala Ile Gln Pro Lys Lys Val Lys Gly Val Gly Phe
200                 205                 210                 215

gga gac att ttc aaa gac aag cca atc aaa cta aga cca agg tca att        966
Gly Asp Ile Phe Lys Asp Lys Pro Ile Lys Leu Arg Pro Arg Ser Ile
            220                 225                 230

gaa gta gaa aat gac ttt ctg ccg gta gaa aag act att ggg aag aag       1014
Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys
            235                 240                 245

tta cct gca act aca gca act cca gac tca tca aaa aca gaa atg gac       1062
Leu Pro Ala Thr Thr Ala Thr Pro Asp Ser Ser Lys Thr Glu Met Asp
        250                 255                 260

agc agg aca aag agc aag gat tac tgc aaa gta ata ttt cca tat gag       1110
Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu
    265                 270                 275

gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act       1158
Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr
280                 285                 290                 295

ctc atc aat aag gac tgc atc gac gta ggc tgg tgg gaa gga gag ctg       1206
Leu Ile Asn Lys Asp Cys Ile Asp Val Gly Trp Trp Glu Gly Glu Leu
            300                 305                 310

aac ggc aga cga ggc gtg ttc ccc gat aac ttc gtg aag tta ctt cca       1254
Asn Gly Arg Arg Gly Val Phe Pro Asp Asn Phe Val Lys Leu Leu Pro
            315                 320                 325

ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca       1302
Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro
        330                 335                 340

tcc gct cct gtc atc aaa caa ggg gca ggc acc act gag aga aaa cat       1350
Ser Ala Pro Val Ile Lys Gln Gly Ala Gly Thr Thr Glu Arg Lys His
    345                 350                 355

gaa att aaa aag ata cct cct gaa aga cca gaa atg ctt cca aac aga       1398
Glu Ile Lys Lys Ile Pro Pro Glu Arg Pro Glu Met Leu Pro Asn Arg
360                 365                 370                 375

aca gaa gaa aaa gaa aga cca gag aga gag cca aaa ctg gat tta cag       1446
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Thr Glu Glu Lys Glu Arg Pro Glu Arg Glu Pro Lys Leu Asp Leu Gln
                380                 385                 390

aag ccc tcc gtt cct gcc ata ccg cca aaa aag cct cgg cca cct aag      1494
Lys Pro Ser Val Pro Ala Ile Pro Pro Lys Lys Pro Arg Pro Pro Lys
            395                 400                 405

acc aat tct ctc agc aga cct ggc gca ctg ccc ccg aga agg ccg gag      1542
Thr Asn Ser Leu Ser Arg Pro Gly Ala Leu Pro Pro Arg Arg Pro Glu
        410                 415                 420

aga ccg gtg ggt ccg ctg aca cac acc agg ggt gac agt cca aag att      1590
Arg Pro Val Gly Pro Leu Thr His Thr Arg Gly Asp Ser Pro Lys Ile
    425                 430                 435

gac ttg gcc ggc agt tcg cta tct ggc atc ctg gac aaa gat ctc tcg      1638
Asp Leu Ala Gly Ser Ser Leu Ser Gly Ile Leu Asp Lys Asp Leu Ser
440                 445                 450                 455

gac cgc agc aat gac att gac tta gaa ggt ttt gac tcc gtg gta tca      1686
Asp Arg Ser Asn Asp Ile Asp Leu Glu Gly Phe Asp Ser Val Val Ser
                460                 465                 470

tct act gag aaa ctc agt cat ccg acc aca agc aga cca aaa gct aca      1734
Ser Thr Glu Lys Leu Ser His Pro Thr Thr Ser Arg Pro Lys Ala Thr
            475                 480                 485

ggg agg cgg cct ccg tcc cag tcc ctc aca tct gtg tct gac aac aaa      1782
Gly Arg Arg Pro Pro Ser Gln Ser Leu Thr Ser Val Ser Asp Asn Lys
        490                 495                 500

gca tcc ctg ccg ccc aag ccg ggg acc atg gca gca ggt ggc ggt ggg      1830
Ala Ser Leu Pro Pro Lys Pro Gly Thr Met Ala Ala Gly Gly Gly Gly
    505                 510                 515

cca gcc cct ctg tcc tca gcg gcg ccc tcc ccc ctg tca tcc tct ttg      1878
Pro Ala Pro Leu Ser Ser Ala Ala Pro Ser Pro Leu Ser Ser Ser Leu
520                 525                 530                 535

gga aca gct gga cac aga gcc aac tcc ccg tct ctg ttc ggc acg gaa      1926
Gly Thr Ala Gly His Arg Ala Asn Ser Pro Ser Leu Phe Gly Thr Glu
                540                 545                 550

gga aaa cca aag atg gag cct gcg gcc agc agc cag gcg gcc gtg gag      1974
Gly Lys Pro Lys Met Glu Pro Ala Ala Ser Ser Gln Ala Ala Val Glu
            555                 560                 565

gag cta agg aca cag gtc cgc gag ctg agg agc atc atc gag acc atg      2022
Glu Leu Arg Thr Gln Val Arg Glu Leu Arg Ser Ile Ile Glu Thr Met
        570                 575                 580

aag gac cag cag aaa cga gag att aaa cag tta ttg tct gag ttg gat      2070
Lys Asp Gln Gln Lys Arg Glu Ile Lys Gln Leu Leu Ser Glu Leu Asp
    585                 590                 595

gaa gag aag aaa atc cgg ctt cgg ttg cag atg gaa gtg aac gac ata      2118
Glu Glu Lys Lys Ile Arg Leu Arg Leu Gln Met Glu Val Asn Asp Ile
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600                 605                 610                 615

aag aaa gct cta caa tca aaa tga atacttgatc aatgaaatgt cacattattc    2172
Lys Lys Ala Leu Gln Ser Lys  *
                620

atcctgagtc cgagactcaa atttctgcc ccagccaaaa taatcttgtg ccaaaagatt   2232

aaaggtttgc ctcaaaatgt ccctgtttga aagattagca caaaagtctt gatagcacaa   2292

cacaaattcc atccaagagg agaatcttcc ccagggttta gtcctggggc tggcactcgt   2352

tgtgacttac acagagcaaa attgtgctaa aggcttttct actctgagat ctcaatgcga   2412

aatgaaaact caggcagttt agtccatagt ggtactattt tgatgatatt ttccattaat   2472

aaaatgtaat ttcagattat tcgtttacaa gctttataat tttatgattt tttaatcgtg   2532

ttttgtcaca gacttcccta gtgtttgtac tacacgtagt cagaagcgag tgtccttttc   2592

ttttgcttca ggctaagagc tgcctcgctc tttgtccccc cattaggatt ctattacata   2652

tgcaattgta ggttcaacct gtccctttcc ctgccagcaa accccaccac cctaagagaa   2712

attttagctt atatatgacg gtatatttac aaaaagagaa agagaaaatc tggtatttgc   2772

aatgatctgt gccttctttt taccaccctc ttgattggag cttttgtgat gcagctacca   2832

tgattcaaaa aaattaaaaa ttaaaaaaaa aaaa                               2866



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     <213> Homo sapiens

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     <222> (404)..(2449)

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tgggtgggcg caggccctga gatgggcgtc agggagaggg gacgccagac acacggcctg    120

agcagggtga ggagcagctg ccagccccgg caggcccagg ccctgtctgg gtgcacagga    180

cagagacaca gcaagatgcc cagggagtgc cgcttcctgg gctagagaca agcaccagcc    240

tgcagtggag aacgcaggac cccgctgccc agaaggagca gccacggcct gcggaggact    300

ggcccagcaa ggtcccaggt cttccctctc ctcagcgcct aagagagagg cccagtgcgg    360

gtgaggagtc gcgaggaaga ggcggaaggc gccggaaggc acc atg ttc cgc aag      415
                                                Met Phe Arg Lys
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aaa aag aag aaa cgc cct gag atc tca gcg cca cag aac ttc cag cac       463
Lys Lys Lys Lys Arg Pro Glu Ile Ser Ala Pro Gln Asn Phe Gln His
  5                  10                  15                  20

cgt gtc cac acc tcc ttc gac ccc aaa gaa ggc aag ttt gtg ggc ctc       511
Arg Val His Thr Ser Phe Asp Pro Lys Glu Gly Lys Phe Val Gly Leu
                 25                  30                  35

ccc cca caa tgg cag aac atc ctg gac aca ctg cgg cgc ccc aag ccc       559
Pro Pro Gln Trp Gln Asn Ile Leu Asp Thr Leu Arg Arg Pro Lys Pro
             40                  45                  50

gtg gtg gac cct tcg cga atc aca cgg gtg cag ctc cag ccc atg aag       607
Val Val Asp Pro Ser Arg Ile Thr Arg Val Gln Leu Gln Pro Met Lys
         55                  60                  65

aca gtg gtg cgg ggc agc gcg atg cct gtg gat ggc tac atc tcg ggg       655
Thr Val Val Arg Gly Ser Ala Met Pro Val Asp Gly Tyr Ile Ser Gly
     70                  75                  80

ctg ctc aac gac atc cag aag ttg tca gtc atc agc tcc aac acc ctg       703
Leu Leu Asn Asp Ile Gln Lys Leu Ser Val Ile Ser Ser Asn Thr Leu
 85                  90                  95                 100

cgt ggc cgc agc ccc acc agc cgg cgg cgg gca cag tcc ctg ggg ctg       751
Arg Gly Arg Ser Pro Thr Ser Arg Arg Arg Ala Gln Ser Leu Gly Leu
                105                 110                 115

ctg ggg gat gag cac tgg gcc acc gac cca gac atg tac ctc cag agc       799
Leu Gly Asp Glu His Trp Ala Thr Asp Pro Asp Met Tyr Leu Gln Ser
            120                 125                 130

ccc cag tct gag cgc act gac ccc cac ggc ctc tac ctc agc tgc aac       847
Pro Gln Ser Glu Arg Thr Asp Pro His Gly Leu Tyr Leu Ser Cys Asn
        135                 140                 145

ggg ggc aca cca gca ggc cac aag cag atg ccg tgg ccc gag cca cag       895
Gly Gly Thr Pro Ala Gly His Lys Gln Met Pro Trp Pro Glu Pro Gln
    150                 155                 160

agc cca cgg gtc ctg ccc aat ggg ctg gct gca aag gca cag tcc ctg       943
Ser Pro Arg Val Leu Pro Asn Gly Leu Ala Ala Lys Ala Gln Ser Leu
165                 170                 175                 180

ggc ccc gcc gag ttt cag ggt gcc tcg cag cgc tgt ctg cag ctg ggt       991
Gly Pro Ala Glu Phe Gln Gly Ala Ser Gln Arg Cys Leu Gln Leu Gly
                185                 190                 195

gcc tgc ctg cag agc tcc cca cca gga gcc tcg ccc ccc acg ggc acc      1039
Ala Cys Leu Gln Ser Ser Pro Pro Gly Ala Ser Pro Pro Thr Gly Thr
            200                 205                 210

aat agg cat gga atg aag gct gcc aag cat ggc tct gag gag gcc cgg      1087
Asn Arg His Gly Met Lys Ala Ala Lys His Gly Ser Glu Glu Ala Arg
        215                 220                 225
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cca cag tcc tgc ctg gtg ggc tca gcc aca ggc agg cca ggt ggg gaa       1135
Pro Gln Ser Cys Leu Val Gly Ser Ala Thr Gly Arg Pro Gly Gly Glu
    230                 235                 240

ggc agc cct agc cct aag acc cgg gag agc agc ctg aag cgc agg cta       1183
Gly Ser Pro Ser Pro Lys Thr Arg Glu Ser Ser Leu Lys Arg Arg Leu
245                 250                 255                 260

ttc cga agc atg ttc ctg tcc act gct gcc aca gcc cct cca agc agc       1231
Phe Arg Ser Met Phe Leu Ser Thr Ala Ala Thr Ala Pro Pro Ser Ser
                265                 270                 275

agc aag cca ggc cct cca cca cag agc aag ccc aac tcc tct ttc cga       1279
Ser Lys Pro Gly Pro Pro Pro Gln Ser Lys Pro Asn Ser Ser Phe Arg
            280                 285                 290

ccg ccg cag aaa gac aac ccc cca agc ctg gtg gcc aag gcc cag tcc       1327
Pro Pro Gln Lys Asp Asn Pro Pro Ser Leu Val Ala Lys Ala Gln Ser
        295                 300                 305

ttg ccc tcg gac cag ccg gtg ggg acc ttc agc cct ctg acc act tcg       1375
Leu Pro Ser Asp Gln Pro Val Gly Thr Phe Ser Pro Leu Thr Thr Ser
    310                 315                 320

gat acc agc agc ccc cag aag tcc ctc cgc aca gcc ccg gcc aca ggc       1423
Asp Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly
325                 330                 335                 340

cag ctt cca ggc cgg tct tcc cca gcg gga tcc ccc cgc acc tgg cac       1471
Gln Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His
                345                 350                 355

gcc cag atc agc acc agc aac ctg tac ctg ccc cag gac ccc acg gtt       1519
Ala Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val
            360                 365                 370

gcc aag ggt gcc ctg gct ggt gag gac aca ggt gtt gtg aca cat gag       1567
Ala Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu
        375                 380                 385

cag ttc aag gct gcg ctc agg atg gtg gtg gac cag ggt gac ccc cgg       1615
Gln Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg
    390                 395                 400

ctg ctg ctg gac agc tac gtg aag att ggc gag ggc tcc acc ggc atc       1663
Leu Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile
405                 410                 415                 420

gtc tgc ttg gcc cgg gag aag cac tcg ggc cgc cag gtg gcc gtc aag       1711
Val Cys Leu Ala Arg Glu Lys His Ser Gly Arg Gln Val Ala Val Lys
                425                 430                 435

atg atg gac ctc agg aag cag cag cgc agg gag ctg ctc ttc aac gag       1759
Met Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu
            440                 445                 450
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gtg gtg atc atg cgg gac tac cag cac ttc aac gtg gtg gag atg tac        1807
Val Val Ile Met Arg Asp Tyr Gln His Phe Asn Val Val Glu Met Tyr
        455                 460                 465

aag agc tac ctg gtg gga gag gag ctg tgg gtg ctc atg gag ttc ctg        1855
Lys Ser Tyr Leu Val Gly Glu Glu Leu Trp Val Leu Met Glu Phe Leu
    470                 475                 480

cag gga gga gcc ctc aca gac atc gtc tcc caa gtc agg ctg aat gag        1903
Gln Gly Gly Ala Leu Thr Asp Ile Val Ser Gln Val Arg Leu Asn Glu
485                 490                 495                 500

gag cag att gcc act gtg tgt gag gct gtg ctg cag gcc ctg gcc tac        1951
Glu Gln Ile Ala Thr Val Cys Glu Ala Val Leu Gln Ala Leu Ala Tyr
                505                 510                 515

ctg cat gct cag ggt gtc atc cac cgg gac atc aag agt gac tcc atc        1999
Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile
            520                 525                 530

ctg ctg acc ctc gat ggc agg gtg aag ctc tcg gac ttc gga ttc tgt        2047
Leu Leu Thr Leu Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys
        535                 540                 545

gct cag atc agc aaa gac gtc cct aag agg aag tcc ctg gtg gga acc        2095
Ala Gln Ile Ser Lys Asp Val Pro Lys Arg Lys Ser Leu Val Gly Thr
    550                 555                 560

ccc tac tgg atg gct cct gaa gtg atc tcc agg tct ttg tat gcc act        2143
Pro Tyr Trp Met Ala Pro Glu Val Ile Ser Arg Ser Leu Tyr Ala Thr
565                 570                 575                 580

gag gtg gat atc tgg tct ctg ggc atc atg gtg att gag atg gta gat        2191
Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp
                585                 590                 595

ggg gag cca ccg tac ttc agt gac tcc cca gtg caa gcc atg aag agg        2239
Gly Glu Pro Pro Tyr Phe Ser Asp Ser Pro Val Gln Ala Met Lys Arg
            600                 605                 610

ctc cgg gac agc ccc cca ccc aag ctg aaa aac tct cac aag gtc tcc        2287
Leu Arg Asp Ser Pro Pro Pro Lys Leu Lys Asn Ser His Lys Val Ser
        615                 620                 625

cca gtg ctg cga gac ttc ctg gag cgg atg ctg gtg cgg gac ccc caa        2335
Pro Val Leu Arg Asp Phe Leu Glu Arg Met Leu Val Arg Asp Pro Gln
    630                 635                 640

gag aga gcc aca gcc cag gag ctc cta gac cac ccc ttc ctg ctg cag        2383
Glu Arg Ala Thr Ala Gln Glu Leu Leu Asp His Pro Phe Leu Leu Gln
645                 650                 655                 660

aca ggg cta cct gag tgc ctg gtg ccc ctg atc cag ctc tac cga aag        2431
Thr Gly Leu Pro Glu Cys Leu Val Pro Leu Ile Gln Leu Tyr Arg Lys
                665                 670                 675

cag acc tcc acc tgc tga gcccac cccaagtatg cctgccacct acgcccacag        2485
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Gln Thr Ser Thr Cys *
680

gcagggcaca ctgggcagcc agcctgccgg caggacttgc ctgcctcctc ctctcagtat 2545

tctctccaaa gattgaaatg tgaagcccca gccccaccct ctgcccttca gcctactggg 2605

ccaggccgga cctgcccccct cagtgtctct ccctcccgag tccccagatg gagacccctt 2665

tctacaggat gacccccttga tatttgcaca gggatatttc taagaaacgc agaggccagc 2725

gttcctggcc tctgcagcca acacagtaga aaaggctgct gtggtttttt aaaggcagtt 2785

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acagaatgga gaga 3099

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tgcagacgta ggagatgcct gggacaagga ggccaccttc tcagggcaaa agaaaaagaa 120

ggtgacaggc gttgagacca ccgaagggaa ccc atg gct agg atc agt ttt tcc 174
Met Ala Arg Ile Ser Phe Ser
1 5

tac ctc tgc cca gcc tcc tgg tac ttc act gtg ccc aca gtg agt cca 222
Tyr Leu Cys Pro Ala Ser Trp Tyr Phe Thr Val Pro Thr Val Ser Pro
10 15 20

ttt ctc cgt cag cgg gtg gca ttc ctg gga ctc ttc ttc ata tcc tgt 270
Phe Leu Arg Gln Arg Val Ala Phe Leu Gly Leu Phe Phe Ile Ser Cys
25 30 35

ctc ctt tta ctt atg tta atc ata gac ttt cga cat tgg agt gct tca 318
Leu Leu Leu Leu Met Leu Ile Ile Asp Phe Arg His Trp Ser Ala Ser
40 45 50 55

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tta cca cga gat agg caa tac gaa agg tat ttg gct cga gta ggg gag       366
Leu Pro Arg Asp Arg Gln Tyr Glu Arg Tyr Leu Ala Arg Val Gly Glu
                 60                  65                  70

ctt gaa gct act gac act gaa gac cca aat ctg aat tat gga ctt gtt       414
Leu Glu Ala Thr Asp Thr Glu Asp Pro Asn Leu Asn Tyr Gly Leu Val
             75                  80                  85

gtt gac tgt ggc agc agt ggt tcc cgg att ttt gtt tat ttc tgg cca       462
Val Asp Cys Gly Ser Ser Gly Ser Arg Ile Phe Val Tyr Phe Trp Pro
         90                  95                 100

aga cat aat ggg aac ccc cat gac ttg ctg gac atc aaa cag atg aga       510
Arg His Asn Gly Asn Pro His Asp Leu Leu Asp Ile Lys Gln Met Arg
    105                 110                 115

gac cgc aac agc caa cca gtg gtt aaa aaa atc aag cca gga atc tct       558
Asp Arg Asn Ser Gln Pro Val Val Lys Lys Ile Lys Pro Gly Ile Ser
120                 125                 130                 135

gca atg gca gac act cca gaa cat gcc agt gat tac ctt cgt cct ctg       606
Ala Met Ala Asp Thr Pro Glu His Ala Ser Asp Tyr Leu Arg Pro Leu
                140                 145                 150

ctg agc ttt gct gct gct cat gtg cct gtg aag aag cac aag gag acc       654
Leu Ser Phe Ala Ala Ala His Val Pro Val Lys Lys His Lys Glu Thr
            155                 160                 165

cct ctt tac atc ctc tgc aca gca ggc atg agg ctt ctc cct gag agg       702
Pro Leu Tyr Ile Leu Cys Thr Ala Gly Met Arg Leu Leu Pro Glu Arg
        170                 175                 180

aag cag ttg gct atc ttg gct gac cta gtg aaa gat tta cca ctg gag       750
Lys Gln Leu Ala Ile Leu Ala Asp Leu Val Lys Asp Leu Pro Leu Glu
    185                 190                 195

ttt gac ttc ctc ttt tca cag tct caa gca gaa gtg atc tct ggg aag       798
Phe Asp Phe Leu Phe Ser Gln Ser Gln Ala Glu Val Ile Ser Gly Lys
200                 205                 210                 215

cag gaa ggg gtt tat gca tgg att gga atc aac ttt gtt ttg gga aga       846
Gln Glu Gly Val Tyr Ala Trp Ile Gly Ile Asn Phe Val Leu Gly Arg
                220                 225                 230

ttc gac cac gag gat gaa tca gat gct gag gct acc cag gaa ttg gca       894
Phe Asp His Glu Asp Glu Ser Asp Ala Glu Ala Thr Gln Glu Leu Ala
            235                 240                 245

gca gga cgg aga agg aca gta ggg ata ctg gat atg gga gga gcc tct       942
Ala Gly Arg Arg Arg Thr Val Gly Ile Leu Asp Met Gly Gly Ala Ser
        250                 255                 260

ctc caa att gct tat gaa gtt cct acc tca acc tct gtc ctt cct gca       990
Leu Gln Ile Ala Tyr Glu Val Pro Thr Ser Thr Ser Val Leu Pro Ala
    265                 270                 275
```

```
aag cag gaa gaa gct gcc aag atc ctg ctg gct gag ttc aac ctg ggc      1038
Lys Gln Glu Glu Ala Ala Lys Ile Leu Leu Ala Glu Phe Asn Leu Gly
280                 285                 290                 295

tgt gat gtg caa cac act gaa cac gtg tac agg gtt tat gtc aca act      1086
Cys Asp Val Gln His Thr Glu His Val Tyr Arg Val Tyr Val Thr Thr
                300                 305                 310

ttt ctg ggt ttc gga ggc aac ttt gcc cgg cag cgc tac gaa gac ctt      1134
Phe Leu Gly Phe Gly Gly Asn Phe Ala Arg Gln Arg Tyr Glu Asp Leu
            315                 320                 325

gtt ctg aat gaa act ctt aac aaa aac aga ttg ctt ggt cag aag aca      1182
Val Leu Asn Glu Thr Leu Asn Lys Asn Arg Leu Leu Gly Gln Lys Thr
        330                 335                 340

ggt ctg agt ccc gac aat cca ttt ctg gat ccc tgc ctg cca gtg gga      1230
Gly Leu Ser Pro Asp Asn Pro Phe Leu Asp Pro Cys Leu Pro Val Gly
    345                 350                 355

ctc aca gat gtg gtg gag agg aac agc caa gtc tta cat gtc cga gga      1278
Leu Thr Asp Val Val Glu Arg Asn Ser Gln Val Leu His Val Arg Gly
360                 365                 370                 375

aga gga gac tgg gtg tct tgt ggg gca atg ctg agc ccc ctg ctg gct      1326
Arg Gly Asp Trp Val Ser Cys Gly Ala Met Leu Ser Pro Leu Leu Ala
                380                 385                 390

cgc tcc aac acc agc cag gcc tca ctc aat ggc ata tat caa tcg cct      1374
Arg Ser Asn Thr Ser Gln Ala Ser Leu Asn Gly Ile Tyr Gln Ser Pro
            395                 400                 405

att gac ttc aac aac agc gag ttc tac ggc ttc tct gag ttt ttt tat      1422
Ile Asp Phe Asn Asn Ser Glu Phe Tyr Gly Phe Ser Glu Phe Phe Tyr
        410                 415                 420

tgt aca gag gat gtg ttg cgc att ggt ggc cgc tac cat ggg cca aca      1470
Cys Thr Glu Asp Val Leu Arg Ile Gly Gly Arg Tyr His Gly Pro Thr
    425                 430                 435

ttt gcc aag gct gct cag gat tac tgt ggc atg gct tgg tcg gta cta      1518
Phe Ala Lys Ala Ala Gln Asp Tyr Cys Gly Met Ala Trp Ser Val Leu
440                 445                 450                 455

act cag aga ttc aag aat ggc ctc ttt tca tca cat gca gat gag cat      1566
Thr Gln Arg Phe Lys Asn Gly Leu Phe Ser Ser His Ala Asp Glu His
                460                 465                 470

cga ctc aaa tat cag tgt ttt aaa tcg gct tgg atg tac caa gtc tta      1614
Arg Leu Lys Tyr Gln Cys Phe Lys Ser Ala Trp Met Tyr Gln Val Leu
            475                 480                 485

cat gaa gga ttc cac ttt ccc tat gac tac cca aac ctg cgg aca gcc      1662
His Glu Gly Phe His Phe Pro Tyr Asp Tyr Pro Asn Leu Arg Thr Ala
        490                 495                 500

cag ctg gtg tat gac cga gag gtt cag tgg acg ctg gga gcc att cta      1710
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Gln Leu Val Tyr Asp Arg Glu Val Gln Trp Thr Leu Gly Ala Ile Leu
    505                 510                 515

tat aaa aca cga ttc tta cca ctc agg gat ctt cgg cag gaa ggt gtc       1758
Tyr Lys Thr Arg Phe Leu Pro Leu Arg Asp Leu Arg Gln Glu Gly Val
520                 525                 530                 535

cga caa gcc cat ggt agc tgg ttc cgt ctc tcc ttt gta tac aac cac       1806
Arg Gln Ala His Gly Ser Trp Phe Arg Leu Ser Phe Val Tyr Asn His
                540                 545                 550

tat ctc ttc ttt gcc tgt atc ctg gtg gtg cta ctg gcc atc ttc cta       1854
Tyr Leu Phe Phe Ala Cys Ile Leu Val Val Leu Leu Ala Ile Phe Leu
            555                 560                 565

tac ctt ctg cgg cta cgc cga att cac cac cga caa aca cga gcc tca       1902
Tyr Leu Leu Arg Leu Arg Arg Ile His His Arg Gln Thr Arg Ala Ser
        570                 575                 580

gct cca ttg gac ttg ctg tgg ctt gaa gag gtg gtg ccc atg atg gga       1950
Ala Pro Leu Asp Leu Leu Trp Leu Glu Glu Val Val Pro Met Met Gly
    585                 590                 595

gta cag gtg ggg ccg tga                                               1968
Val Gln Val Gly Pro  *
600                 605




    <210> 43
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    <213> Homo sapiens

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    <222> (418)..(1023)

    <400> 43
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aagaggttag acagaagggc taaagaaagc agaagcaaag aacagagtat attagttact     120

tttcaattag ttactttttc ttacaaggct gggagaggga gacagaacaa tagaaaaata     180

actggttgat tcatatggag gtcagagtgg aagcaggtgt gagagggtcc cacagaagaa     240

aacatggcag ccaaagtgtt tgagtccacg gtaagtttgg cttggcctta gctgttgcag     300

gagacctgtg aactctgcct tatataatgt ggatgttggg cacagagctg tcatctttga     360

ctgattccag gacaaaaatg acaggacatt gtggtagggg actcactttc tcatccc       417
atg ggt aca gaa acc aat tat ctt tgc ctt tct cca cca cgt aat gta       465
Met Gly Thr Glu Thr Asn Tyr Leu Cys Leu Ser Pro Pro Arg Asn Val
 1               5                  10                  15
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cca atc atc act ggt agc aaa gat tta cag aat gtc aat atc aca ctg       513
Pro Ile Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu
             20                  25                  30

cgc atc atc ttc cag cct gtt gct agc cag ctt cct cgc atc ttc acc       561
Arg Ile Ile Phe Gln Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr
         35                  40                  45

agc atc gga gag gac tat gat gag cct gtg ctg acg tac atc acg acc       609
Ser Ile Gly Glu Asp Tyr Asp Glu Pro Val Leu Thr Tyr Ile Thr Thr
     50                  55                  60

gag atc ctc aag tca gtg gtg gct cgc ttt gat gct gga gaa gtt atc       657
Glu Ile Leu Lys Ser Val Val Ala Arg Phe Asp Ala Gly Glu Val Ile
 65                  70                  75                  80

act cag aga gag ctg gtc tcc agg cag gtg agc aac gac ctt acg gag       705
Thr Gln Arg Glu Leu Val Ser Arg Gln Val Ser Asn Asp Leu Thr Glu
                 85                  90                  95

caa gca gcc aca ttt ggg ctc atc ctg gac gac gtg tcc ttg aca tat       753
Gln Ala Ala Thr Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr
            100                 105                 110

ctg acc ttt gga aag gag ttc aca gaa gca gtg gaa gcc aaa cag gtg       801
Leu Thr Phe Gly Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val
        115                 120                 125

gct cag cag gaa gca gag agg gcc aga ttt gtg aag gaa aag gct gag       849
Ala Gln Gln Glu Ala Glu Arg Ala Arg Phe Val Lys Glu Lys Ala Glu
    130                 135                 140

cag cag aaa aag gct gag cag cag aaa aag gtt gag cag cag aaa aag       897
Gln Gln Lys Lys Ala Glu Gln Gln Lys Lys Val Glu Gln Gln Lys Lys
145                 150                 155                 160

gca gcc gtg atc tct gct gag ggc gac tcc aag gca acc gag ctg att       945
Ala Ala Val Ile Ser Ala Glu Gly Asp Ser Lys Ala Thr Glu Leu Ile
                165                 170                 175

gcc aac tca ctg gcc acc gcg ggg gac ggc ctg atg gag ctg tgc aag       993
Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Met Glu Leu Cys Lys
            180                 185                 190

ttg gaa gcc gcg gag gct ctc gga aca tga c ctacctgccg gcggggcagt      1044
Leu Glu Ala Ala Glu Ala Leu Gly Thr  *
        195                 200

ccgctcctcc ggctgcccca tgagggccca ccctgcctgc acctccgcag gctgactggg    1104

ccacagcccc aatgattctt aacactgcct tacccccta ccccagaaat cactgaaatt     1164

tcataattgg cttaaagtga aggaaataaa agtaaaatca cttcagaact cttaaaaaaa    1224

aaaaa                                                                1229
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     <210>  44
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     <213>  Homo sapiens

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atttggccct cgaggccaag aattcggcac gaggttcaga aatataagcc gtacaacaat     60

ggagctgcca atcaaaagtg gcattac    atg aaa aat ata aaa gca ctt gtg     111
                                 Met Lys Asn Ile Lys Ala Leu Val
                                   1               5

gcc ttt cat agc act gcc ttg gat aag gaa att aca tca gca aat tat      159
Ala Phe His Ser Thr Ala Leu Asp Lys Glu Ile Thr Ser Ala Asn Tyr
     10                  15                  20

gct ggt gtc tgt aca tca tct gtg att aaa gaa gaa aac att gat caa      207
Ala Gly Val Cys Thr Ser Ser Val Ile Lys Glu Glu Asn Ile Asp Gln
 25                  30                  35                  40

cca gga tac tgt tat ctc tca cct gat gga aag aga aaa act atg ctc      255
Pro Gly Tyr Cys Tyr Leu Ser Pro Asp Gly Lys Arg Lys Thr Met Leu
                 45                  50                  55

tgc ttg gct tgt gga caa tcc atg aga aca gag aaa gga ctg aaa caa      303
Cys Leu Ala Cys Gly Gln Ser Met Arg Thr Glu Lys Gly Leu Lys Gln
             60                  65                  70

ttg ctt cca ggg gtt cca ttc ctc tgt att tca ggc acc aag act cag      351
Leu Leu Pro Gly Val Pro Phe Leu Cys Ile Ser Gly Thr Lys Thr Gln
         75                  80                  85

aag ccc ttc tta caa ggg ccc ttc aag gtc atc agt gtg gct gag gtt      399
Lys Pro Phe Leu Gln Gly Pro Phe Lys Val Ile Ser Val Ala Glu Val
     90                  95                 100

gat ttg tcg tgt gac aag gct gaa aaa act cta agt tac tac caa gca      447
Asp Leu Ser Cys Asp Lys Ala Glu Lys Thr Leu Ser Tyr Tyr Gln Ala
105                 110                 115                 120

cgt cta ttg tct tta cgg atg aag acc tgc acg caa gct gca tct cac      495
Arg Leu Leu Ser Leu Arg Met Lys Thr Cys Thr Gln Ala Ala Ser His
                125                 130                 135

agt ggc atg gca gcc aca cac cag aag gca gtg aaa ata att gca tac      543
Ser Gly Met Ala Ala Thr His Gln Lys Ala Val Lys Ile Ile Ala Tyr
            140                 145                 150

aaa aat ggg gat ggg tat cgt aat ggg aag tta att gtg gct gga aca      591
Lys Asn Gly Asp Gly Tyr Arg Asn Gly Lys Leu Ile Val Ala Gly Thr
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        155                 160                 165

ttc ccc atg ctt ctt aca gaa tgc acg gaa caa ctt ggg ctt gcc aga       639
Phe Pro Met Leu Leu Thr Glu Cys Thr Glu Gln Leu Gly Leu Ala Arg
    170                 175                 180

gca gcc tcc aaa gta tat acc aaa gat gga acc cca atc ttt acc ttg       687
Ala Ala Ser Lys Val Tyr Thr Lys Asp Gly Thr Pro Ile Phe Thr Leu
185                 190                 195                 200

cgt gat ttg gtt tta tgg gct cta gat gaa tcc ttt ctc cag aga gac       735
Arg Asp Leu Val Leu Trp Ala Leu Asp Glu Ser Phe Leu Gln Arg Asp
                205                 210                 215

tct gag aaa caa aag caa gat gca gct cct gtt gga aaa gaa cag ata       783
Ser Glu Lys Gln Lys Gln Asp Ala Ala Pro Val Gly Lys Glu Gln Ile
            220                 225                 230

att gtt gaa agt atg gaa gaa aat cca aga atg aaa gtg aaa aac aga       831
Ile Val Glu Ser Met Glu Glu Asn Pro Arg Met Lys Val Lys Asn Arg
        235                 240                 245

tta ttt gca aaa tct gtg aca tcc gat agt ttg gat ggt ata gac aag       879
Leu Phe Ala Lys Ser Val Thr Ser Asp Ser Leu Asp Gly Ile Asp Lys
    250                 255                 260

tct ttg ctt acc ctc atc ctc aga aat cct att gcc atc tgg gtg tct       927
Ser Leu Leu Thr Leu Ile Leu Arg Asn Pro Ile Ala Ile Trp Val Ser
265                 270                 275                 280

tgt ggt gaa cca ttt cta cct cca aat gct ttg cag aaa gca gaa aaa       975
Cys Gly Glu Pro Phe Leu Pro Pro Asn Ala Leu Gln Lys Ala Glu Lys
                285                 290                 295

tta gag aaa cag aac tgg cta aaa aag gac aga att ttg gct gat cta      1023
Leu Glu Lys Gln Asn Trp Leu Lys Lys Asp Arg Ile Leu Ala Asp Leu
            300                 305                 310

gat acc atg aga cac aaa atg aga cag tta aaa ggg cgg cga gta gcg      1071
Asp Thr Met Arg His Lys Met Arg Gln Leu Lys Gly Arg Arg Val Ala
        315                 320                 325

gca tgt cag cca gcc acc atg gtt cct acc aag agc cct gtg cag ccc      1119
Ala Cys Gln Pro Ala Thr Met Val Pro Thr Lys Ser Pro Val Gln Pro
    330                 335                 340

gtg gtg gtt gaa gga ggc tgg acc gaa cag act caa cag gaa att aaa      1167
Val Val Val Glu Gly Gly Trp Thr Glu Gln Thr Gln Gln Glu Ile Lys
345                 350                 355                 360

ctc atg gaa ctt ata aga cat aca gag gca cac ctt tct gaa atc caa      1215
Leu Met Glu Leu Ile Arg His Thr Glu Ala His Leu Ser Glu Ile Gln
                365                 370                 375

gaa atg gaa tcc aaa ata aat ttt cca att gca acc aaa cgt ata gca      1263
Glu Met Glu Ser Lys Ile Asn Phe Pro Ile Ala Thr Lys Arg Ile Ala
            380                 385                 390
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gtc aag ccg agc aac ctg tat aag cag ccc aac aca aaa cga gtg tgg     1311
Val Lys Pro Ser Asn Leu Tyr Lys Gln Pro Asn Thr Lys Arg Val Trp
        395                 400                 405

att tat cta aat gga ggc aga cct gaa gat ggc act tat gcc tgg ggc     1359
Ile Tyr Leu Asn Gly Gly Arg Pro Glu Asp Gly Thr Tyr Ala Trp Gly
    410                 415                 420

aaa act att tca gag ctg ctg caa gac tgc tcc tct cgt ctc aaa atg     1407
Lys Thr Ile Ser Glu Leu Leu Gln Asp Cys Ser Ser Arg Leu Lys Met
425                 430                 435                 440

acc cac cca gct aga gca ctg tac acc ccc agt gga gag cca att cag     1455
Thr His Pro Ala Arg Ala Leu Tyr Thr Pro Ser Gly Glu Pro Ile Gln
                445                 450                 455

tcc tgg gac gac ata gag cga gat atg gtc atc tgt gtg tct atg gga     1503
Ser Trp Asp Asp Ile Glu Arg Asp Met Val Ile Cys Val Ser Met Gly
            460                 465                 470

cat ggt ttc aaa acc cca aaa gag tta aaa caa ctg atg gag atc aga     1551
His Gly Phe Lys Thr Pro Lys Glu Leu Lys Gln Leu Met Glu Ile Arg
        475                 480                 485

gca aat tat gcc aga atc cga agg cag cag ggc cct caa gcc aca gac     1599
Ala Asn Tyr Ala Arg Ile Arg Arg Gln Gln Gly Pro Gln Ala Thr Asp
    490                 495                 500

att gtg gtg tca cca tcc acg aag ctg ctg tct ctg gca cat ctc cac     1647
Ile Val Val Ser Pro Ser Thr Lys Leu Leu Ser Leu Ala His Leu His
505                 510                 515                 520

aat taa ctcctatcag aaccatcgga ttttctgctg tatttttctg gaaagaaaac      1703
Asn  *

tttctttacc cacttataaa cagaagactg tgacaagaag gccaattatt tccatcgctg   1763

aagactctaa atttggcaaa tcttctaaat aacaatcctg catagtttat taaaaaaaat   1823

tagtcgtaaa atttatcctt caaaaatctg cattttaaat aaaccctgac agtgatttct   1883

caagactgta aagatattag tctgagaatg caactctaac agactgctct gggcatcttt   1943

tctctttgcc ttggccaggc ctctcagaat tgagtgagcg tgtgactcca tttgcacagt   2003

gggacagata gtacaactga aataaaaagt ggaggcctct gcaaaaaata aaaaataaaa   2063

aataaattta tccttcaaaa taactcagtt ttttcaatgg gcctattttt aagaatgaac   2123

attgaaaaat gagacaatat atccataaat tcatagtatg acataccata              2173


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     <222> (186)..(929)

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caacgctggc aagtctcaaa gtcgccacag aaacatgccc ctgattcagt gcctctgctt     120

agctgtaaca tgttaatcag aactacctgg catcttcctg aacaagactt tcaatagggg     180

ccagt    atg ctt cgc ttc atc cag aag ttt tct caa gca tct tca aag      227
         Met Leu Arg Phe Ile Gln Lys Phe Ser Gln Ala Ser Ser Lys
           1               5                  10

ata ctg aag tac tct ttc cca gtg gga cta aga acc agc aga aca gat      275
Ile Leu Lys Tyr Ser Phe Pro Val Gly Leu Arg Thr Ser Arg Thr Asp
 15                  20                  25                  30

ata ctt tct ctc aag atg tct ctc cag caa aac ttt tcc cca tgt cca      323
Ile Leu Ser Leu Lys Met Ser Leu Gln Gln Asn Phe Ser Pro Cys Pro
                 35                  40                  45

agg cct tgg ctt tcc tca tca ttt cca gcg tat atg agc aag aca cag      371
Arg Pro Trp Leu Ser Ser Ser Phe Pro Ala Tyr Met Ser Lys Thr Gln
             50                  55                  60

tgc tat cat aca tcc ccc tgc agc ttt aaa aag cag cag aag caa gca      419
Cys Tyr His Thr Ser Pro Cys Ser Phe Lys Lys Gln Gln Lys Gln Ala
         65                  70                  75

ctt cta gcc aga ccc tca agc acc atc act tac cta act gac agc cca      467
Leu Leu Ala Arg Pro Ser Ser Thr Ile Thr Tyr Leu Thr Asp Ser Pro
     80                  85                  90

aag cca gca tta tgt gta act ctg gca gga cta atc ccc ttc gtt gct      515
Lys Pro Ala Leu Cys Val Thr Leu Ala Gly Leu Ile Pro Phe Val Ala
 95                 100                 105                 110

cca cca ctg gtc atg ctg atg aca aaa act tat att ccc ata tta gct      563
Pro Pro Leu Val Met Leu Met Thr Lys Thr Tyr Ile Pro Ile Leu Ala
                115                 120                 125

ttt act cag atg gct tat gga gcc agt ttc cta tct ttc ttg ggt ggg      611
Phe Thr Gln Met Ala Tyr Gly Ala Ser Phe Leu Ser Phe Leu Gly Gly
            130                 135                 140

atc aga tgg ggt ttt gct cta cca gaa ggt agt cca gcc aaa cca gac      659
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```
Ile Arg Trp Gly Phe Ala Leu Pro Glu Gly Ser Pro Ala Lys Pro Asp
        145                 150                 155

tac ctt aat tta gct agc agt gca gct cct ctt ttc ttt tca tgg ttt      707
Tyr Leu Asn Leu Ala Ser Ser Ala Ala Pro Leu Phe Phe Ser Trp Phe
    160                 165                 170

gcc ttc ctt att tct gaa aga ctt agt gaa gcc ata gtc aca gta ata      755
Ala Phe Leu Ile Ser Glu Arg Leu Ser Glu Ala Ile Val Thr Val Ile
175                 180                 185                 190

atg ggt atg gga gta gca ttc cac ctt gaa ctt ttt ctc tta cca cat      803
Met Gly Met Gly Val Ala Phe His Leu Glu Leu Phe Leu Leu Pro His
                195                 200                 205

tat ccc aac tgg ttt aaa gcc ctg agg ata gta gtc act tta ttg gcc      851
Tyr Pro Asn Trp Phe Lys Ala Leu Arg Ile Val Val Thr Leu Leu Ala
            210                 215                 220

act ttt tca ttt ata atc act tta gta gtt aaa agt agt ttt cca gaa      899
Thr Phe Ser Phe Ile Ile Thr Leu Val Val Lys Ser Ser Phe Pro Glu
        225                 230                 235

aaa gga cat aag aga cct ggt caa gta taa a aaatataaaa gtctgggaag      950
Lys Gly His Lys Arg Pro Gly Gln Val  *
    240                 245

tgaggagcac ctctgcccag ctgctgcccc gtctgggaag tgaggagcgc ctctgcctgg   1010

ccgcctgacc atctgggaag tgtgacaagc gcctctgccc ggccgctgtg caaccttcca   1070

cgtgtgaagt gacagccttg tgtgtgatct ttctgtcttc ccccaagttt gcattttcga   1130

cattaaagtt tactttttag ttaaaagttt aaaaaatata tataaataca ctgtagagan   1190

aacatgtgtn tgccagctac acctttctcn acttctgttt ggcttttttt ccccacacca   1250

atggtaattt atcttcacag atngttcttc atttctagaa attgttactt catggtaatt   1310

acttgagcaa aagcttgaaa atccctgaca agtacttntc atctcatagt atattagttt   1370

tcactcagtc attttatgaa taatanagtt atccacttaa acatttcaat aatgtaacca   1430

gc                                                                  1432


<210> 46
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<212> DNA
<213> Homo sapiens

<220>
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<222> (269)..(1372)
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cggaggggca gtcgggggaa ccgcgaagaa gccgaggagc ccggagcccc gcgtgacgct     120

cctctctcag tccaaaagcg gcttttggtt cggcgcagag agacccgggg gtctagcttt     180

tcctcgaaaa gcgccgccct gcccttggcc ccgagaacag acaaagagca ccgcagggcc     240

gatcacgctg ggggcgctga ggccggcc   atg gtc atg gaa gtg ggc acc ctg      292
                                 Met Val Met Glu Val Gly Thr Leu
                                   1               5

gac gct gga ggc ctg cgg gcg ctg ctg ggg gag cga gcg gcg caa tgc      340
Asp Ala Gly Gly Leu Arg Ala Leu Leu Gly Glu Arg Ala Ala Gln Cys
     10                  15                  20

ctg ctg ctg gac tgc cgc tcc ttc ttc gct ttc aac gcc ggc cac atc      388
Leu Leu Leu Asp Cys Arg Ser Phe Phe Ala Phe Asn Ala Gly His Ile
 25                  30                  35                  40

gcc ggc tct gtc aac gtg cgc ttc agc acc atc gtg cgg cgc cgg gcc      436
Ala Gly Ser Val Asn Val Arg Phe Ser Thr Ile Val Arg Arg Arg Ala
                 45                  50                  55

aag ggc gcc atg ggc ctg gag cac atc gtg ccc aac gcc gag ctc cgc      484
Lys Gly Ala Met Gly Leu Glu His Ile Val Pro Asn Ala Glu Leu Arg
             60                  65                  70

ggc cgc ctg ctg gcc ggc gcc tac cac gcc gtg gtg ttg ctg gac gag      532
Gly Arg Leu Leu Ala Gly Ala Tyr His Ala Val Val Leu Leu Asp Glu
         75                  80                  85

cgc agc gcc gcc ctg gac ggc gcc aag cgc gac ggc acc ctg gcc ctg      580
Arg Ser Ala Ala Leu Asp Gly Ala Lys Arg Asp Gly Thr Leu Ala Leu
     90                  95                 100

gcg gcc ggc gcg ctc tgc cgc gag gcg cgc gcc gcg caa gtc ttc ttc      628
Ala Ala Gly Ala Leu Cys Arg Glu Ala Arg Ala Ala Gln Val Phe Phe
105                 110                 115                 120

ctc aaa gga gga tac gaa gcg ttt tcg gct tcc tgc ccg gag ctg tgc      676
Leu Lys Gly Gly Tyr Glu Ala Phe Ser Ala Ser Cys Pro Glu Leu Cys
                125                 130                 135

agc aaa cag tcg acc ccc atg ggg ctc agc ctt ccc ctg agt act agc      724
Ser Lys Gln Ser Thr Pro Met Gly Leu Ser Leu Pro Leu Ser Thr Ser
            140                 145                 150

gtc cct gac agc gcg gaa tct ggg tgc agt tcc tgc agt acc cca ctc      772
Val Pro Asp Ser Ala Glu Ser Gly Cys Ser Ser Cys Ser Thr Pro Leu
        155                 160                 165

tac gat cag ggt ggc ccg gtg gaa atc ctg ccc ttt ctg tac ctg ggc      820
Tyr Asp Gln Gly Gly Pro Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly
    170                 175                 180
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agt gcg tat cac gct tcc cgc aag gac atg ctg gat gcc ttg ggc ata        868
Ser Ala Tyr His Ala Ser Arg Lys Asp Met Leu Asp Ala Leu Gly Ile
185                 190                 195                 200

act gcc ttg atc aac gtc tca gcc aat tgt ccc aac cat ttt gag ggt        916
Thr Ala Leu Ile Asn Val Ser Ala Asn Cys Pro Asn His Phe Glu Gly
                205                 210                 215

cac tac cag tac aag agc atc cct gtg gag gac aac cac aag gca gac        964
His Tyr Gln Tyr Lys Ser Ile Pro Val Glu Asp Asn His Lys Ala Asp
            220                 225                 230

atc agc tcc tgg ttc aac gag gcc att gac ttc ata gac tcc atc aag       1012
Ile Ser Ser Trp Phe Asn Glu Ala Ile Asp Phe Ile Asp Ser Ile Lys
        235                 240                 245

aat gct gga gga agg gtg ttt gtc cac tgc cag gca ggc att tcc cgg       1060
Asn Ala Gly Gly Arg Val Phe Val His Cys Gln Ala Gly Ile Ser Arg
    250                 255                 260

tca gcc acc atc tgc ctt gct tac ctt atg agg act aat cga gtc aag       1108
Ser Ala Thr Ile Cys Leu Ala Tyr Leu Met Arg Thr Asn Arg Val Lys
265                 270                 275                 280

ctg gac gag gcc ttt gag ttt gtg aag cag agg cga agc atc atc tct       1156
Leu Asp Glu Ala Phe Glu Phe Val Lys Gln Arg Arg Ser Ile Ile Ser
                285                 290                 295

ccc aac ttc agc ttc atg ggc cag ctg ctg cag ttt gag tcc cag gtg       1204
Pro Asn Phe Ser Phe Met Gly Gln Leu Leu Gln Phe Glu Ser Gln Val
            300                 305                 310

ctg gct ccg cac tgt tcg gca gag gct ggg agc ccc gcc atg gct gtg       1252
Leu Ala Pro His Cys Ser Ala Glu Ala Gly Ser Pro Ala Met Ala Val
        315                 320                 325

ctc gac cga ggc acc tcc acc acc acc gtg ttc aac ttc ccc gtc tcc       1300
Leu Asp Arg Gly Thr Ser Thr Thr Thr Val Phe Asn Phe Pro Val Ser
    330                 335                 340

atc cct gtc cac tcc acg aac agt gcg ctg agc tac ctt cag agc ccc       1348
Ile Pro Val His Ser Thr Asn Ser Ala Leu Ser Tyr Leu Gln Ser Pro
345                 350                 355                 360

att acg acc tct ccc agc tgc tga aaggccacgg gaggtgaggc tcttcacatc      1402
Ile Thr Thr Ser Pro Ser Cys  *
                365

ccattgggac tccatgctcc ttgagaggag aaatgcaata actctgggag gggctcgaga     1462

gggctggtcc ttatttattt aacttcaccc gagttcctct gggtttctaa gcagttatgg     1522

tgatgactta gcgtcaagac atttgctgaa ctcagcacat tcgggaccaa tatatagtgg     1582

gtacatcaag tccatctgac aaaatggggc agaagagaaa ggactcagtg tgtgatccgg     1642

tttcttttttg ctcgcccctg ttttttgtag aatctcttca tgcttgacat acctaccagt    1702
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attattcccg acgacacata tacatatgag aatatacctt atttattttt gtgtaggtgt    1762

ctgccttcac aaatgtcatt gtctactcct agaagaacca aatacctcaa tttttgtttt    1822

tgagtactgt actatcctgt aaatatatct taagcaggtt tgttttcagc actgatggaa    1882

aataccagtg ttgggttttt ttttagttgc caacagttgt atgtttgctg attatttatg    1942

acctgaaata atatatttct tcttctaaga agacattttg ttacataagg atgacttttt    2002

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cattatgatg tgtttatgtt cacagaaatt tttgtaattt ctctatggta acaacttttt     180

atgccttaag agtgtctctg aggcaggatt ctaagagatt ctctttgact caatcccaga     240

tagaggataa atctcctggc aaagcccaga atg acc aca gcc ctg gaa cct         291
                                 Met Thr Thr Ala Leu Glu Pro
                                  1               5

gag gac caa aaa gga ctt ctg ata att aag gca gag gac cat tac tgg      339
Glu Asp Gln Lys Gly Leu Leu Ile Ile Lys Ala Glu Asp His Tyr Trp
        10                  15                  20

gga cag gat tcc agc tca caa aag tgc agt cct cac agg agg gaa ctc      387
Gly Gln Asp Ser Ser Ser Gln Lys Cys Ser Pro His Arg Arg Glu Leu
    25                  30                  35

tat aga caa cac ttc agg aag ctc tgc tat cag gat gca cct gga ccc      435
Tyr Arg Gln His Phe Arg Lys Leu Cys Tyr Gln Asp Ala Pro Gly Pro
40                  45                  50                  55

cgt gaa gct ctt acc cag ctg tgg gag ctc tgc cgt cag tgg ctg agg      483
Arg Glu Ala Leu Thr Gln Leu Trp Glu Leu Cys Arg Gln Trp Leu Arg
                60                  65                  70

cca gaa tgc cac acc aag gag cag att tta gac ctg ctg gtg cta gaa      531
Pro Glu Cys His Thr Lys Glu Gln Ile Leu Asp Leu Leu Val Leu Glu
            75                  80                  85
```

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cag ttc ctg agc att ctt cct aaa gac ctg caa gca tgg gtg cgt gca        579
Gln Phe Leu Ser Ile Leu Pro Lys Asp Leu Gln Ala Trp Val Arg Ala
         90                  95                 100

cac cat cca gag act gga gag gag gca gtg acg gta ctg gag gat ctg        627
His His Pro Glu Thr Gly Glu Glu Ala Val Thr Val Leu Glu Asp Leu
    105                 110                 115

gag aga gag ctt gat gaa cct gga aag cag gtc cca ggc aat tca gaa        675
Glu Arg Glu Leu Asp Glu Pro Gly Lys Gln Val Pro Gly Asn Ser Glu
120                 125                 130                 135

aga cgg gac ata ctc atg gac aag ttg gcc ccc ttg gga agg cca tat        723
Arg Arg Asp Ile Leu Met Asp Lys Leu Ala Pro Leu Gly Arg Pro Tyr
                140                 145                 150

gaa tca ctg act gtc cag ctc cat ccc aaa aag acc cag ctg gag cag        771
Glu Ser Leu Thr Val Gln Leu His Pro Lys Lys Thr Gln Leu Glu Gln
            155                 160                 165

gaa gct ggg aaa cca caa agg aat ggt gat aaa act agg act aag aat        819
Glu Ala Gly Lys Pro Gln Arg Asn Gly Asp Lys Thr Arg Thr Lys Asn
        170                 175                 180

gaa gag ttg ttc cag aag gaa gat atg ccc aaa gac aag gaa ttc ctt        867
Glu Glu Leu Phe Gln Lys Glu Asp Met Pro Lys Asp Lys Glu Phe Leu
    185                 190                 195

ggg gag ata aat gac aga ctg aac aaa gat act cct cag cat cct aag        915
Gly Glu Ile Asn Asp Arg Leu Asn Lys Asp Thr Pro Gln His Pro Lys
200                 205                 210                 215

tcc aaa gat att att gaa aat gag ggc aga tca gaa tgg caa cag agg        963
Ser Lys Asp Ile Ile Glu Asn Glu Gly Arg Ser Glu Trp Gln Gln Arg
                220                 225                 230

gaa aga aga cga tat aaa tgt gat gaa tgt ggg aaa agt ttc agt cat       1011
Glu Arg Arg Arg Tyr Lys Cys Asp Glu Cys Gly Lys Ser Phe Ser His
            235                 240                 245

agc tca gac ctt agt aaa cac agg aga act cac acg gga gag aag ccc       1059
Ser Ser Asp Leu Ser Lys His Arg Arg Thr His Thr Gly Glu Lys Pro
        250                 255                 260

tat aaa tgt gat gag tgt gga aaa gcc ttc att cag cgc tca cat ctc       1107
Tyr Lys Cys Asp Glu Cys Gly Lys Ala Phe Ile Gln Arg Ser His Leu
    265                 270                 275

att gga cat cat aga gta cac acg gga gta aaa ccc tat aaa tgt aaa       1155
Ile Gly His His Arg Val His Thr Gly Val Lys Pro Tyr Lys Cys Lys
280                 285                 290                 295

gaa tgt ggg aaa gac ttc agt ggg cgc aca ggt ctt att cag cat cag       1203
Glu Cys Gly Lys Asp Phe Ser Gly Arg Thr Gly Leu Ile Gln His Gln
                300                 305                 310
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aga atc cac aca ggt gaa aaa ccc tat gaa tgt gat gag tgt gga agg     1251
Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asp Glu Cys Gly Arg
            315                 320                 325

cct ttc cga gta agt tca gct ctt att aga cat caa aga att cat acc     1299
Pro Phe Arg Val Ser Ser Ala Leu Ile Arg His Gln Arg Ile His Thr
        330                 335                 340

gca aat aaa ctc tac taa tatagc agtaatatca aaagttcttt ggacactcag     1353
Ala Asn Lys Leu Tyr  *
    345

gcctaactag ttatcaaaga atctatttta gaaaccttga gtttcctcaa tgtggtcaaa   1413

gcttcagtca tcattaaact tctctggacc aaaaaaaa                           1451
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actggaaaat taggggcctg tcgagcgatg ttggaagaag aaacagatca aacctatgag    120

aatgtcctgg ctgagattca gtctttcgaa ctgcctattg aagctacttt aagtcaacag    180

gaagagatac ctctttggtc aggaatgtaa aaacaggaag gaggaagtct attgcaaatc    240

tgtgctggct gattatgaat tcaggtttca ccatggagga tgttcatta    atg atc     295
                                                          Met Ile
                                                           1

atc agt gtg ctg tgc tgt tat tca aaa tta cag tct gtg tat gat gac      343
Ile Ser Val Leu Cys Cys Tyr Ser Lys Leu Gln Ser Val Tyr Asp Asp
        5                   10                  15

caa cca aat gcg cac aag aag ttt atg gaa aag tta gat gct tgt atc      391
Gln Pro Asn Ala His Lys Lys Phe Met Glu Lys Leu Asp Ala Cys Ile
    20                  25                  30

cgt aat cat gac aag gaa att gaa aag atg tgt aat ttt cat cat cag      439
Arg Asn His Asp Lys Glu Ile Glu Lys Met Cys Asn Phe His His Gln
35                  40                  45                  50

ggt ttt gta gat gct att aca gaa ctc ctt aaa gta agg act gat gca      487
Gly Phe Val Asp Ala Ile Thr Glu Leu Leu Lys Val Arg Thr Asp Ala
                55                  60                  65
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gaa aaa ctg aag gtg caa gtt act gat acc aac cga agg ttt caa gat      535
Glu Lys Leu Lys Val Gln Val Thr Asp Thr Asn Arg Arg Phe Gln Asp
             70                  75                  80

gct gga aaa gag gtg ata gtc cac aca gaa gat atc att cga tgt aga      583
Ala Gly Lys Glu Val Ile Val His Thr Glu Asp Ile Ile Arg Cys Arg
         85                  90                  95

att cag cag aga aat att aca act gta gta gaa aaa ttg cag tta tgc      631
Ile Gln Gln Arg Asn Ile Thr Thr Val Val Glu Lys Leu Gln Leu Cys
    100                 105                 110

ctt cct gtg cta gaa atg tac agt aag ctg aaa gaa cag atg agt gcc      679
Leu Pro Val Leu Glu Met Tyr Ser Lys Leu Lys Glu Gln Met Ser Ala
115                 120                 125                 130

aaa agg tac tat tct gcc cta aaa act atg gaa caa tta gag aat gtg      727
Lys Arg Tyr Tyr Ser Ala Leu Lys Thr Met Glu Gln Leu Glu Asn Val
                135                 140                 145

tac ttt ccc tgg gtt agt caa tac cgg ttt tgt cag ctc atg ata gaa      775
Tyr Phe Pro Trp Val Ser Gln Tyr Arg Phe Cys Gln Leu Met Ile Glu
            150                 155                 160

aat ctt ccc aaa ctc cgt gag gat att aaa gaa atc tcc atg tct gat      823
Asn Leu Pro Lys Leu Arg Glu Asp Ile Lys Glu Ile Ser Met Ser Asp
        165                 170                 175

ctc aaa gac ttt ttg gaa agt att cga aaa cat tct gac aaa ata ggt      871
Leu Lys Asp Phe Leu Glu Ser Ile Arg Lys His Ser Asp Lys Ile Gly
    180                 185                 190

gaa aca gca atg aaa cag gca cag cat cag aaa acc ttc agt gtt tct      919
Glu Thr Ala Met Lys Gln Ala Gln His Gln Lys Thr Phe Ser Val Ser
195                 200                 205                 210

ctg cag aaa caa aat aaa atg aaa ttt ggg aaa aat atg tat ata aat      967
Leu Gln Lys Gln Asn Lys Met Lys Phe Gly Lys Asn Met Tyr Ile Asn
                215                 220                 225

cgt gat aga att cca gag gaa agg aat gaa act gta ttg aaa cat tca     1015
Arg Asp Arg Ile Pro Glu Glu Arg Asn Glu Thr Val Leu Lys His Ser
            230                 235                 240

ctt gaa gaa gag gat gag aat gaa gaa gag atc tta act gtt cag gat     1063
Leu Glu Glu Glu Asp Glu Asn Glu Glu Glu Ile Leu Thr Val Gln Asp
        245                 250                 255

ctt gtt gat ttt tcc cct gtt tat cga tgt ttg cac att tat tct gtt     1111
Leu Val Asp Phe Ser Pro Val Tyr Arg Cys Leu His Ile Tyr Ser Val
    260                 265                 270

ttg ggt gac gag gaa aca ttt gaa aac tat tat cga aaa caa aga aag     1159
Leu Gly Asp Glu Glu Thr Phe Glu Asn Tyr Tyr Arg Lys Gln Arg Lys
275                 280                 285                 290

aaa caa gca aga ctg gta ttg caa ccc cag tcg aat atg cat gaa aca     1207
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Lys Gln Ala Arg Leu Val Leu Gln Pro Gln Ser Asn Met His Glu Thr
                295                 300                 305

gtt gat ggc tat aga aga tat ttc act caa att gta ggg ttc ttt gtg      1255
Val Asp Gly Tyr Arg Arg Tyr Phe Thr Gln Ile Val Gly Phe Phe Val
            310                 315                 320

gta gaa gat cac att tta cat gtg acc caa gga tta gta acc agg gca      1303
Val Glu Asp His Ile Leu His Val Thr Gln Gly Leu Val Thr Arg Ala
        325                 330                 335

tac act gat gaa ctt tgg aac atg gcc ctc tca aag ata att gct gtc      1351
Tyr Thr Asp Glu Leu Trp Asn Met Ala Leu Ser Lys Ile Ile Ala Val
    340                 345                 350

ctt aga gct cat tca tcc tat tgc act gat cct gat ctt gtt ctg gag      1399
Leu Arg Ala His Ser Ser Tyr Cys Thr Asp Pro Asp Leu Val Leu Glu
355                 360                 365                 370

ctg aag aat ctt act gta ata ttt gca gat act tta cag ggt tat ggt      1447
Leu Lys Asn Leu Thr Val Ile Phe Ala Asp Thr Leu Gln Gly Tyr Gly
                375                 380                 385

ttt cca gtg aac cga ctt ttt gac ctt tta ttt gaa ata aga gac caa      1495
Phe Pro Val Asn Arg Leu Phe Asp Leu Leu Phe Glu Ile Arg Asp Gln
            390                 395                 400

tac aat gaa aca ctg ctt aag aaa tgg gct gga gtt ttc agg gac att      1543
Tyr Asn Glu Thr Leu Leu Lys Lys Trp Ala Gly Val Phe Arg Asp Ile
        405                 410                 415

ttt gaa gaa gat aat tac agc ccc atc cct gtt gtc aat gaa gaa gaa      1591
Phe Glu Glu Asp Asn Tyr Ser Pro Ile Pro Val Val Asn Glu Glu Glu
    420                 425                 430

tat aaa att gtc atc agc aaa ttt ccc ttt caa gat cca gac ctt gaa      1639
Tyr Lys Ile Val Ile Ser Lys Phe Pro Phe Gln Asp Pro Asp Leu Glu
435                 440                 445                 450

aag cag tct ttc cca aag aaa ttc ccc atg tct cag tca gtg cct cat      1687
Lys Gln Ser Phe Pro Lys Lys Phe Pro Met Ser Gln Ser Val Pro His
                455                 460                 465

att tac att caa gtt aaa gaa ttt att tat gcc agc ctt aaa ttt tca      1735
Ile Tyr Ile Gln Val Lys Glu Phe Ile Tyr Ala Ser Leu Lys Phe Ser
            470                 475                 480

gag tca cta cac cgg agc tca aca gaa ata gac gat atg ctt aga aaa      1783
Glu Ser Leu His Arg Ser Ser Thr Glu Ile Asp Asp Met Leu Arg Lys
        485                 490                 495

tca aca aat ctg ctg ctg acc aga act ttg agt agc tgt tta ctg aac      1831
Ser Thr Asn Leu Leu Leu Thr Arg Thr Leu Ser Ser Cys Leu Leu Asn
    500                 505                 510

ctt att aga aaa cct cat ata ggt ttg aca gag ctg gta caa atc atc      1879
Leu Ile Arg Lys Pro His Ile Gly Leu Thr Glu Leu Val Gln Ile Ile
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515                 520                 525                 530

ata aac aca aca cac ctg gag caa gct tgt aaa tat ctt gag gac ttt      1927
Ile Asn Thr Thr His Leu Glu Gln Ala Cys Lys Tyr Leu Glu Asp Phe
                535                 540                 545

ata act aac att aca aat att tcc caa gaa act gtt cat act aca aga      1975
Ile Thr Asn Ile Thr Asn Ile Ser Gln Glu Thr Val His Thr Thr Arg
            550                 555                 560

ctt tat gga ctt tct act ttc aag gat gct cga cat gca gca gaa gga      2023
Leu Tyr Gly Leu Ser Thr Phe Lys Asp Ala Arg His Ala Ala Glu Gly
        565                 570                 575

gaa ata tat acc aaa ctg aat caa aaa att gat gaa ttt gtt cag ctt      2071
Glu Ile Tyr Thr Lys Leu Asn Gln Lys Ile Asp Glu Phe Val Gln Leu
    580                 585                 590

gct gat tat gac tgg aca atg tct gag cca gat gga aga gct agt ggt      2119
Ala Asp Tyr Asp Trp Thr Met Ser Glu Pro Asp Gly Arg Ala Ser Gly
595                 600                 605                 610

tat tta atg gac ctt ata aat ttt ttg aga agc atc ttt caa gtg ttt      2167
Tyr Leu Met Asp Leu Ile Asn Phe Leu Arg Ser Ile Phe Gln Val Phe
                615                 620                 625

act cat ttg cct ggg aaa gtt gct cag aca gct tgc atg tca gcc tgc      2215
Thr His Leu Pro Gly Lys Val Ala Gln Thr Ala Cys Met Ser Ala Cys
            630                 635                 640

cag cat ctg tca aca tcc tta atg cag atg cta ctg gac agt gag tta      2263
Gln His Leu Ser Thr Ser Leu Met Gln Met Leu Leu Asp Ser Glu Leu
        645                 650                 655

aaa caa ata agc atg gga gct gtt cag cag ttt aac tta gat gtc ata      2311
Lys Gln Ile Ser Met Gly Ala Val Gln Gln Phe Asn Leu Asp Val Ile
    660                 665                 670

cag tgt gaa ttg ttt gcc agc tct gag cct gtg cca gga ttc cag ggg      2359
Gln Cys Glu Leu Phe Ala Ser Ser Glu Pro Val Pro Gly Phe Gln Gly
675                 680                 685                 690

gat acc ctg cag cta gca ttc att gac ctc aga caa ctc ctt gac ctg      2407
Asp Thr Leu Gln Leu Ala Phe Ile Asp Leu Arg Gln Leu Leu Asp Leu
                695                 700                 705

ttt atg gtt tgg gat tgg tct act tac cta gct gat tat ggg cag cca      2455
Phe Met Val Trp Asp Trp Ser Thr Tyr Leu Ala Asp Tyr Gly Gln Pro
            710                 715                 720

gct tct aag tac ctt cgg gtg aat cca aac aca gcc ctt act ctt ttg      2503
Ala Ser Lys Tyr Leu Arg Val Asn Pro Asn Thr Ala Leu Thr Leu Leu
        725                 730                 735

gag aag atg aag gat act agc aaa aag aac aat ata ttt gct cag ttc      2551
Glu Lys Met Lys Asp Thr Ser Lys Lys Asn Asn Ile Phe Ala Gln Phe
    740                 745                 750
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agg aag aat gat cga gac aaa cag aag ttg ata gag aca gtc gtg aaa      2599
Arg Lys Asn Asp Arg Asp Lys Gln Lys Leu Ile Glu Thr Val Val Lys
755                 760                 765                 770

cag ctg aga agt ttg gtg aat ggt atg tcc cag cac atg tag acctcac      2648
Gln Leu Arg Ser Leu Val Asn Gly Met Ser Gln His Met  *
                775                 780

atggcttgca ctcagtgaca ccaaatccat gattcaatgt tgatcttgag caagtattgg    2708

tcatgataca gtaatttgtt tacagaatcc aaaaatacaa tagagaagat acatgagggc    2768

ttaaacaaga aatagtaata aatatcattt gtatggattt ttaaataatc gaatactatt    2828

ttatatatgg aaaaaaatga ccattttttc acttttaggg gaaaatgcaa aagtgtaata    2888

cataaattgt cacaaattat acctgaaatt gattacaaat acatttgaaa aacatatgcc    2948

tctactcata agtatttttt tctatttaga cttgaatgat aatctgtttt ttgatcagta    3008

tatggctttg gaattcaatc atgtctgata tggtagtatt tcactaccat tttctgactt    3068

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taagaatgtg aattatttgt tctacttggg tggtttaatt taatcgttct gaatatgaac    3248

aaaaggtttt ggattttcta aagatgcagt gttgtttctg ttcatcaggg ttaatatttc    3308

taactatatt gcttgtaggt gaccccattc tggatttgtt tggtttggtt tggttccagt    3368

taaaagagag gacaggaact aaatggggct aaccacttca ggtgcagctt gtgcgagggt    3428

agatggttcc tgcacacaga agttaccaca ggggtcaggt tactttcttc aaatagcaga    3488

tttcagtact ttatcctcat tgtggaaaca agccaaacca aatgaactct ggaaaaccta    3548

aaacaaatgt acattttcct ttgtgtatgt ttctgtggtc caaatggcaa tataaatcca    3608

gtctttattc tccctttgtt gtatttatgc tgaatcttcc ctttgccttt tcaggattta    3668

ggcctgtaag aaactatgcc tgattctgta aaataagtgt aaagaattat atgtacatct    3728

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Lys Lys Glu Ala Pro Ala Pro Pro Lys Ala Glu Ala Lys Ala Lys Ala
                10                  15                  20

ttg caa ggc caa gaa ggc agt gtt gaa aga tgt cca cag cca caa aaa       151
Leu Gln Gly Gln Glu Gly Ser Val Glu Arg Cys Pro Gln Pro Gln Lys
            25                  30                  35

aaa caa gat cca cat gtc acc cac ctt ccg gcg gcc caa gac act gtg       199
Lys Gln Asp Pro His Val Thr His Leu Pro Ala Ala Gln Asp Thr Val
        40                  45                  50

act ccg gag gca gcc caa ata tcc ttg gaa gag cac ccc cag gag aaa       247
Thr Pro Glu Ala Ala Gln Ile Ser Leu Glu Glu His Pro Gln Glu Lys
    55                  60                  65

taa gctt gaccaccatg ttatcatcaa gtttccgctg accactgagt aggctgtgaa       304
 *
 70

gaagatagaa aacaacagcc tacttgtgtt cactgtggat gttaaagcca acaagcacca    364

gatcaaacag gctgtgaaga agtttgtgac attgatgtgg ccaaagtcaa cactctgatt    424

cagtctgatg gagagaggaa ggcatatgtt cgactggctc ctgactacga tgctttggtt    484

gttgccacca aaattgggat cacctaaact gagtcaagct ggctaattcc aaatatatgt    544

atatcttttc accattaaaa gaatcttaat ctctcaaaaa aaaaaaa                  591



<210> 50
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<213> Homo sapiens

<220>
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<222> (150)..(2729)

<400> 50
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actgacttgt ccatttgcta agcttcatcc caccgggcaa ttttcctgca cagcagccct    120

cggccccgga gcccctcggc ggcgccacc  atg tac tcg gga gcc ggc ccc gca     173
                                 Met Tyr Ser Gly Ala Gly Pro Ala
                                  1               5
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ctt gca cct cct gcg ccg ccg ccc ccc atc caa gga tat gcc ttc aag      221
Leu Ala Pro Pro Ala Pro Pro Pro Pro Ile Gln Gly Tyr Ala Phe Lys
     10                  15                  20

cct cca cct aga ccc gac ttt ggg acc tcc ggg aga aca atc aaa tta      269
Pro Pro Pro Arg Pro Asp Phe Gly Thr Ser Gly Arg Thr Ile Lys Leu
 25                  30                  35                  40

cag gcc aat ttc ttc gaa atg gac atc ccc aaa att gac atc tat cat      317
Gln Ala Asn Phe Phe Glu Met Asp Ile Pro Lys Ile Asp Ile Tyr His
                 45                  50                  55

tat gaa ttg gat atc aag cca gag aag tgc ccg agg aga gtt aac agg      365
Tyr Glu Leu Asp Ile Lys Pro Glu Lys Cys Pro Arg Arg Val Asn Arg
             60                  65                  70

gaa atc gtg gaa cac atg gtc cag cac ttt aaa aca cag atc ttt ggg      413
Glu Ile Val Glu His Met Val Gln His Phe Lys Thr Gln Ile Phe Gly
         75                  80                  85

gat cgg aag ccc gtg ttt gac ggc agg aag aat cta tac aca gcc atg      461
Asp Arg Lys Pro Val Phe Asp Gly Arg Lys Asn Leu Tyr Thr Ala Met
     90                  95                 100

ccc ctt ccg att ggg agg gac aag gtg gag ctg gag gtc acg ctg cca      509
Pro Leu Pro Ile Gly Arg Asp Lys Val Glu Leu Glu Val Thr Leu Pro
105                 110                 115                 120

gga gaa ggc aag gat cgc atc ttc aag gtg tcc atc aag tgg gtg tcc      557
Gly Glu Gly Lys Asp Arg Ile Phe Lys Val Ser Ile Lys Trp Val Ser
                125                 130                 135

tgc gtg agc ttg cag gcg tta cac gat gca ctt tca ggg cgg ctg ccc      605
Cys Val Ser Leu Gln Ala Leu His Asp Ala Leu Ser Gly Arg Leu Pro
            140                 145                 150

agc gtc cct ttt gag acg atc cag gcc ctg gac gtg gtc atg agg cac      653
Ser Val Pro Phe Glu Thr Ile Gln Ala Leu Asp Val Val Met Arg His
        155                 160                 165

ttg cca tcc atg agg tac acc ccc gtg ggc cgc tcc ttc ttc acc gcg      701
Leu Pro Ser Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Thr Ala
    170                 175                 180

tcc gaa ggc tgc tct aac cct ctt ggc ggg ggc cga gaa gtg tgg ttt      749
Ser Glu Gly Cys Ser Asn Pro Leu Gly Gly Gly Arg Glu Val Trp Phe
185                 190                 195                 200

ggc ttc cat cag tcc gtc cgg cct tct ctc tgg aaa atg atg ctg aat      797
Gly Phe His Gln Ser Val Arg Pro Ser Leu Trp Lys Met Met Leu Asn
                205                 210                 215

att gat gtg tca gca aca gcg ttt tac aag gca cag cca gta atc gag      845
Ile Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu
            220                 225                 230
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ttt gtt tgt gaa gtt ttg gat ttt aaa agt att gaa gaa caa caa aaa       893
Phe Val Cys Glu Val Leu Asp Phe Lys Ser Ile Glu Glu Gln Gln Lys
        235                 240                 245

cct ctg aca gat tcc caa agg gta aag ttt acc aaa gaa att aaa ggt       941
Pro Leu Thr Asp Ser Gln Arg Val Lys Phe Thr Lys Glu Ile Lys Gly
    250                 255                 260

cta aag gtg gag ata acg cac tgt ggg cag atg aag agg aag tac cgt       989
Leu Lys Val Glu Ile Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg
265                 270                 275                 280

gtc tgc aat gtg acc cgg cgg ccc gcc agt cac caa aca ttc ccg ctg      1037
Val Cys Asn Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu
                285                 290                 295

cag cag gag agc ggg cag acg gtg gag tgc acg gtg gcc cag tat ttc      1085
Gln Gln Glu Ser Gly Gln Thr Val Glu Cys Thr Val Ala Gln Tyr Phe
            300                 305                 310

aag gac agg cac aag ttg gtt ctg cgc tac ccc cac ctc cca tgt tta      1133
Lys Asp Arg His Lys Leu Val Leu Arg Tyr Pro His Leu Pro Cys Leu
        315                 320                 325

caa gtc gga cag gag cag aaa cac acc tac ctt ccc ctg gag gtc tgt      1181
Gln Val Gly Gln Glu Gln Lys His Thr Tyr Leu Pro Leu Glu Val Cys
    330                 335                 340

aac att gtg gca gga caa aga tgt att aaa aaa tta acg gac aat cag      1229
Asn Ile Val Ala Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Asn Gln
345                 350                 355                 360

acc tca acc atg atc aga gcg act gct agg tcg gcg ccc gat cgg caa      1277
Thr Ser Thr Met Ile Arg Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln
                365                 370                 375

gaa gag att agc aaa ttg atg cga agt gca agt ttc aac aca gat cca      1325
Glu Glu Ile Ser Lys Leu Met Arg Ser Ala Ser Phe Asn Thr Asp Pro
            380                 385                 390

tac gtc cgt gaa ttt gga atc atg gtc aaa gat gag atg aca gac gtg      1373
Tyr Val Arg Glu Phe Gly Ile Met Val Lys Asp Glu Met Thr Asp Val
        395                 400                 405

act ggg cgg gtg ctg cag ccg ccc tcc atc ctc tac ggg ggc agg aat      1421
Thr Gly Arg Val Leu Gln Pro Pro Ser Ile Leu Tyr Gly Gly Arg Asn
    410                 415                 420

aaa gct att gcg acc cct gtc cag ggc gtc tgg gac atg cgg aac aag      1469
Lys Ala Ile Ala Thr Pro Val Gln Gly Val Trp Asp Met Arg Asn Lys
425                 430                 435                 440

cag ttc cac acg ggc atc gag atc aag gtg tgg gcc att gcg tgc ttc      1517
Gln Phe His Thr Gly Ile Glu Ile Lys Val Trp Ala Ile Ala Cys Phe
                445                 450                 455

gcc ccc cag cgc cag tgc acg gaa gtc cat ctg aag tcc ttc aca gag      1565
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Ala Pro Gln Arg Gln Cys Thr Glu Val His Leu Lys Ser Phe Thr Glu
            460                 465                 470

cag ctc aga aag atc tcg aga gac gcc ggc atg ccc atc cag ggc cag      1613
Gln Leu Arg Lys Ile Ser Arg Asp Ala Gly Met Pro Ile Gln Gly Gln
        475                 480                 485

ccg tgc ttc tgc aaa tac gcg cag ggg gcg gac agc gtg gag ccc atg      1661
Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro Met
    490                 495                 500

ttc cgg cac ctg aag aac acg tat gcg ggc ctg cag ctg gtg gtg gtc      1709
Phe Arg His Leu Lys Asn Thr Tyr Ala Gly Leu Gln Leu Val Val Val
505                 510                 515                 520

atc ctg ccc ggc aag acg ccc gtg tac gcc gag gtc aag cgc gtg gga      1757
Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val Gly
                525                 530                 535

gac acg gtg ctg ggg atg gcc acg cag tgc gtg cag atg aag aac gtg      1805
Asp Thr Val Leu Gly Met Ala Thr Gln Cys Val Gln Met Lys Asn Val
            540                 545                 550

cag agg acc acg cca cag acc ctg tcc aac ctc tgc ctg aag atc aac      1853
Gln Arg Thr Thr Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile Asn
        555                 560                 565

gtc aag ctg gga ggc gtg aac aac atc ctg ctg ccc cag ggc agg ccg      1901
Val Lys Leu Gly Gly Val Asn Asn Ile Leu Leu Pro Gln Gly Arg Pro
    570                 575                 580

ccg gtg ttc cag cag ccc gtc atc ttt ctg gga gca gac gtc act cac      1949
Pro Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr His
585                 590                 595                 600

ccc ccc gcc ggg gat ggg aag aag ccc tcc att gcc gcc gtg gtg ggc      1997
Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val Gly
                605                 610                 615

agc atg gac gcc cac ccc aat cgc tac tgc gcc acc gtg cgt gtg cag      2045
Ser Met Asp Ala His Pro Asn Arg Tyr Cys Ala Thr Val Arg Val Gln
            620                 625                 630

cag cac cgg cag gag atc ata caa gac ctg gcc gcc atg gtc cgc gag      2093
Gln His Arg Gln Glu Ile Ile Gln Asp Leu Ala Ala Met Val Arg Glu
        635                 640                 645

ctc ctc atc cag ttc tac aag tcc acg cgc ttc aag ccc acc cgc atc      2141
Leu Leu Ile Gln Phe Tyr Lys Ser Thr Arg Phe Lys Pro Thr Arg Ile
    650                 655                 660

atc ttc tac cgc gac ggt gtc tct gaa ggc cag ttc cag cag gtt ctc      2189
Ile Phe Tyr Arg Asp Gly Val Ser Glu Gly Gln Phe Gln Gln Val Leu
665                 670                 675                 680

cac cac gag ttg ctg gcc atc cgt gag gcc tgt atc aag cta gaa aaa      2237
His His Glu Leu Leu Ala Ile Arg Glu Ala Cys Ile Lys Leu Glu Lys
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                685                 690                 695

gac tac cag ccc ggg atc acc ttc atc gtg gtg cag aag agg cac cac      2285
Asp Tyr Gln Pro Gly Ile Thr Phe Ile Val Val Gln Lys Arg His His
            700                 705                 710

acc cgg ctc ttc tgc act gac aag aac gag cgg gtt ggg aaa agt gga      2333
Thr Arg Leu Phe Cys Thr Asp Lys Asn Glu Arg Val Gly Lys Ser Gly
        715                 720                 725

aac att cca gca ggc acg act gtg gac acg aaa atc acc cac ccc acc      2381
Asn Ile Pro Ala Gly Thr Thr Val Asp Thr Lys Ile Thr His Pro Thr
    730                 735                 740

gag ttc gac ttc tac ctg tgt agt cac gct ggc atc cag ggg aca agc      2429
Glu Phe Asp Phe Tyr Leu Cys Ser His Ala Gly Ile Gln Gly Thr Ser
745                 750                 755                 760

agg cct tcg cac tat cac gtc ctc tgg gac gac aat cgt ttc tcc tct      2477
Arg Pro Ser His Tyr His Val Leu Trp Asp Asp Asn Arg Phe Ser Ser
                765                 770                 775

gat gag ctg cag atc cta acc tac cag ctg tgt cac acc tac gtg cgc      2525
Asp Glu Leu Gln Ile Leu Thr Tyr Gln Leu Cys His Thr Tyr Val Arg
            780                 785                 790

tgc aca cgc tcc gtg tcc atc cca gcg cca gca tac tac gct cac ctg      2573
Cys Thr Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala His Leu
        795                 800                 805

gtg gcc ttc cgg gcc agg tac cac ctg gtg gat aag gaa cat gac agt      2621
Val Ala Phe Arg Ala Arg Tyr His Leu Val Asp Lys Glu His Asp Ser
    810                 815                 820

gct gaa gga agc cat acc tct ggg cag agt aac ggg cga gac cac caa      2669
Ala Glu Gly Ser His Thr Ser Gly Gln Ser Asn Gly Arg Asp His Gln
825                 830                 835                 840

gca ctg gcc aag gcg gtc cag gtt cac caa gac act ctg cgc acc atg      2717
Ala Leu Ala Lys Ala Val Gln Val His Gln Asp Thr Leu Arg Thr Met
                845                 850                 855

tac ttt gct tga cat gttttagtgt ttagcgattg tgtaccgagt gggattcacg      2772
Tyr Phe Ala  *
            860

agaccagcta cactcagacc aacagatggc cagcccttcc gtgacagcca gcatcgaaca    2832

tgagacgtca ttgattttat tagattctcc gttttccaga atgccttccg tcccagattt    2892

caaacttgga ttttgaactg cagacctgta tgagaaccca atgtcatagg aaatatggtt    2952

tgctaaaatc tataagctgc ttattaaaac agagtcccgt gtgtcctaaa aaaaaaaa      3011
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<212> DNA
<213> Homo sapiens

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<222> (639)..(935)

<400> 51
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cagccaacat cctccaggtt tgccaaagga gaagggtgcc caggttagtt tacaccagca     120

ctttcaatgt catctttgga ggtcaagtta tcagaaatgg ggatgaatct ctgccgtacc     180

tgcctcttca cctccaccct gatcactact ctcggacaaa gtcaattgca gagcagaagg     240

tgctggaggc gaatgctaca cccctggaca gaggcgacgg tgtcttaaga acctgcgctc     300

tgaggccagc tggcatctat gggcctggag aacaaagaca ccttcccagg atagtcagct     360

acatcgagaa gggtctgttc aagtttgtct acggcgaccc caggagcctg gttgagtttg     420

tccacgtgga taacttggtg caggctcaca ttctggcctc agaagccctg agagctgaca     480

agggccatat tgcctctggg cagccctact tcatctcaga tggcagaccc gtgaacaact     540

ttgagttctt ccggcctctg gttgagggcc tgggctacac attcccgtct acccgcctgc     600

cattgacctt ggtctactgc tttgcttttc taacagag    atg gtt cac ttc att      653
                                             Met Val His Phe Ile
                                               1               5

ttg ggt cga ctc tac aac ttc cag ccc ttc ctc act cgc act gaa gtt       701
Leu Gly Arg Leu Tyr Asn Phe Gln Pro Phe Leu Thr Arg Thr Glu Val
                 10                  15                  20

tac aaa act ggt gtc aca cat tat ttt agc tta gag aaa gcc aag aaa       749
Tyr Lys Thr Gly Val Thr His Tyr Phe Ser Leu Glu Lys Ala Lys Lys
             25                  30                  35

gag cta ggt tat aag gct cag cca ttt gac ctc cag gaa gca gtg gaa       797
Glu Leu Gly Tyr Lys Ala Gln Pro Phe Asp Leu Gln Glu Ala Val Glu
         40                  45                  50

tgg ttt aaa gcc cat ggt cat ggc aga agt tct gga agt cgt gac tcg       845
Trp Phe Lys Ala His Gly His Gly Arg Ser Ser Gly Ser Arg Asp Ser
     55                  60                  65

gag tgt ttt gtt tgg gat ggg cta ttg gtc ttc ctc ctg att ata gca       893
Glu Cys Phe Val Trp Asp Gly Leu Leu Val Phe Leu Leu Ile Ile Ala
 70                  75                  80                  85

gtt ctc atg tgg ctg cct tct tct gtg att ctg tca ctg tga aggaggg       942
Val Leu Met Trp Leu Pro Ser Ser Val Ile Leu Ser Leu  *
                 90                  95
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gccagaaata aggtgatcac agttggctga gatggttctc aagaaacatg ggttttaaaa   1002

tgtgtacagt gatatctggt gccaaacatt ggctcttcaa attgctactt aaaaaaaaaa   1062

aa                                                                  1064




    <210> 52
    <211> 710
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (158)..(682)

    <400> 52
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tgtccactaa ccggactcag aagggacttc cctgctcggc tggctttcgg tttctctgct    120

cacctccgga taaatcacgg ggtctcccgc gccgctc atg gcg cct ccc gtc cgt     175
                                         Met Ala Pro Pro Val Arg
                                          1               5

ctc gag cgt ccc ttt cct tcc cgg cgc ttt cct ggg ttg ctt ctg gcg      223
Leu Glu Arg Pro Phe Pro Ser Arg Arg Phe Pro Gly Leu Leu Leu Ala
            10                  15                  20

gcc ctg gtg ttg ctg ctg tcc tcc ttc tcc gat caa tgc aat gtc ccg      271
Ala Leu Val Leu Leu Leu Ser Ser Phe Ser Asp Gln Cys Asn Val Pro
        25                  30                  35

gaa tgg ctt cca ttt gcc agg cct acc aac cta act gat gac ttt gag      319
Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Asp Phe Glu
    40                  45                  50

ttt ccc att ggg aca tat ctg aac tat gaa tgc cgc cct ggt tat tcc      367
Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser
55                  60                  65                  70

gga aga ccg ttt tct atc atc tgc cta aaa aac tca gtc tgg aca agt      415
Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr Ser
                75                  80                  85

gct aag gac aag tgc aaa cgt aaa tca tgt cgt aat cct cca gat cct      463
Ala Lys Asp Lys Cys Lys Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro
            90                  95                  100

gtg aat ggc atg gca cat gtg atc aaa gac atc cag ttc gga tcc caa      511
Val Asn Gly Met Ala His Val Ile Lys Asp Ile Gln Phe Gly Ser Gln
        105                 110                 115

att aaa tat tct tgt cct aaa gga tac cga ctc att ggt tcc tcg tct      559
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Ile Lys Tyr Ser Cys Pro Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser
    120                 125                 130

gcc aca tgc atc atc tca ggc aac act gtc att tgg gat aat aaa aca      607
Ala Thr Cys Ile Ile Ser Gly Asn Thr Val Ile Trp Asp Asn Lys Thr
135                 140                 145                 150

cct gtt tgt gac agt gag ttg aaa tat gca ttc cta ttt ctt tta ccg      655
Pro Val Cys Asp Ser Glu Leu Lys Tyr Ala Phe Leu Phe Leu Leu Pro
                155                 160                 165

ata cat tct aat ttt tct ctg gaa taa taaaa atctattccg aaaaaaaaaa      707
Ile His Ser Asn Phe Ser Leu Glu  *
            170                 175

aaa                                                                  710




     <210> 53
     <211> 1685
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (174)..(1613)

     <400> 53
tttcgtccgg aaggaagagg aaattccagt agccgatcag gagtctgcaa actccggtgg      60

taggggagcg cgctgctgtt tagagccacg agttaccgga gcgcctgatt cctgcgccga     120

agtcagtggt ggccgaaagt ccggagtcgc tgtaaaacct gagattgtga gcc   atg     176
                                                             Met
                                                               1

gtg ggg aga tcc cgg cgg cgc gga gca gct aag tgg gca gct gtg cga      224
Val Gly Arg Ser Arg Arg Arg Gly Ala Ala Lys Trp Ala Ala Val Arg
              5                  10                  15

gcc aag gca ggt ccc acg ctc acc gac gaa aat gga gat gat tta gga      272
Ala Lys Ala Gly Pro Thr Leu Thr Asp Glu Asn Gly Asp Asp Leu Gly
         20                  25                  30

ttg cca ccc tca cca ggg gac acc agc tac tac caa gat cag gta gat      320
Leu Pro Pro Ser Pro Gly Asp Thr Ser Tyr Tyr Gln Asp Gln Val Asp
     35                  40                  45

gac ttt cat gag gca cga tcc cgg gcc gcc tta gct aag ggc tgg aat      368
Asp Phe His Glu Ala Arg Ser Arg Ala Ala Leu Ala Lys Gly Trp Asn
 50                  55                  60                  65

gaa gta cag agt gga gac gag gag gat ggc gag gag gag gag gag gag      416
Glu Val Gln Ser Gly Asp Glu Glu Asp Gly Glu Glu Glu Glu Glu Glu
                 70                  75                  80
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gtg cta gcc cta gat atg gac gat gag gac gac gaa gat gga ggg aat        464
Val Leu Ala Leu Asp Met Asp Asp Glu Asp Asp Glu Asp Gly Gly Asn
             85                  90                  95

gcg ggg gag gag gag gag gag gag aat gcc gat gat gat ggt ggg agc        512
Ala Gly Glu Glu Glu Glu Glu Glu Asn Ala Asp Asp Asp Gly Gly Ser
        100                 105                 110

tcc gtg caa agt gaa gct gag gcc tct gtg gat ccc agt ttg tcg tgg        560
Ser Val Gln Ser Glu Ala Glu Ala Ser Val Asp Pro Ser Leu Ser Trp
    115                 120                 125

ggt cag agg aaa aaa ctt tac tat gac acg gac tat ggt tcc aag tcc        608
Gly Gln Arg Lys Lys Leu Tyr Tyr Asp Thr Asp Tyr Gly Ser Lys Ser
130                 135                 140                 145

cga ggc cgg cag agt caa cag gag gca gag gag gag gaa aga gag gag        656
Arg Gly Arg Gln Ser Gln Gln Glu Ala Glu Glu Glu Glu Arg Glu Glu
                150                 155                 160

gag gag gag gca cag atc att cag cgg cgc cta gcc caa gcg ctg caa        704
Glu Glu Glu Ala Gln Ile Ile Gln Arg Arg Leu Ala Gln Ala Leu Gln
            165                 170                 175

gag gat gat ttt ggt gtc gcc tgg gtt gag gcc ttt gca aaa cca gtg        752
Glu Asp Asp Phe Gly Val Ala Trp Val Glu Ala Phe Ala Lys Pro Val
        180                 185                 190

cct cag gta gat gag gct gag aca cgg gtc gtg aag gat ttg gct aaa        800
Pro Gln Val Asp Glu Ala Glu Thr Arg Val Val Lys Asp Leu Ala Lys
    195                 200                 205

gtt tca gtg aaa gag aag ctg aaa atg ttg cga aag gaa tca cca gaa        848
Val Ser Val Lys Glu Lys Leu Lys Met Leu Arg Lys Glu Ser Pro Glu
210                 215                 220                 225

ctc ttg gag ctg ata gaa gac ctg aaa gtc aag ttg aca gag gtt aag        896
Leu Leu Glu Leu Ile Glu Asp Leu Lys Val Lys Leu Thr Glu Val Lys
                230                 235                 240

gat gag ctg gag cca ttg tta gag ttg gtg gaa caa ggg atc att cca        944
Asp Glu Leu Glu Pro Leu Leu Glu Leu Val Glu Gln Gly Ile Ile Pro
            245                 250                 255

ccc gga aaa gga agc caa tac ttg agg acc aag tac aac ctc tac ttg        992
Pro Gly Lys Gly Ser Gln Tyr Leu Arg Thr Lys Tyr Asn Leu Tyr Leu
        260                 265                 270

aat tat tgc tcg aac atc agt ttt tat ttg atc ctg aaa gct agg aga       1040
Asn Tyr Cys Ser Asn Ile Ser Phe Tyr Leu Ile Leu Lys Ala Arg Arg
    275                 280                 285

gtc cca gca cat gga cat cct gtc ata gaa agg ctt gtt acc tac cga       1088
Val Pro Ala His Gly His Pro Val Ile Glu Arg Leu Val Thr Tyr Arg
290                 295                 300                 305
```

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aat ttg atc aac aag ctg tcc gtt gtg gat cag aag ctg tcc tca gaa      1136
Asn Leu Ile Asn Lys Leu Ser Val Val Asp Gln Lys Leu Ser Ser Glu
                310                 315                 320

att cgt cat ctg ttg aca ctt aag gat gat gct gta aag aaa gaa ctg      1184
Ile Arg His Leu Leu Thr Leu Lys Asp Asp Ala Val Lys Lys Glu Leu
            325                 330                 335

att cca aaa gca aaa tcc acc aag ccc aaa cca aag tct gtt tca aag      1232
Ile Pro Lys Ala Lys Ser Thr Lys Pro Lys Pro Lys Ser Val Ser Lys
        340                 345                 350

act tct gct gct gcc tgt gct gtt aca gat ctt tct gat gat tct gat      1280
Thr Ser Ala Ala Ala Cys Ala Val Thr Asp Leu Ser Asp Asp Ser Asp
    355                 360                 365

ttt gat gaa aaa gca aaa ctg aag tac tat aaa gaa ata gaa gac agg      1328
Phe Asp Glu Lys Ala Lys Leu Lys Tyr Tyr Lys Glu Ile Glu Asp Arg
370                 375                 380                 385

caa aag cta aag aga aag aaa gaa gaa aat agc act gaa gaa cag gct      1376
Gln Lys Leu Lys Arg Lys Lys Glu Glu Asn Ser Thr Glu Glu Gln Ala
                390                 395                 400

ctt gaa gat caa aat gca aag aga gct att acc tat caa att gct aaa      1424
Leu Glu Asp Gln Asn Ala Lys Arg Ala Ile Thr Tyr Gln Ile Ala Lys
            405                 410                 415

aat agg gga ctt act cct agg aga aag aag att gat cgc aat ccc aga      1472
Asn Arg Gly Leu Thr Pro Arg Arg Lys Lys Ile Asp Arg Asn Pro Arg
        420                 425                 430

gtg aaa cac aga gag aag ttc aga aga gcc aaa att aga aga aga ggc      1520
Val Lys His Arg Glu Lys Phe Arg Arg Ala Lys Ile Arg Arg Arg Gly
    435                 440                 445

cag gtt cgt gaa gtt cgt aaa gaa gag caa cgt tat agt ggt gaa tta      1568
Gln Val Arg Glu Val Arg Lys Glu Glu Gln Arg Tyr Ser Gly Glu Leu
450                 455                 460                 465

tct ggc att cgt gca gga gtt aaa aag agc att aag ctt aaa tga agt      1616
Ser Gly Ile Arg Ala Gly Val Lys Lys Ser Ile Lys Leu Lys  *
                470                 475                 480

ttttgcttag cataaggttt ttggcagttt tggatcaata aatttttact tttaactaaa    1676

aaaaaaaaa                                                            1685


      <210> 54
      <211> 2600
      <212> DNA
      <213> Homo sapiens

      <220>
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     <221> CDS
     <222> (289)..(831)

     <400> 54
tgaatatctc tccctgatga taatcataca catgaagctg ggattttctt tccctttgtg      60

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aaggaagaaa attggtaact ttaagtggga cttatcattt gttgtgtgtg ctttcctcat     180

agtgagtcta attttcacaa ttacaccttg gtctcattga atgaagaatt taatcgtgga     240

cgaggactaa atgtgggtgc ccgagcttgg gacaagggag aggtcttg atg ttt ttc      297
                                                     Met Phe Phe
                                                       1

tgt gat gtt gat atc tat ttc tca gcc gaa ttc ctt aac agc tgc cgg       345
Cys Asp Val Asp Ile Tyr Phe Ser Ala Glu Phe Leu Asn Ser Cys Arg
      5                  10                  15

tta aat gct gag cca ggt aag aag gtg ttt tac cct gtg gtg ttc agt       393
Leu Asn Ala Glu Pro Gly Lys Lys Val Phe Tyr Pro Val Val Phe Ser
 20                  25                  30                  35

ctt tac aat cct gcc att gtt tat gcc aac cag gaa gtg cca cca cct       441
Leu Tyr Asn Pro Ala Ile Val Tyr Ala Asn Gln Glu Val Pro Pro Pro
                 40                  45                  50

gtg gag cag cag ctg gtt cac aaa aag gat tct ggc ttt tgg cga gat       489
Val Glu Gln Gln Leu Val His Lys Lys Asp Ser Gly Phe Trp Arg Asp
             55                  60                  65

ttt ggc ttt gga atg act tgt cag tat cgt tca gat ttc ctg acc att       537
Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Leu Thr Ile
         70                  75                  80

ggt gga ttt gac atg gaa gtg aaa ggt tgg ggt gga gaa gat gtt cat       585
Gly Gly Phe Asp Met Glu Val Lys Gly Trp Gly Gly Glu Asp Val His
     85                  90                  95

ctt tat cga aaa tac tta cat ggt gac ctc att gtg att cgg act ccg       633
Leu Tyr Arg Lys Tyr Leu His Gly Asp Leu Ile Val Ile Arg Thr Pro
100                 105                 110                 115

gtt cct ggt ctt ttc cac ctc tgg cat gaa aag cgc tgt gct gat gag       681
Val Pro Gly Leu Phe His Leu Trp His Glu Lys Arg Cys Ala Asp Glu
                120                 125                 130

ctg acc ccc gag cag tac cgc atg tgc atc cag tct aaa gcc atg aat       729
Leu Thr Pro Glu Gln Tyr Arg Met Cys Ile Gln Ser Lys Ala Met Asn
            135                 140                 145

gag gcc tct cac tcc cac ctg gga atg ctg gtc ttc agg gag gaa ata       777
Glu Ala Ser His Ser His Leu Gly Met Leu Val Phe Arg Glu Glu Ile
        150                 155                 160

gag acg cat ctt cat aaa cag gca tac agg aca aac agt gaa gct gtt       825
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Glu Thr His Leu His Lys Gln Ala Tyr Arg Thr Asn Ser Glu Ala Val
    165                 170                 175

ggt tga aatcataatt aatgcgttac tgtatgaacc acaaaacagc actatttatt       881
Gly  *
180

tagccttact tctacttcca gatgcagtgc ctcttttgga gaagacatgt ttatttttca    941

tgttctttct gacattactt tagcaattca acttgatgtg agaagaaaaa acaaatgttt   1001

caacacaaaa tctctgtttt gtgagaatac tgcactatgg aataattgac aaattgaaat   1061

ctcatatttg tcccaaaagt tgttttgagt tagttctacc tggtgcccat gttctgattg   1121

tgtgtgggat tgcatggtgt cctgattgca tctaggtgga gcggatggaa tgtgctgggc   1181

cactgttggg tggagagcag cacattctta cagaggagat ggagcgttat gagcatagta   1241

tgtggatagg tatcttcacc tgcccgcccc tgagtcagcc tccttgactt gatagcttga   1301

agaatccttt tccactgaaa tagaggataa ttaattgaca catctgaaat ccccaatcaa   1361

tcaatcaaga gaaaggtaga actaaaaact ccttaactta ctgttgctta cacccctgaa   1421

agtctgtttt taagcaaatg ggtaatagta gaaaataggt tagaatctat ggcttgatta   1481

aaaatatgtt attacattat catgttcagg attaggatta gtagtcagtt gctgtaaact   1541

attttgaaca aacagaaaag aacacggaaa catttttaac agagcattta attatgttgg   1601

aatacaggat cctagctctg tctgggaaca ttagtttatg tgagccagct ctatcagggt   1661

cttcccatgg tggttcagaa tagatgagca tagcatggtt ttgtttgttt ttgctttcaa   1721

ttttctaatt tggcatggat ccatatgtat ttactatcct ttttctaata tattaatata   1781

tgctacattt gtatttgcat tactataata ctttgagttg aaaaagagtt tcattgtgga   1841

gagaaaaagc aaatggtatg ccacaagatc actctgattt gagaaaaggg aggaggggaa   1901

gatagtctga atggaaatct gaaatacgga atgttttaga gaaatatgtc acttgcatat   1961

agaatgtttt aattgaggta taaattaatg agacaaagtg aaaaagaaat tatattcaga   2021

taggactgca ctacattatt tgtcacacat ggatctgtta ccatcaggtc aattcctagt   2081

atgcataaat tttttaaccc ttttaaaaga gacctatgtt gaaaacccct gaaaattcac   2141

tgaagaaaaa tcattactct ttttctcagt aaatcatatc atctgaaata ttacaaattt   2201

caaatttcta ggtgctatat taattcaata ttacaataac tcttacctaa ttattcttac   2261

aagttttaag ttgtggtagt ttagtgattt ttttaaaaga tgtgtgaaat gttctctgca   2321

aaataattca ggccactgtc tccttttata tattattata attatttatt atgaagacca   2381
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gtgaattacg atatttaaag tgagagaact taattatttg caaaggtaag ttacagcttg   2441

tttttgaga gaatcaaatg agtttacttt tgttcctgtt gtttttaact agctttaagt   2501

ttaaagatgg aagctaagca atggaaatgc tatacgtttt tgacatttat taaatggtac   2561

caataaagta ttttattacc aaaagttaaa aaaaaaaa                          2600
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<210> 55
<211> 1949
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (23)..(1369)

<400> 55
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cggccgcccg cccggtcggg cg atg aag tgt cac tat gag gcg ctg ggg gtg      52
                         Met Lys Cys His Tyr Glu Ala Leu Gly Val
                           1               5                  10

cgg cgc gac gcc agc gag gag gag ctc aag aag gcc tat cgg aag ctg      100
Arg Arg Asp Ala Ser Glu Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu
                 15                  20                  25

gcc ctg aaa tgg cac ccg gat aaa aat ctg gat aat gcc gca gaa gca      148
Ala Leu Lys Trp His Pro Asp Lys Asn Leu Asp Asn Ala Ala Glu Ala
             30                  35                  40

gct gaa caa ttt aaa tta atc caa gca gca tat gat gtg ttg agt gac      196
Ala Glu Gln Phe Lys Leu Ile Gln Ala Ala Tyr Asp Val Leu Ser Asp
         45                  50                  55

cct cag gaa aga gca tgg tat gat aat cat aga gag gcc cta ctt aaa      244
Pro Gln Glu Arg Ala Trp Tyr Asp Asn His Arg Glu Ala Leu Leu Lys
     60                  65                  70

ggt ggg ttt gat ggc gaa tat caa gat gac agc tta gat ttg cta cgc      292
Gly Gly Phe Asp Gly Glu Tyr Gln Asp Asp Ser Leu Asp Leu Leu Arg
 75                  80                  85                  90

tat ttc acc gtt acc tgt tat tct ggt tat gga gat gat gaa aag gga      340
Tyr Phe Thr Val Thr Cys Tyr Ser Gly Tyr Gly Asp Asp Glu Lys Gly
                 95                 100                 105

ttt tac acg gtg tat cgt aat gtt ttt gaa atg att gcc aag gaa gaa      388
Phe Tyr Thr Val Tyr Arg Asn Val Phe Glu Met Ile Ala Lys Glu Glu
            110                 115                 120

cta gaa tct gtg tta gag gaa gag gtt gat gat ttc cca act ttt gga      436
Leu Glu Ser Val Leu Glu Glu Glu Val Asp Asp Phe Pro Thr Phe Gly
        125                 130                 135
```

```
gac tcc cag agt gac tat gat acg gta gtc cat cct ttc tac gct tat       484
Asp Ser Gln Ser Asp Tyr Asp Thr Val Val His Pro Phe Tyr Ala Tyr
    140                 145                 150

tgg cag agt ttc tgc act caa aag aat ttt gca tgg aag gaa gaa tat       532
Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr
155                 160                 165                 170

gat aca cga cag gct tca aac cgc tgg gaa aaa cga gcc atg gaa aaa       580
Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys
                175                 180                 185

gaa aac aaa aag att cgg gac aaa gca agg aaa gag aag aat gag ctt       628
Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu
            190                 195                 200

gtc cgt cag ctg gta gct ttc att cgt aaa aga gat aaa aga gtg cag       676
Val Arg Gln Leu Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln
        205                 210                 215

gcg cat cga aaa ctt gtg gaa gaa cag aat gca gag aag gcg agg aaa       724
Ala His Arg Lys Leu Val Glu Glu Gln Asn Ala Glu Lys Ala Arg Lys
    220                 225                 230

gcc gaa gag atg agg cgg cag cag aag cta aag cag gcc aaa ctg gtg       772
Ala Glu Glu Met Arg Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val
235                 240                 245                 250

gag cag tac aga gaa cag agc tgg atg act atg gcc aat ttg gag aaa       820
Glu Gln Tyr Arg Glu Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys
                255                 260                 265

gag ctc cag gag atg gag gca cgg tac gag aag gag ttt gga gat gga       868
Glu Leu Gln Glu Met Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly
            270                 275                 280

tcg gat gaa aat gaa atg gaa gaa cat gaa ctc aaa gat gag gag gat       916
Ser Asp Glu Asn Glu Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp
        285                 290                 295

ggt aaa gac agt gat gag gcc gag gac gct gag ctc tat gat gac ctt       964
Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu
    300                 305                 310

tac tgc cca gca tgt gac aaa tcg ttc aag aca gaa aag gcc atg aag      1012
Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys
315                 320                 325                 330

aat cac gag aag tca aag aag cat cgg gaa atg gtg gcc ttg cta aaa      1060
Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys
                335                 340                 345

caa cag ctg gag gag gaa gaa gaa aat ttt tca aga cct caa att gat      1108
Gln Gln Leu Glu Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp
            350                 355                 360

gaa aat cca tta gat gac aat tct gag gaa gaa atg gaa gat gca cca      1156
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```
Glu Asn Pro Leu Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro
        365                 370                 375

aaa caa aag ctt tct aaa aaa cag aag aca caa gaa aca gta aac cag      1204
Lys Gln Lys Leu Ser Lys Lys Gln Lys Thr Gln Glu Thr Val Asn Gln
    380                 385                 390

cac agg atg tac ctg gca aag att cat atc tgc ctg cag ctc act ttc      1252
His Arg Met Tyr Leu Ala Lys Ile His Ile Cys Leu Gln Leu Thr Phe
395                 400                 405                 410

aga tgg ctt ggg gaa aaa agt gtg tgt agg gag aga gaa gag atg gag      1300
Arg Trp Leu Gly Glu Lys Ser Val Cys Arg Glu Arg Glu Glu Met Glu
                415                 420                 425

aga gcg agc aca aat gtg cca aaa tgt tgc ttg aaa aca gac aga att      1348
Arg Ala Ser Thr Asn Val Pro Lys Cys Cys Leu Lys Thr Asp Arg Ile
            430                 435                 440

atg atg acc att tca atg taa at ggacctggac gaaggagtaa aggttgatcc      1401
Met Met Thr Ile Ser Met  *
        445

atgaagatac taacttatat caagacagtg ccaaagaatt ggaagatagt ccccaggaaa    1461

atgtcagtgt cacagatgat cattacacca tgtgatgatc caaaaagtga agctaaaagg    1521

taagtcaaag ttgcatatta tttgtaaatt actgaatatt gatagtaagg atgtagcttt    1581

tcatatatca aataaaatct tctttcccat gactgaccag gtaatttaga tgtatctgta    1641

catatttatg tatagataca cacacacata tgtatacaga tgaagagcgt tgagaagagg    1701

atgctagagg aatgtgccca cacacatctc agcagcatgg ccaaaatcag aaagatgtca    1761

ctttgatcca gttctcgttt accttatcct gctgtggcgc tgatctcgtc gtggatcatt    1821

aacacttgac actcacatga gaacaagact cctgctgcgt ccctggagtg tcactaagca    1881

aatctccatg ctcacgacag cagcctgtgt agggccccac catgttgtga ggacacatgg    1941

cagcagct                                                             1949


     <210> 56
     <211> 2439
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (23)..(1618)

     <400> 56
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                        Met Lys Cys His Tyr Glu Ala Leu Gly Val
                         1               5                   10

cgg cgc gac gcc agc gag gag gag ctc aag aag gcc tat cgg aag ctg       100
Arg Arg Asp Ala Ser Glu Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu
                 15                  20                  25

gcc ctg aaa tgg cac ccg gat aaa aat ctg gat aat gcc gca gaa gca       148
Ala Leu Lys Trp His Pro Asp Lys Asn Leu Asp Asn Ala Ala Glu Ala
             30                  35                  40

gct gaa caa ttt aaa tta atc caa gca gca tat gat gtg ttg agt gac       196
Ala Glu Gln Phe Lys Leu Ile Gln Ala Ala Tyr Asp Val Leu Ser Asp
         45                  50                  55

cct cag gaa aga gca tgg tat gat aat cat aga gag gcc cta ctt aaa       244
Pro Gln Glu Arg Ala Trp Tyr Asp Asn His Arg Glu Ala Leu Leu Lys
     60                  65                  70

ggt ggg ttt gat ggc gaa tat caa gat gac agc tta gat ttg cta cgc       292
Gly Gly Phe Asp Gly Glu Tyr Gln Asp Asp Ser Leu Asp Leu Leu Arg
 75                  80                  85                  90

tat ttc acc gtt acc tgt tat tct ggt tat gga gat gat gaa aag gga       340
Tyr Phe Thr Val Thr Cys Tyr Ser Gly Tyr Gly Asp Asp Glu Lys Gly
                 95                 100                 105

ttt tac acg gtg tat cgt aat gtt ttt gaa atg att gcc aag gaa gaa       388
Phe Tyr Thr Val Tyr Arg Asn Val Phe Glu Met Ile Ala Lys Glu Glu
            110                 115                 120

cta gaa tct gtg tta gag gaa gag gtt gat gat ttc cca act ttt gga       436
Leu Glu Ser Val Leu Glu Glu Glu Val Asp Asp Phe Pro Thr Phe Gly
        125                 130                 135

gac tcc cag agt gac tat gat acg gta gtc cat cct ttc tac gct tat       484
Asp Ser Gln Ser Asp Tyr Asp Thr Val Val His Pro Phe Tyr Ala Tyr
    140                 145                 150

tgg cag agt ttc tgc act caa aag aat ttt gca tgg aag gaa gaa tat       532
Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr
155                 160                 165                 170

gat aca cga cag gct tca aac cgc tgg gaa aaa cga gcc atg gaa aaa       580
Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys
                175                 180                 185

gaa aac aaa aag att cgg gac aaa gca agg aaa gag aag aat gag ctt       628
Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu
            190                 195                 200

gtc cgt cag ctg gta gct ttc att cgt aaa aga gat aaa aga gtg cag       676
Val Arg Gln Leu Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln
        205                 210                 215

gcg cat cga aaa ctt gtg gaa gaa cag aat gca gag aag gcg agg aaa       724
Ala His Arg Lys Leu Val Glu Glu Gln Asn Ala Glu Lys Ala Arg Lys
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```
    220                 225                 230

gcc gaa gag atg agg cgg cag cag aag cta aag cag gcc aaa ctg gtg       772
Ala Glu Glu Met Arg Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val
235                 240                 245                 250

gag cag tac aga gaa cag agc tgg atg act atg gcc aat ttg gag aaa       820
Glu Gln Tyr Arg Glu Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys
                255                 260                 265

gag ctc cag gag atg gag gca cgg tac gag aag gag ttt gga gat gga       868
Glu Leu Gln Glu Met Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly
            270                 275                 280

tcg gat gaa aat gaa atg gaa gaa cat gaa ctc aaa gat gag gag gat       916
Ser Asp Glu Asn Glu Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp
        285                 290                 295

ggt aaa gac agt gat gag gcc gag gac gct gag ctc tat gat gac ctt       964
Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu
    300                 305                 310

tac tgc cca gca tgt gac aaa tcg ttc aag aca gaa aag gcc atg aag      1012
Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys
315                 320                 325                 330

aat cac gag aag tca aag aag cat cgg gaa atg gtg gcc ttg cta aaa      1060
Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys
                335                 340                 345

caa cag ctg gag gag gaa gaa gaa aat ttt tca aga cct caa att gat      1108
Gln Gln Leu Glu Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp
            350                 355                 360

gaa aat cca tta gat gac aat tct gag gaa gaa atg gaa gat gca cca      1156
Glu Asn Pro Leu Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro
        365                 370                 375

aaa caa aag ctt tct aaa aaa cag aag aaa aag aaa cag aaa cca gca      1204
Lys Gln Lys Leu Ser Lys Lys Gln Lys Lys Lys Lys Gln Lys Pro Ala
    380                 385                 390

cag aat tat gat gac aat ttc aat gta aat gga cct gga gaa gga gta      1252
Gln Asn Tyr Asp Asp Asn Phe Asn Val Asn Gly Pro Gly Glu Gly Val
395                 400                 405                 410

aag gtt gat cca gaa gat act aac tta aat caa gac agt gcc aaa gaa      1300
Lys Val Asp Pro Glu Asp Thr Asn Leu Asn Gln Asp Ser Ala Lys Glu
                415                 420                 425

ttg gaa gat agt ccc cag gaa aat gtc agt gtc aca gag atc att aaa      1348
Leu Glu Asp Ser Pro Gln Glu Asn Val Ser Val Thr Glu Ile Ile Lys
            430                 435                 440

cca tgt gat gat cca aaa agt gaa gct aaa agt gtt cct aaa ccc aaa      1396
Pro Cys Asp Asp Pro Lys Ser Glu Ala Lys Ser Val Pro Lys Pro Lys
        445                 450                 455
```

```
gga aag aaa acc aaa gat atg aaa aaa cct gtc aga gta cct gct gaa     1444
Gly Lys Lys Thr Lys Asp Met Lys Lys Pro Val Arg Val Pro Ala Glu
    460             465                     470

cca caa aca atg agt gtt ctt atc agc tgt aca acc tgc cat agt gaa     1492
Pro Gln Thr Met Ser Val Leu Ile Ser Cys Thr Thr Cys His Ser Glu
475                 480                 485                 490

ttt cca tct cgg aat aaa ctt ttt gac cat cta aag gcc aca ggt cat     1540
Phe Pro Ser Arg Asn Lys Leu Phe Asp His Leu Lys Ala Thr Gly His
                495                 500                 505

gca aga gca cct tca tca tcg tct tta aac agc gca aca agt agt caa     1588
Ala Arg Ala Pro Ser Ser Ser Ser Leu Asn Ser Ala Thr Ser Ser Gln
            510                 515                 520

agc aag aaa gag aaa cgt aaa aac aga tag a gattctgcct gtgcttttgt     1639
Ser Lys Lys Glu Lys Arg Lys Asn Arg  *
        525                 530

ttgactgtct ctagattttg aaaccaaaaa actgaactga aatcatctaa agagttaaaa   1699

tttcagtgat ctgcaattaa ttacattgtg gaagattatt ttttatcttg taaaaacact   1759

tttttggttt aatatatatt tttaaaacat ttcactagtg attgaattct acttttgcca   1819

tctgaattga cttgaatgtc ttaaaacagg taaatactgt aaagtgtgta ttcttgatgt   1879

ttattggctc atgtggacag aaatgtacag ggagaattac attattttaa cacacagaag   1939

tgcaactttc tgctttattt tctgaatttc acattacttt tacttaatgc ttttgtgttt   1999

tgttaatact tcataatatg tgaaaaactc ggatctttta aaaagcatca tagatcattt   2059

ttccatatga cactggttcc gattttaaaa attattttta aataaccgat tattgattac   2119

tgtatttttt ttctcaagaa cagtgatagg tagaaactaa ttgaacattt ggtagtcttt   2179

caagaatagt gtctcttcaa ggttttactt gatttaattt gatattttac tggtttacca   2239

gtaaggtgta ttgttcagtt ttttgctccg atttgaattg tggaggtgga agcaaattag   2299

tttacatggc atgtcctccc taggcacagt gacagctgta aagtatgacg gaacaaggta   2359

gcagatggta cagaatttat actatttaag aagagatgtg gcgttcttca ttgagttttt   2419

ttcttcacta ttttcagaag                                               2439
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<211> 2331
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (27)..(1784)

<400> 57
ggcacgaggc gagtccgagc gccgcc atg gct ctg ctg tcc gag ggc ctg gac       53
                             Met Ala Leu Leu Ser Glu Gly Leu Asp
                              1               5

gag gtg ccc gcc gcc tgc ctg tcg ccg tgc ggg ccg ccc aac ccg acc      101
Glu Val Pro Ala Ala Cys Leu Ser Pro Cys Gly Pro Pro Asn Pro Thr
 10                  15                  20                  25

gag ctg ttc agc gag tca cgg cgc ctg gct ctg gag gag ctg gtg gcg      149
Glu Leu Phe Ser Glu Ser Arg Arg Leu Ala Leu Glu Glu Leu Val Ala
                 30                  35                  40

ggc ggc ccc gaa gcc ttc gcg gcc ttc ctg cga cgc gag cgc ctg gct      197
Gly Gly Pro Glu Ala Phe Ala Ala Phe Leu Arg Arg Glu Arg Leu Ala
             45                  50                  55

cgt ttc ctg aac ccc gat gag gtg cac gcc att ctg cgc gcg gcg gag      245
Arg Phe Leu Asn Pro Asp Glu Val His Ala Ile Leu Arg Ala Ala Glu
         60                  65                  70

agg ccg gga gag gag ggc gcg gcg gcg gcg gcg gcg gcc gag gac tcg      293
Arg Pro Gly Glu Glu Gly Ala Ala Ala Ala Ala Ala Ala Glu Asp Ser
     75                  80                  85

ttc ggc tcc tcg cac gac tgc tct tcg ggc acc tac ttc ccc gag cag      341
Phe Gly Ser Ser His Asp Cys Ser Ser Gly Thr Tyr Phe Pro Glu Gln
 90                  95                 100                 105

tcg gac ctg gag cca ccg ctg ttg gag ctt ggc tgg ccc gcc ttc tac      389
Ser Asp Leu Glu Pro Pro Leu Leu Glu Leu Gly Trp Pro Ala Phe Tyr
                110                 115                 120

cag ggc gcc tac cgc ggc gcc acg cgt gtc gag acg cac ttc cag ccc      437
Gln Gly Ala Tyr Arg Gly Ala Thr Arg Val Glu Thr His Phe Gln Pro
            125                 130                 135

cgc ggc gct ggc gaa ggt ggc ccc tac ggc tgc aag gac gct ctg cgc      485
Arg Gly Ala Gly Glu Gly Gly Pro Tyr Gly Cys Lys Asp Ala Leu Arg
        140                 145                 150

cag cag ctc cgc tcg gcg cga gag gtg att gca gtg gtc atg gac gtg      533
Gln Gln Leu Arg Ser Ala Arg Glu Val Ile Ala Val Val Met Asp Val
    155                 160                 165

ttc aca gac atc gac atc ttc aga gac ctg caa gaa ata tgc agg aaa      581
Phe Thr Asp Ile Asp Ile Phe Arg Asp Leu Gln Glu Ile Cys Arg Lys
170                 175                 180                 185

cag gga gtt gct gtg tat atc ctt ctg gac cag gct ctc ctc tct caa      629
Gln Gly Val Ala Val Tyr Ile Leu Leu Asp Gln Ala Leu Leu Ser Gln
                190                 195                 200
```

```
ttt ctg gat atg tgc atg gat ctg aaa gtt cat cct gaa cag gaa aag      677
Phe Leu Asp Met Cys Met Asp Leu Lys Val His Pro Glu Gln Glu Lys
            205                 210                 215

tta atg aca gtt cgg act atc aca gga aat atc tac tat gca agg tca      725
Leu Met Thr Val Arg Thr Ile Thr Gly Asn Ile Tyr Tyr Ala Arg Ser
        220                 225                 230

gga act aag att att ggg aag gtt cac gaa aag ttc acg ttg att gat      773
Gly Thr Lys Ile Ile Gly Lys Val His Glu Lys Phe Thr Leu Ile Asp
    235                 240                 245

ggc atc cgc gtg gca aca ggc tcc tac agt ttt aca tgg acg gat ggc      821
Gly Ile Arg Val Ala Thr Gly Ser Tyr Ser Phe Thr Trp Thr Asp Gly
250                 255                 260                 265

aaa tta aac agc agt aac ttg gta att ctg tct ggc caa gtg gtt gaa      869
Lys Leu Asn Ser Ser Asn Leu Val Ile Leu Ser Gly Gln Val Val Glu
                270                 275                 280

cac ttt gat ctg gag ttc cga atc ctg tat gcc cag tcc aag ccc atc      917
His Phe Asp Leu Glu Phe Arg Ile Leu Tyr Ala Gln Ser Lys Pro Ile
            285                 290                 295

agc ccc aaa ctc ctg tct cac ttc cag agc agc aac aag ttt gat cac      965
Ser Pro Lys Leu Leu Ser His Phe Gln Ser Ser Asn Lys Phe Asp His
        300                 305                 310

ctc acc aac cga aaa cca cag tcc aag gag ctc acc ctg ggc aac ctg     1013
Leu Thr Asn Arg Lys Pro Gln Ser Lys Glu Leu Thr Leu Gly Asn Leu
    315                 320                 325

ctg cgg atg cgg ctg gct agg ctg tca agt act ccc agg aag gcg gac     1061
Leu Arg Met Arg Leu Ala Arg Leu Ser Ser Thr Pro Arg Lys Ala Asp
330                 335                 340                 345

ctg gac cca gag atg ccc gca gag ggc aag gca gag cgc aag ccc cat     1109
Leu Asp Pro Glu Met Pro Ala Glu Gly Lys Ala Glu Arg Lys Pro His
                350                 355                 360

gac tgt gag tcc tct act gtt agt gag gaa gac tac ttc agc agc cac     1157
Asp Cys Glu Ser Ser Thr Val Ser Glu Glu Asp Tyr Phe Ser Ser His
            365                 370                 375

agg gac gag ctc cag agc aga aag gcc att gac gct gcc act caa aca     1205
Arg Asp Glu Leu Gln Ser Arg Lys Ala Ile Asp Ala Ala Thr Gln Thr
        380                 385                 390

gag cca gga gag gag atg cca ggg ctg agt gtg agt gag gtg gga aca     1253
Glu Pro Gly Glu Glu Met Pro Gly Leu Ser Val Ser Glu Val Gly Thr
    395                 400                 405

caa acc agc atc acc aca gca tgt gct ggt acc cag act gca gtc atc     1301
Gln Thr Ser Ile Thr Thr Ala Cys Ala Gly Thr Gln Thr Ala Val Ile
410                 415                 420                 425

acc agg ata gca agc tct caa acc acg att tgg tcc aga tcg acc act     1349
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Thr Arg Ile Ala Ser Ser Gln Thr Thr Ile Trp Ser Arg Ser Thr Thr
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act cag act gac atg gat gag aac att ctc ttt cct cga gga act caa      1397
Thr Gln Thr Asp Met Asp Glu Asn Ile Leu Phe Pro Arg Gly Thr Gln
            445                 450                 455

tct aca gaa ggg tca cca gtc tca aaa atg tct gta tcg aga tct tcc      1445
Ser Thr Glu Gly Ser Pro Val Ser Lys Met Ser Val Ser Arg Ser Ser
        460                 465                 470

agt ttg aag tct tcc tcc tct gtg tct tcc caa ggc tct gtg gca agc      1493
Ser Leu Lys Ser Ser Ser Ser Val Ser Ser Gln Gly Ser Val Ala Ser
    475                 480                 485

tcc act ggt tct ccc gct tcc atc aga acc act gac ttc cac aat cct      1541
Ser Thr Gly Ser Pro Ala Ser Ile Arg Thr Thr Asp Phe His Asn Pro
490                 495                 500                 505

ggc tat ccc aag tac ctg ggc acc ccc cac ctg gaa ctg tac ttg agt      1589
Gly Tyr Pro Lys Tyr Leu Gly Thr Pro His Leu Glu Leu Tyr Leu Ser
                510                 515                 520

gac tca ctt aga aac ttg aac aaa gag cgg caa ttc cac ttc gct ggt      1637
Asp Ser Leu Arg Asn Leu Asn Lys Glu Arg Gln Phe His Phe Ala Gly
            525                 530                 535

atc agg tcc cgg ctc aac cac atg ctg gct atg ctg tca agg aga aca      1685
Ile Arg Ser Arg Leu Asn His Met Leu Ala Met Leu Ser Arg Arg Thr
        540                 545                 550

ctc ttt act gaa aac cac ctt ggc ctt cat tct ggc aat ttc agc aga      1733
Leu Phe Thr Glu Asn His Leu Gly Leu His Ser Gly Asn Phe Ser Arg
    555                 560                 565

gtt aat ttg ctt gct gtt aga gat gta gca ctt tat cct tcc tat cag      1781
Val Asn Leu Leu Ala Val Arg Asp Val Ala Leu Tyr Pro Ser Tyr Gln
570                 575                 580                 585

taa ctgc tccgtgttca gactcctggt ttcttccagg cttacagtgg acatcatcag      1838
 *

cttcctgctt taaaaaatat cttatgtccc taattgcctt tcttttacct gactttgtca   1898

cctttgttgt ctttgaattc tttaggctgc atattatttt acatgctttg ttttgtcatg   1958

tatataccag gtattggttt tatggtttaa acactatgga tacaggggtt tgttttgcac   2018

aattttaata gtcatgcact acataatgat gttttggtca atgacagacc acgtatatgt   2078

tggcagtctc ataagattat aatactgtat ttttactata ccttttctgt gtttagatac   2138

aaataccatt atgttacagt tgcctacagt attcagtgca gtaacatgat gtacaggttt   2198

gtagcctgtt ttgcattttt cttaggttgt atgctcttct gttttaaagg tttgaatcac   2258
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ttaaaaaaaa aaa                                                       2331




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accagagatt atttctgaca acccaggata tcccgaaagc ttggaggcat atggctggaa    180

aatgaaacga cccaggacat cgtttctggc tgcatcatta ttttgtgtcg cgtagtacca    240

gatgggcagt cagtgagcgg cgcagggatg tgaacggacg gttttataat gtgaaaattt    300

tcccttggta aagctaaaac agatttaatt tccctctctt ttctttcact acttccccct    360

ctttattccc cctctgtctg caatatcagt gaactcaact ttgcagtgag gtggccaaaa    420

agagagagaa tgaggagatc ttgatcatct tagtgtcaga ggagtcgcag cggactggga    480

actgcagctg cgaccccccg cgtcctgtgc ggatttcagg gctgataccg cataggcggt    540

tatggaaagg acggtacacc ggagcggcgg aggatagaga ccctggcccc cggagaggtc    600

tgctgatttc gcagcagcct tcgaagccgt ggctgccttt catctgctgc gttttattac    660

tattatcgcc gttccggaaa agtc   atg gaa gac agc ccg ctg cca gac ctc      711
                             Met Glu Asp Ser Pro Leu Pro Asp Leu
                              1               5

aga gac atc gag ctg aag ctg ggg cgc aaa gta ccc gag agt cta gtg      759
Arg Asp Ile Glu Leu Lys Leu Gly Arg Lys Val Pro Glu Ser Leu Val
 10                  15                  20                  25

cgc tct ctc cgt ggg gag gag ccg gtt ccc agg gaa agg gac agg gac      807
Arg Ser Leu Arg Gly Glu Glu Pro Val Pro Arg Glu Arg Asp Arg Asp
                30                  35                  40

ccc tgc ggg ggg agc ggt ggt ggt ggc ggc ggc ggc ggc ggc ggc ggc      855
Pro Cys Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
            45                  50                  55

ggc tgc agt agc agc agc agc tac tgc agc ttc cct ccc tcc ttg tcg      903
Gly Cys Ser Ser Ser Ser Ser Tyr Cys Ser Phe Pro Pro Ser Leu Ser
```

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        60                  65                  70

tcc tcc tct tcg tcc tcc cca acc tct ggc tcc cca cga ggt agc cac      951
Ser Ser Ser Ser Ser Ser Pro Thr Ser Gly Ser Pro Arg Gly Ser His
     75                  80                  85

tct agc gcc ctg gag agg cta gaa acc aag ctt cac ctc ctc agg caa      999
Ser Ser Ala Leu Glu Arg Leu Glu Thr Lys Leu His Leu Leu Arg Gln
 90                  95                 100                 105

gag atg gtt aac ctc aga gcc aca gac gtc agg ctc atg cgc cag ttg     1047
Glu Met Val Asn Leu Arg Ala Thr Asp Val Arg Leu Met Arg Gln Leu
                110                 115                 120

ctt gta atc aat gag agc atc gag tcc atc aag tgg atg atc gaa gaa     1095
Leu Val Ile Asn Glu Ser Ile Glu Ser Ile Lys Trp Met Ile Glu Glu
            125                 130                 135

aaa gcc acc att acc agc aga ggc agc agc ctc agt ggc agc ctg tgc     1143
Lys Ala Thr Ile Thr Ser Arg Gly Ser Ser Leu Ser Gly Ser Leu Cys
        140                 145                 150

agt ttg ttg gag agt cag agc acc tcc tta cgt ggc agc tac aac agc     1191
Ser Leu Leu Glu Ser Gln Ser Thr Ser Leu Arg Gly Ser Tyr Asn Ser
    155                 160                 165

cta cac gat ggc agt gat ggg ctg gat ggc att tcc gtg gga agt tat     1239
Leu His Asp Gly Ser Asp Gly Leu Asp Gly Ile Ser Val Gly Ser Tyr
170                 175                 180                 185

ctg gac acg ttg gcg gat gat gtc cca ggc cat cag acc cct tca gac     1287
Leu Asp Thr Leu Ala Asp Asp Val Pro Gly His Gln Thr Pro Ser Asp
                190                 195                 200

ttg gac caa ttc agt gac agc tcc ctc ata gag gac tca cag gca cta     1335
Leu Asp Gln Phe Ser Asp Ser Ser Leu Ile Glu Asp Ser Gln Ala Leu
            205                 210                 215

cac aag cgt cct aaa ttg gat tct gaa tac tac tgc ttt ggc tag tga     1383
His Lys Arg Pro Lys Leu Asp Ser Glu Tyr Tyr Cys Phe Gly  *
        220                 225                 230

cagtttttg catgggactg gtgtgcaatg aacttgtatt tatccttctt ctccgctgct    1443

atatttttgg tgtgattttt attttaataa gatgaccttt ttaaaagaag ctgattttga   1503

aactgcttaa tggtattgct gttgctccta atacttctca tctgagctga tttatttttc   1563

tctgttacat ctctattttt tatttattac aatgattttc tcccttcttt tacagtagca   1623

caaacaaagt agggggaaaa gaataagcaa taattatgtt tttgcttttg ttttcagagc   1683

aatgggtcag ggattacaag aaaaactttg ctaaatttta caataaacca aagtctgata   1743

acagttaaaa aaaaaaaaa                                                1762
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ctttctcctg gacattgaag atatggccct ttggaggtga cccaggagag aaggg atg      118
                                                             Met
                                                             1

aag gcc ttt ggt cct cca cat gag ggc ccc ctc caa gga ctc gtg gcc      166
Lys Ala Phe Gly Pro Pro His Glu Gly Pro Leu Gln Gly Leu Val Ala
            5                   10                  15

tcc cgc att gag act tat ggg ggc cgg cat cga gcc tct gct cag agc      214
Ser Arg Ile Glu Thr Tyr Gly Gly Arg His Arg Ala Ser Ala Gln Ser
        20                  25                  30

act act ggc aga ctc tat ccc cga gga tac cct gtg ctg gat ccc agt      262
Thr Thr Gly Arg Leu Tyr Pro Arg Gly Tyr Pro Val Leu Asp Pro Ser
    35                  40                  45

cgc cga cgc ctc cag cag tat gtc ccc ttt gcc agg ggt tct ggc cag      310
Arg Arg Arg Leu Gln Gln Tyr Val Pro Phe Ala Arg Gly Ser Gly Gln
50                  55                  60                  65

gcc cga ggc ctg tca ccc atg aga ctg cga gat cca gag ccc gag aag      358
Ala Arg Gly Leu Ser Pro Met Arg Leu Arg Asp Pro Glu Pro Glu Lys
                70                  75                  80

agg cac ggg ggc cat gtg ggg gct ggc ctg ctt cac tcc ccc aaa ctc      406
Arg His Gly Gly His Val Gly Ala Gly Leu Leu His Ser Pro Lys Leu
            85                  90                  95

aag gaa ctc acc aag gcc cat gag ctg gag gtg agg ctg cac act ttc      454
Lys Glu Leu Thr Lys Ala His Glu Leu Glu Val Arg Leu His Thr Phe
        100                 105                 110

agc atg ttt ggg atg ccc cgg ctg ccc cct gag gac cgg cgg cac tgg      502
Ser Met Phe Gly Met Pro Arg Leu Pro Pro Glu Asp Arg Arg His Trp
    115                 120                 125

gag ata gga gag ggt ggc gac agt ggc ctg acc atc gag aag tcc tgg      550
Glu Ile Gly Glu Gly Gly Asp Ser Gly Leu Thr Ile Glu Lys Ser Trp
130                 135                 140                 145

agg gag ctg gtg cct ggg cac aag gag atg agc cag gag ctc tgc cac      598
Arg Glu Leu Val Pro Gly His Lys Glu Met Ser Gln Glu Leu Cys His
                150                 155                 160
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caa cag gag gcc ctg tgg gag ctc ctg acc acc gag ctg atc tac gtg        646
Gln Gln Glu Ala Leu Trp Glu Leu Leu Thr Thr Glu Leu Ile Tyr Val
            165                 170                 175

aga aag ctc aag atc atg act gat ctg cta gcc gcc ggc ctg ctg aac        694
Arg Lys Leu Lys Ile Met Thr Asp Leu Leu Ala Ala Gly Leu Leu Asn
        180                 185                 190

ctg cag cga gtg gga ctg ctg atg gaa gtg tca gct gag acc ctg ttt        742
Leu Gln Arg Val Gly Leu Leu Met Glu Val Ser Ala Glu Thr Leu Phe
    195                 200                 205

gga aat gtc ccc agc ctg att cga acc cac cgg agc ttt tgg gat gag        790
Gly Asn Val Pro Ser Leu Ile Arg Thr His Arg Ser Phe Trp Asp Glu
210                 215                 220                 225

gtg ctg ggg ccc acc ctg gag gag act cgg gcc tcg ggc cag cct ctg        838
Val Leu Gly Pro Thr Leu Glu Glu Thr Arg Ala Ser Gly Gln Pro Leu
                230                 235                 240

gac ccc att ggt ctg caa agt ggc ttc ctg acg ttt ggc cag cgg ttc        886
Asp Pro Ile Gly Leu Gln Ser Gly Phe Leu Thr Phe Gly Gln Arg Phe
            245                 250                 255

cac ccc tat gtc cag tac tgc ctc cga gtg aag cag acc atg gct tac        934
His Pro Tyr Val Gln Tyr Cys Leu Arg Val Lys Gln Thr Met Ala Tyr
        260                 265                 270

gcc cga gaa cag caa gaa act aac cct ctc ttc cat gcc ttc gtg cag        982
Ala Arg Glu Gln Gln Glu Thr Asn Pro Leu Phe His Ala Phe Val Gln
    275                 280                 285

tgg tgt gag aag cac aag cgc tct ggg agg cag atg ctc tgt gac ttg       1030
Trp Cys Glu Lys His Lys Arg Ser Gly Arg Gln Met Leu Cys Asp Leu
290                 295                 300                 305

ctt atc aag ccc cac cag cgc atc acc aag tac cca ctg ctg ctc cat       1078
Leu Ile Lys Pro His Gln Arg Ile Thr Lys Tyr Pro Leu Leu Leu His
                310                 315                 320

gct gtg ctc aag agg agc ccc gag gca cga gcc caa gag gcc ctg aat       1126
Ala Val Leu Lys Arg Ser Pro Glu Ala Arg Ala Gln Glu Ala Leu Asn
            325                 330                 335

gcc atg att gaa gcc gtg gag tca ttc ctg cga cat atc aat ggg cag       1174
Ala Met Ile Glu Ala Val Glu Ser Phe Leu Arg His Ile Asn Gly Gln
        340                 345                 350

gtc cgc cag ggc gaa gag caa gag agc ttg gcg gct gca gca caa cgc       1222
Val Arg Gln Gly Glu Glu Gln Glu Ser Leu Ala Ala Ala Ala Gln Arg
    355                 360                 365

atc ggg ccc tac gag gtg ctg gag cca ccc agt gat gag gtg gag aag       1270
Ile Gly Pro Tyr Glu Val Leu Glu Pro Pro Ser Asp Glu Val Glu Lys
370                 375                 380                 385
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aac ctg cgc cca ttc tcc acc ctg gac ctg acg tcc ccc atg ctg ggg         1318
Asn Leu Arg Pro Phe Ser Thr Leu Asp Leu Thr Ser Pro Met Leu Gly
                390                 395                 400

gtt gca tct gag cac acc aga cag ctg ctg ctg gag ggg cct gtg cga         1366
Val Ala Ser Glu His Thr Arg Gln Leu Leu Leu Glu Gly Pro Val Arg
            405                 410                 415

gtg aag gag gga cga gaa ggg aag ctg gac gtg tac ctg ttc ctc ttc         1414
Val Lys Glu Gly Arg Glu Gly Lys Leu Asp Val Tyr Leu Phe Leu Phe
        420                 425                 430

tct gat gtg ctc ctt gtg acc aag ccc cag cgc aag gcg gac aaa gcc         1462
Ser Asp Val Leu Leu Val Thr Lys Pro Gln Arg Lys Ala Asp Lys Ala
    435                 440                 445

aag gtc atc cga ccc cct ctc atg ctg gag aag ctc gtg tgc caa ccc         1510
Lys Val Ile Arg Pro Pro Leu Met Leu Glu Lys Leu Val Cys Gln Pro
450                 455                 460                 465

ctg cga gac ccc aac agc ttc ctg ctg atc cac ctc act gaa ttc cag         1558
Leu Arg Asp Pro Asn Ser Phe Leu Leu Ile His Leu Thr Glu Phe Gln
                470                 475                 480

tgt gtc tcc agc gcc ctc ctt gtg cac tgt ccc agt cct aca gac cgt         1606
Cys Val Ser Ser Ala Leu Leu Val His Cys Pro Ser Pro Thr Asp Arg
            485                 490                 495

gcc cag tgg ctg gag aag acc cag cag gcc cag gcc gcc cta cag aag         1654
Ala Gln Trp Leu Glu Lys Thr Gln Gln Ala Gln Ala Ala Leu Gln Lys
        500                 505                 510

ctg aag gca gag gag tat gtt caa cag aag agg gag ctc ctg acc ctc         1702
Leu Lys Ala Glu Glu Tyr Val Gln Gln Lys Arg Glu Leu Leu Thr Leu
    515                 520                 525

tat cgg gac cag gac agg gag tcc ccc agc acc agg ccc tcc acg cct         1750
Tyr Arg Asp Gln Asp Arg Glu Ser Pro Ser Thr Arg Pro Ser Thr Pro
530                 535                 540                 545

tcc ctg gag ggc tct cag agc agc gca gag ggg agg act cct gag ttc         1798
Ser Leu Glu Gly Ser Gln Ser Ser Ala Glu Gly Arg Thr Pro Glu Phe
                550                 555                 560

tcg acc att atc ccc cac ctg gtg gtg aca gaa gac aca gat gaa gat         1846
Ser Thr Ile Ile Pro His Leu Val Val Thr Glu Asp Thr Asp Glu Asp
            565                 570                 575

gct ccc ctt gtg cca gat gat acc tca gac tct ggc tac ggc act ttg         1894
Ala Pro Leu Val Pro Asp Asp Thr Ser Asp Ser Gly Tyr Gly Thr Leu
        580                 585                 590

atc cca ggc acc ccc acg ggg tcc cgc tcc cca ctg agc cgt cta cgc         1942
Ile Pro Gly Thr Pro Thr Gly Ser Arg Ser Pro Leu Ser Arg Leu Arg
    595                 600                 605

caa aga gcc ctt cgg cgg gac cct cgc ctc acc ttc tcc acc ctg gaa         1990
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Gln Arg Ala Leu Arg Arg Asp Pro Arg Leu Thr Phe Ser Thr Leu Glu
610                 615                 620                 625

ctc cgg gac atc cct ctg cgt ccc cac cct ccc gac ccc caa gct cct       2038
Leu Arg Asp Ile Pro Leu Arg Pro His Pro Pro Asp Pro Gln Ala Pro
                630                 635                 640

caa cgc cga agc gcc ccc gaa ctg ccg gaa gga atc cta aaa gga ggc       2086
Gln Arg Arg Ser Ala Pro Glu Leu Pro Glu Gly Ile Leu Lys Gly Gly
            645                 650                 655

agt ctt ccc cag gaa gac cca cca acc tgg tct gag gaa gaa gat ggg       2134
Ser Leu Pro Gln Glu Asp Pro Pro Thr Trp Ser Glu Glu Glu Asp Gly
        660                 665                 670

gcc tcc gag cga ggg aat gtg gtg gtg gaa aca ctc cac agg gcc cgg       2182
Ala Ser Glu Arg Gly Asn Val Val Val Glu Thr Leu His Arg Ala Arg
    675                 680                 685

ctt cgg ggc cag ctt ccc tcc tcc cca acc cat gct gac tct gcc ggg       2230
Leu Arg Gly Gln Leu Pro Ser Ser Pro Thr His Ala Asp Ser Ala Gly
690                 695                 700                 705

gaa agc ccc tgg gag tcc tca ggg gag gag gaa gaa gag ggg cct ctg       2278
Glu Ser Pro Trp Glu Ser Ser Gly Glu Glu Glu Glu Glu Gly Pro Leu
                710                 715                 720

ttc ctg aaa gct ggc cac aca tcc ctg cgc cca atg cgg gct gag gac       2326
Phe Leu Lys Ala Gly His Thr Ser Leu Arg Pro Met Arg Ala Glu Asp
            725                 730                 735

atg ctc aga gag atc cgg gag gag ctg gcc agc caa agg att gag ggg       2374
Met Leu Arg Glu Ile Arg Glu Glu Leu Ala Ser Gln Arg Ile Glu Gly
        740                 745                 750

gcc gag gag ccc cgg gac agc agg cca cgg aag ctg act cgg gcc cag       2422
Ala Glu Glu Pro Arg Asp Ser Arg Pro Arg Lys Leu Thr Arg Ala Gln
    755                 760                 765

ctg cag agg atg cgg ggg ccc cac atc att cag ctg gac acc cct ctg       2470
Leu Gln Arg Met Arg Gly Pro His Ile Ile Gln Leu Asp Thr Pro Leu
770                 775                 780                 785

tcc gca tca gag gta tga ggaatg cagaggacct ttggcatgca tctctcccag       2524
Ser Ala Ser Glu Val  *
                790

aggagatctc tccccagtag tgctggtcac cctccggcat ctgtgactct acctcaagga     2584

ccacatttcc caaaggaagc ctggcccagg caccctgcct cctgctctgt ttggggatca     2644

agaactgtaa atttatgtat cataggtgca cctgagcccc acagaaagtt gtgcataaaa     2704

atgactgccc tggctgggca tggctgcctg taatcccagc actttgggag gctgaggtgg     2764

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cacgtgcata tgatcaactt tggacttctt ttgagattgc caggcgtttg ca atg 175
Met
1

gct gct act gtg aac ttg gaa ctt gat ccc att ttt ttg aaa gca cta 223
Ala Ala Thr Val Asn Leu Glu Leu Asp Pro Ile Phe Leu Lys Ala Leu
5 10 15

ggt ttc ttg cat tca aag agt aaa gat tct gct gaa aag cta aaa gca 271
Gly Phe Leu His Ser Lys Ser Lys Asp Ser Ala Glu Lys Leu Lys Ala
20 25 30

ctg ctt gat gaa tct ttg gct cgg ggc att gat tcc agt tac cgt cca 319
Leu Leu Asp Glu Ser Leu Ala Arg Gly Ile Asp Ser Ser Tyr Arg Pro
35 40 45

tct caa aag gat gtg gag cca ccc aaa att tca agc aca aaa aac att 367
Ser Gln Lys Asp Val Glu Pro Pro Lys Ile Ser Ser Thr Lys Asn Ile
50 55 60 65

tcc att aag caa gag ccc aaa ata tca tcc agt ctt cct tct ggt aat 415
Ser Ile Lys Gln Glu Pro Lys Ile Ser Ser Ser Leu Pro Ser Gly Asn
70 75 80

aat aat ggc aag gtc ctc aca act gaa aag gta aag aag gaa gct gaa 463
Asn Asn Gly Lys Val Leu Thr Thr Glu Lys Val Lys Lys Glu Ala Glu
85 90 95

aag aga cct gct gat aaa atg aaa tca gac atc act gaa gga gtt gat 511
Lys Arg Pro Ala Asp Lys Met Lys Ser Asp Ile Thr Glu Gly Val Asp
100 105 110

att cca aag aaa cct aga ttg gag aaa cca gaa aca cag tca tct ccc 559
Ile Pro Lys Lys Pro Arg Leu Glu Lys Pro Glu Thr Gln Ser Ser Pro
115 120 125

att act gtc caa agt agc aag gat tta cct atg gct gac ctt tcc agt 607
Ile Thr Val Gln Ser Ser Lys Asp Leu Pro Met Ala Asp Leu Ser Ser

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130                 135                 140                 145

ttt gag gag acc agt gct gat gat ttt gcc atg gag atg gga ttg gcc      655
Phe Glu Glu Thr Ser Ala Asp Asp Phe Ala Met Glu Met Gly Leu Ala
                150                 155                 160

tgc gtt gtt tgt agg caa atg atg gtg gca tct ggc aat caa tta gta      703
Cys Val Val Cys Arg Gln Met Met Val Ala Ser Gly Asn Gln Leu Val
            165                 170                 175

gaa tgt cag gag tgc cat aat ctc tac cac cga gat tgt cat aaa ccc      751
Glu Cys Gln Glu Cys His Asn Leu Tyr His Arg Asp Cys His Lys Pro
        180                 185                 190

cag gtg aca gac aag gaa gcg aat gac cct cgc ctg gtg tgg tat tgt      799
Gln Val Thr Asp Lys Glu Ala Asn Asp Pro Arg Leu Val Trp Tyr Cys
    195                 200                 205

gcc cga tgt acc aga caa atg aaa aga atg gct caa aaa act cag aaa      847
Ala Arg Cys Thr Arg Gln Met Lys Arg Met Ala Gln Lys Thr Gln Lys
210                 215                 220                 225

cca ccg cag aaa cca gcc cct gca gtt gtt tct gta act cca gct gtc      895
Pro Pro Gln Lys Pro Ala Pro Ala Val Val Ser Val Thr Pro Ala Val
                230                 235                 240

aaa gat cca ttg gtt aag aaa cca gaa act aaa ctg aaa caa gag aca      943
Lys Asp Pro Leu Val Lys Lys Pro Glu Thr Lys Leu Lys Gln Glu Thr
            245                 250                 255

act ttt cta gcg ttt aag aga aca gaa gtc aag aca tcc aca gtt att      991
Thr Phe Leu Ala Phe Lys Arg Thr Glu Val Lys Thr Ser Thr Val Ile
        260                 265                 270

tca gga aat tct tct agt gcc agc gtt tcc tcg tca gta act agt ggc     1039
Ser Gly Asn Ser Ser Ser Ala Ser Val Ser Ser Ser Val Thr Ser Gly
    275                 280                 285

tta act gga tgg gca gct ttt gca gcc aaa act tcc tct gct ggt cct     1087
Leu Thr Gly Trp Ala Ala Phe Ala Ala Lys Thr Ser Ser Ala Gly Pro
290                 295                 300                 305

tca aca gca aaa ttg agt tca aca aca caa aac aat act ggg aaa cct     1135
Ser Thr Ala Lys Leu Ser Ser Thr Thr Gln Asn Asn Thr Gly Lys Pro
                310                 315                 320

gct act tcg tca gct aac cag aaa cct gtg ggt ttg act ggt ctg gca     1183
Ala Thr Ser Ser Ala Asn Gln Lys Pro Val Gly Leu Thr Gly Leu Ala
            325                 330                 335

aca tca tcc aaa ggt gga ata ggt tcc aaa ata ggt tcc aat aac agc     1231
Thr Ser Ser Lys Gly Gly Ile Gly Ser Lys Ile Gly Ser Asn Asn Ser
        340                 345                 350

act acg ccc act gta cct tta aaa cca cct cca cct cta acc ttg ggt     1279
Thr Thr Pro Thr Val Pro Leu Lys Pro Pro Pro Pro Leu Thr Leu Gly
    355                 360                 365
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aaa act ggc ctt agt cgc tca gtt agt tgt gac aat gtc agc aaa gta 1327
Lys Thr Gly Leu Ser Arg Ser Val Ser Cys Asp Asn Val Ser Lys Val
370 375 380 385

ggt ctt cct agt cca agt agt tta gtt cca gga agc agc agc caa cta 1375
Gly Leu Pro Ser Pro Ser Ser Leu Val Pro Gly Ser Ser Ser Gln Leu
390 395 400

agt ggg aat gga aat agt gga aca tca gga cct agt gga agt act acc 1423
Ser Gly Asn Gly Asn Ser Gly Thr Ser Gly Pro Ser Gly Ser Thr Thr
405 410 415

agc aaa act act tca gaa tcc agc agc tct ccc tca gca tcc ctt aaa 1471
Ser Lys Thr Thr Ser Glu Ser Ser Ser Ser Pro Ser Ala Ser Leu Lys
420 425 430

ggc cca act tca caa gaa tca cag ctc aat gct atg aag cga tta cag 1519
Gly Pro Thr Ser Gln Glu Ser Gln Leu Asn Ala Met Lys Arg Leu Gln
435 440 445

atg gtc aag aag aaa gct gcc caa aag aaa ctc aag aag taa tgtggcc 1568
Met Val Lys Lys Lys Ala Ala Gln Lys Lys Leu Lys Lys *
450 455 460

aagtaggttt ttgtatcata ttagcctaaa gatgaaaggc ttattattat gatataatct 1628

gtaatacact gtaatttaat aaaagtcttc ataatcaaaa aaaaaaaa 1676

<210> 61
<211> 1110
<212> DNA
<213> Homo sapiens

<220>
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<222> (158)..(1051)

<400> 61
gcgagactcg caggcgcaaa gagccccatt cacgccggcc caggtggcct caggtgaggg 60

ggggcggagc gcacctgtgg ggacgggacg acgagttcaa gcctccgtgg gtgcagttgg 120

tcgccagcga gggatgcgga gacgcccctg aacgacc atg gca tcg gcc gac gag 175
Met Ala Ser Ala Asp Glu
1 5

ctg acc ttc cat gaa ttc gag gag gcc act aat ctt ctg gct gac acc 223
Leu Thr Phe His Glu Phe Glu Glu Ala Thr Asn Leu Leu Ala Asp Thr
10 15 20

cca gat gca gcc acc acc agc aga agc gat cag ctg acc cca caa ggg 271
Pro Asp Ala Ala Thr Thr Ser Arg Ser Asp Gln Leu Thr Pro Gln Gly
25 30 35

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cac gtg gct gtg gcc gtg ggc tca ggt ggc agc tat gga gcc gag gat        319
His Val Ala Val Ala Val Gly Ser Gly Gly Ser Tyr Gly Ala Glu Asp
     40                  45                  50

gag gtg gag gag gag agt gac aag gcc gcg ctc ctg cag gag cag cag        367
Glu Val Glu Glu Glu Ser Asp Lys Ala Ala Leu Leu Gln Glu Gln Gln
 55                  60                  65                  70

cag cag cag cag ccg gga ttc tgg acc ttc agc tac tat cag agc ttc        415
Gln Gln Gln Gln Pro Gly Phe Trp Thr Phe Ser Tyr Tyr Gln Ser Phe
                 75                  80                  85

ttt gac gtg gac acc tca cag gtc ctg gac cgg atc aaa ggc tca ctg        463
Phe Asp Val Asp Thr Ser Gln Val Leu Asp Arg Ile Lys Gly Ser Leu
             90                  95                 100

ctg ccc cgg cct ggc cac aac ttt gtg cgg cac cat ctg cgg aat cgg        511
Leu Pro Arg Pro Gly His Asn Phe Val Arg His His Leu Arg Asn Arg
        105                 110                 115

ccg gat ctg tat ggc ccc ttc tgg atc tgt gcc acg ttg gcc ttt gtc        559
Pro Asp Leu Tyr Gly Pro Phe Trp Ile Cys Ala Thr Leu Ala Phe Val
    120                 125                 130

ctg gcc gtc act ggc aac ctg acg ctg gtg ctg gcc cag agg agg gac        607
Leu Ala Val Thr Gly Asn Leu Thr Leu Val Leu Ala Gln Arg Arg Asp
135                 140                 145                 150

ccc tcc atc cac tac agc ccc cag ttc cac aag gtg acc gtg gca ggc        655
Pro Ser Ile His Tyr Ser Pro Gln Phe His Lys Val Thr Val Ala Gly
                155                 160                 165

atc agc atc tac tgc tat gcg tgg ctg gtg ccc ctg gcc ctg tgg ggc        703
Ile Ser Ile Tyr Cys Tyr Ala Trp Leu Val Pro Leu Ala Leu Trp Gly
            170                 175                 180

ttc ctg cgg tgg cgc aag ggt gtc cag gag cgc atg ggg ccc tac acc        751
Phe Leu Arg Trp Arg Lys Gly Val Gln Glu Arg Met Gly Pro Tyr Thr
        185                 190                 195

ttc ctg gag act gtg tgc atc tac ggc tac tcc ctc ttt gtc ttc atc        799
Phe Leu Glu Thr Val Cys Ile Tyr Gly Tyr Ser Leu Phe Val Phe Ile
    200                 205                 210

ccc atg gtg gtc ctg tgg ctc atc cct gtg cct tgg ctg cag tgg ctc        847
Pro Met Val Val Leu Trp Leu Ile Pro Val Pro Trp Leu Gln Trp Leu
215                 220                 225                 230

ttt ggg gcg ctg gcc ctg ggc ctg tca gcc gcc ggg ctg gta ttc acc        895
Phe Gly Ala Leu Ala Leu Gly Leu Ser Ala Ala Gly Leu Val Phe Thr
                235                 240                 245

ctc tgg ccc gtg gtc cgt gag gac acc agg ctg gtg gcc aca gtg ctg        943
Leu Trp Pro Val Val Arg Glu Asp Thr Arg Leu Val Ala Thr Val Leu
            250                 255                 260
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ctg tcc gtg gtc gtg ctg ctc cag gcc ctc ctg gcc atg ggc tgt gaa       991
Leu Ser Val Val Val Leu Leu Gln Ala Leu Leu Ala Met Gly Cys Glu
        265                 270                 275

gtt gga ctt ctt ccg gtg tgc ctc ggg gac gtg gtc ctc ccc cca ttc      1039
Val Gly Leu Leu Pro Val Cys Leu Gly Asp Val Val Leu Pro Pro Phe
    280                 285                 290

att ttg ccc taa att gggggcctac tgtcgggccg ggcccctcag aggcgggccg      1094
Ile Leu Pro  *
295

gcccttggac ccttgg                                                    1110




     <210> 62
     <211> 1011
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (51)..(716)

     <400> 62
gcggcacgag gccccaaccc tgccctctct catgaccccg ctccgggatt   atg gcc        56
                                                         Met Ala
                                                           1

ggg act ggg ctg ctg gcg ctg cgg acg ctg cca ggg ccc agc tgg gtg       104
Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser Trp Val
        5                   10                  15

cga ggc tcg ggc cct tcc gtg ctg agc cgc ctg cag gac gcg gcc gtg       152
Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala Ala Val
    20                  25                  30

gtg cgg cct ggc ttc ctg agc acg gca gag gag gag acg ctg agc cga       200
Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu Ser Arg
35                  40                  45                  50

gaa ctg gag ccc gag ctg cgc cgc cgc cgc tac gaa tac gat cac tgg       248
Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp His Trp
                55                  60                  65

gac gcg gcc atc cac ggc ttc cga gag aca gag aag tcg cgc tgg tca       296
Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg Trp Ser
            70                  75                  80

gaa gcc agc cgg gcc atc ctg cag cgc gtg cag gcg gcc gcc ttt ggc       344
Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala Phe Gly
        85                  90                  95

ccc ggc cag acc ctg ctc tcc tcc gtg cac gtg ctg gac ctg gaa gcc       392
Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu Glu Ala
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    100                 105                 110

cgc ggc tac atc aag ccc cac gtg gac agc atc aag ttc tgc ggg gcc      440
Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys Gly Ala
115                 120                 125                 130

acc atc gcc ggc ctg tct ctc ctg tct ccc agc gtt atg cgg ctg gtg      488
Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg Leu Val
                135                 140                 145

cac acc cag gag ccg ggg gag tgg ctg gaa ctc ttg ctg gag ccg ggc      536
His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Leu Glu Pro Gly
            150                 155                 160

tcc ctc tac atc ctt agg ggc tca gcc cgt tat gac ttc tcc cat gag      584
Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser His Glu
        165                 170                 175

atc ctt cgg gat gaa gag tcc ttc ttt ggg gaa cgc cag att ccc cgg      632
Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Gln Ile Pro Arg
    180                 185                 190

ggc cgg cgc atc tcc gtg atc tgc cgc tcc ctc cct gag ggc atg ggg      680
Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly Met Gly
195                 200                 205                 210

cca ggg gag tct gga cag ccg ccc cca gcc tgc tga cccc cagctttcta      730
Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys  *
                215                 220

cagacaccag atttgtgaat aaagttgggg aatggacagc ctaactggga cattgcagtg    790

gctgcttgct ggggccggga tttgcagggg aacccaggat ggcactggcc catagggagc    850

tccaggtgtg gctggctgga cacatggtca aagtcacaag gccgggagag tggtgtcctt    910

tattgcactc actgctggtc gccccagccc actcccctcc tcgttgtctc tgcatccagg    970

tctccaataa ataagtcagc cgagaaaaag aaaaaaaaaa a                       1011



      <210> 63
      <211> 842
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (194)..(736)

      <400> 63
ctggaccgcc ccttcgaggg gctgatgtat ataactatct attcgatgat gaagataccc     60

caccaaaccc aaaaaaagag atctctcgag gatccgaatt cgcggccgcg tcgacatcgc    120
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agggagccgg tccgccgccg gaacgggagc ctgggtgtgc gtgtggagtc cggactcgtg    180

ggagacgatc gcg   atg aac acg gtg ctg tcg cgg gcg aac tca ctg ttc     229
                 Met Asn Thr Val Leu Ser Arg Ala Asn Ser Leu Phe
                   1               5                  10

gcc ttc tcg ctg agc gtg atg gcg gcg ctc acc ttc ggc tgc ttc atc      277
Ala Phe Ser Leu Ser Val Met Ala Ala Leu Thr Phe Gly Cys Phe Ile
         15                  20                  25

acc acc gcc ttc aaa gac agg agc gtc ccg gtg cgg ctg cac gtc tcg      325
Thr Thr Ala Phe Lys Asp Arg Ser Val Pro Val Arg Leu His Val Ser
     30                  35                  40

cgg atc ata cta aaa aat gta gaa gat ttc act gga cct aga gaa aga      373
Arg Ile Ile Leu Lys Asn Val Glu Asp Phe Thr Gly Pro Arg Glu Arg
 45                  50                  55                  60

agt gat ctg gga ttt atc aca ttt gat ata act gct gat cta gag aat      421
Ser Asp Leu Gly Phe Ile Thr Phe Asp Ile Thr Ala Asp Leu Glu Asn
                 65                  70                  75

ata ttt gat tgg aat gtt aag cag ttg ttt ctt tat tta tca gca gaa      469
Ile Phe Asp Trp Asn Val Lys Gln Leu Phe Leu Tyr Leu Ser Ala Glu
             80                  85                  90

tat tca aca aaa aat aat gct ctg aac caa gtt gtc cta tgg gac aag      517
Tyr Ser Thr Lys Asn Asn Ala Leu Asn Gln Val Val Leu Trp Asp Lys
         95                 100                 105

att gtt ttg aga ggt gat aat ccg aag ctg ctg ctg aaa gat atg aaa      565
Ile Val Leu Arg Gly Asp Asn Pro Lys Leu Leu Leu Lys Asp Met Lys
    110                 115                 120

aca aaa tat ttt ttc ttt gac gat gga aat ggt ctc aag gga aac agg      613
Thr Lys Tyr Phe Phe Phe Asp Asp Gly Asn Gly Leu Lys Gly Asn Arg
125                 130                 135                 140

aat gtc act ttg acc ctg tct tgg aac gtc gta cca aat gct gga att      661
Asn Val Thr Leu Thr Leu Ser Trp Asn Val Val Pro Asn Ala Gly Ile
                145                 150                 155

cta cct ctt gtg aca gga tca gga cac gta tct gtc cca ttt cca gat      709
Leu Pro Leu Val Thr Gly Ser Gly His Val Ser Val Pro Phe Pro Asp
            160                 165                 170

aca tat gaa ata acg aag agt tat taa attat tctgaatttg aaacaacata      761
Thr Tyr Glu Ile Thr Lys Ser Tyr  *
        175                 180

tttttatact taatgaattg tatctcatta atctcttccc ttacatcttc atgtattgtt    821

ggtttgtttt ttggttttgg g                                              842
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<210> 64
<211> 4027
<212> DNA
<213> Homo sapiens

<220>
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<222> (1021)..(3825)

<400> 64
gcaaacatac tttaataagt taaagaaaat aacaaaaaca gtacagcaaa gatactgggc       60

aatgaaagaa agaaacatac aatttcaaag gtataacaaa ctgaggcatt ctgtaatata      120

cattcaggct atttttaggg gaaagaaagc tagaagacat ttaaaaatga tgcatatagc      180

cgcaactctc attcagagga gatttagaac tctaatgatg agaagaagat tcctctctct      240

caagaaaact gctattttga ttcagagaaa atatcgggca catctttgta caaagcatca      300

cttacagttc cttcaggtac aaaatgcagt tattaaaatc cagtcatcat acagaagatg      360

gatgataagg aaaaggatgc gagagatgca cagggctgct actttcatcc agtctacttt      420

cagaatgcac agattacata tgagatatca ggctttgaaa caggcctccg ttgtgatcca      480

acagcaatac caagcaaata gagctgcaaa actgcagagg cagcattatc tcagacaaag      540

acactctgct gtgatccttc aggctgcatt caggggtatg aaaactagaa gacatttgaa      600

gagtatgcat tcctctgcaa cccttattca gagtaggttt agatcattac tggtgaggag      660

aagattcatt tccctcaaaa aagctactat tttgttcag aggaaatatc gagccaccat       720

ttgtgccaaa cataaattgt accaattctt gcacttaaga aaggcagcca ttacaataca      780

gtcatcttac agaagactga tggtaaagaa gaagttacaa gaaatgcaaa gggctgcagt      840

tctcattcag gctactttca ggatgcacag aaaaaaaaat atattacatt tcagacttgg      900

aaacatgctt caattctaat tcagcaacat tatcgaacat atagagctgc aaaattgcaa      960

agagaaaatt atatcagaca atggcattct gctgtggtta ttcaggctgc atataaagga     1020

atg aaa gca aga caa ctt tta agg gaa aaa cac aaa gct tct atc gta       1068
Met Lys Ala Arg Gln Leu Leu Arg Glu Lys His Lys Ala Ser Ile Val
 1               5                   10                  15

ata caa agc acc tac aga atg tat agg cag tat tgt ttc tac caa aag       1116
Ile Gln Ser Thr Tyr Arg Met Tyr Arg Gln Tyr Cys Phe Tyr Gln Lys
             20                  25                  30

ctt cag tgg gct aca aaa atc ata caa gaa aaa tat aga gca aat aaa       1164
Leu Gln Trp Ala Thr Lys Ile Ile Gln Glu Lys Tyr Arg Ala Asn Lys
         35                  40                  45

aag aaa cag aaa gta ttt caa cac aat gaa ctt aag aaa gag act tgt       1212
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Lys Lys Gln Lys Val Phe Gln His Asn Glu Leu Lys Lys Glu Thr Cys
     50                  55                  60

gtt cag gca ggt ttt cag gac atg aac ata aaa aaa cag att cag gaa       1260
Val Gln Ala Gly Phe Gln Asp Met Asn Ile Lys Lys Gln Ile Gln Glu
 65                  70                  75                  80

cag cac cag gct gcc att att att cag aag cat tgt aaa gcc ttt aaa       1308
Gln His Gln Ala Ala Ile Ile Ile Gln Lys His Cys Lys Ala Phe Lys
                 85                  90                  95

ata agg aag cat tat ctc cac ctt aga gca aca gta gtt tct att caa       1356
Ile Arg Lys His Tyr Leu His Leu Arg Ala Thr Val Val Ser Ile Gln
            100                 105                 110

aga aga tac aga aaa cta act gca gtg cgt acc caa gca gtt att tgt       1404
Arg Arg Tyr Arg Lys Leu Thr Ala Val Arg Thr Gln Ala Val Ile Cys
        115                 120                 125

ata cag tct tat tac aga ggc ttt aaa gta cga aag gat att caa aat       1452
Ile Gln Ser Tyr Tyr Arg Gly Phe Lys Val Arg Lys Asp Ile Gln Asn
    130                 135                 140

atg cac cgg gct gcc aca cta att cag tca ttc tat cga atg cac agg       1500
Met His Arg Ala Ala Thr Leu Ile Gln Ser Phe Tyr Arg Met His Arg
145                 150                 155                 160

gcc aaa gtt gat tat gaa aca aag aaa act gca att gtg gtt ata cag       1548
Ala Lys Val Asp Tyr Glu Thr Lys Lys Thr Ala Ile Val Val Ile Gln
                165                 170                 175

aat tat tat agg ttg tat gtt aga gta aaa aaa aaa aaa aaa aac ttt       1596
Asn Tyr Tyr Arg Leu Tyr Val Arg Val Lys Lys Lys Lys Lys Asn Phe
            180                 185                 190

tta gca gtt cag aaa tct gta cga act att cag gct gct ttt aga ggc       1644
Leu Ala Val Gln Lys Ser Val Arg Thr Ile Gln Ala Ala Phe Arg Gly
        195                 200                 205

atg aaa gtt aga caa aaa ttg aaa aat gta tca gag gaa aag atg gca       1692
Met Lys Val Arg Gln Lys Leu Lys Asn Val Ser Glu Glu Lys Met Ala
    210                 215                 220

gcc att gtt aac caa tct gca ctc tgc tgt tac aga agc aaa act cag       1740
Ala Ile Val Asn Gln Ser Ala Leu Cys Cys Tyr Arg Ser Lys Thr Gln
225                 230                 235                 240

tat gaa gct gtt caa agt gaa ggt gtt atg att caa gag tgg tat aaa       1788
Tyr Glu Ala Val Gln Ser Glu Gly Val Met Ile Gln Glu Trp Tyr Lys
                245                 250                 255

gct tct ggc ctt gct tgt tca cag gaa gca gag tat cat tct caa agt       1836
Ala Ser Gly Leu Ala Cys Ser Gln Glu Ala Glu Tyr His Ser Gln Ser
            260                 265                 270

agg gct gca gta aca att caa aaa gct ttt tgt aga atg gtc aca aga       1884
Arg Ala Ala Val Thr Ile Gln Lys Ala Phe Cys Arg Met Val Thr Arg
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        275                 280                 285

aaa ctg gaa aca cag aaa tgt gct gcc cta cgg att cag ttc ttc ctt      1932
Lys Leu Glu Thr Gln Lys Cys Ala Ala Leu Arg Ile Gln Phe Phe Leu
    290                 295                 300

cag atg gct gtg tat cgg aga aga ttt gtt cag cag aaa aga gct gct      1980
Gln Met Ala Val Tyr Arg Arg Arg Phe Val Gln Gln Lys Arg Ala Ala
305                 310                 315                 320

atc act tta cag cat tat ttt agg acg tgg caa acc aga aaa cag ttt      2028
Ile Thr Leu Gln His Tyr Phe Arg Thr Trp Gln Thr Arg Lys Gln Phe
                325                 330                 335

tta cta tat aga aaa gca gca gtg gtt tta caa aat cac tac aga gca      2076
Leu Leu Tyr Arg Lys Ala Ala Val Val Leu Gln Asn His Tyr Arg Ala
            340                 345                 350

ttt ctg tct gca aaa cat caa aga caa gtc tat tta cag atc aga agc      2124
Phe Leu Ser Ala Lys His Gln Arg Gln Val Tyr Leu Gln Ile Arg Ser
        355                 360                 365

agt gtt atc att att caa gct aga agt aaa gga ttt ata cag aaa cgg      2172
Ser Val Ile Ile Ile Gln Ala Arg Ser Lys Gly Phe Ile Gln Lys Arg
    370                 375                 380

aag ttt cag gaa att aaa aat agc acc ata aaa att cag gct atg tgg      2220
Lys Phe Gln Glu Ile Lys Asn Ser Thr Ile Lys Ile Gln Ala Met Trp
385                 390                 395                 400

agg aga tat aga gcc aag aaa tat tta tgt aaa gtg aaa gct gcc tgc      2268
Arg Arg Tyr Arg Ala Lys Lys Tyr Leu Cys Lys Val Lys Ala Ala Cys
                405                 410                 415

aag att caa gcc tgg tat aga tgt tgg aga gca cac aaa gaa tat cta      2316
Lys Ile Gln Ala Trp Tyr Arg Cys Trp Arg Ala His Lys Glu Tyr Leu
            420                 425                 430

gct gta tta aaa gct gtt aaa att att caa ggt tgc ttc tat acc aaa      2364
Ala Val Leu Lys Ala Val Lys Ile Ile Gln Gly Cys Phe Tyr Thr Lys
        435                 440                 445

cta gag aga aca cgg ttt ttg aat gtg aga gca tca gca att atc att      2412
Leu Glu Arg Thr Arg Phe Leu Asn Val Arg Ala Ser Ala Ile Ile Ile
    450                 455                 460

cag aga aaa tgg aga gct ata ctt cct gca aag ata gct cat gaa cac      2460
Gln Arg Lys Trp Arg Ala Ile Leu Pro Ala Lys Ile Ala His Glu His
465                 470                 475                 480

ttc tta atg ata aaa aga cat cga gct gct tgt ttg atc caa gca cat      2508
Phe Leu Met Ile Lys Arg His Arg Ala Ala Cys Leu Ile Gln Ala His
                485                 490                 495

tat aga gga tat aaa gga agg cag gtc tct ctt cgg cag aaa tct gct      2556
Tyr Arg Gly Tyr Lys Gly Arg Gln Val Ser Leu Arg Gln Lys Ser Ala
            500                 505                 510
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gct ttg atc ata caa aaa tat ata cga gcc agg gag gct gga aag cat      2604
Ala Leu Ile Ile Gln Lys Tyr Ile Arg Ala Arg Glu Ala Gly Lys His
        515                 520                 525

gaa agg ata aaa tat att gaa ttt aaa aaa tct aca gtt atc cta caa      2652
Glu Arg Ile Lys Tyr Ile Glu Phe Lys Lys Ser Thr Val Ile Leu Gln
    530                 535                 540

gca ctg gtg cgt ggt tgg cta gta cga aaa aga ttt tta gaa cag aga      2700
Ala Leu Val Arg Gly Trp Leu Val Arg Lys Arg Phe Leu Glu Gln Arg
545                 550                 555                 560

gcc aaa att cga ctt ctt cac ttc act gca gct gca tat tat cac ctg      2748
Ala Lys Ile Arg Leu Leu His Phe Thr Ala Ala Ala Tyr Tyr His Leu
                565                 570                 575

aat gct gtt aga att caa aga gcc tat aaa ctt tac ctg gct gtg aag      2796
Asn Ala Val Arg Ile Gln Arg Ala Tyr Lys Leu Tyr Leu Ala Val Lys
        580                 585                 590

aat gct aac aag cag gtt aat tca gtc atc tgt att cag aga tgg ttt      2844
Asn Ala Asn Lys Gln Val Asn Ser Val Ile Cys Ile Gln Arg Trp Phe
        595                 600                 605

cga gca aga tta caa gaa aag aga ttt att cag aaa tat cat agc atc      2892
Arg Ala Arg Leu Gln Glu Lys Arg Phe Ile Gln Lys Tyr His Ser Ile
    610                 615                 620

aaa aag att gag cat gaa ggt caa gaa tgt ctg agc cag cga aat agg      2940
Lys Lys Ile Glu His Glu Gly Gln Glu Cys Leu Ser Gln Arg Asn Arg
625                 630                 635                 640

gct gca tca gta ata cag aaa gca gtg cgc cat ttt ctc ctc cgt aaa      2988
Ala Ala Ser Val Ile Gln Lys Ala Val Arg His Phe Leu Leu Arg Lys
                645                 650                 655

aag cag gaa aaa ttc act agt gga atc att aaa att cag gca tta tgg      3036
Lys Gln Glu Lys Phe Thr Ser Gly Ile Ile Lys Ile Gln Ala Leu Trp
                660                 665                 670

aga ggc tat tct tgg agg aag aaa aat gat tgt aca aaa att aaa gct      3084
Arg Gly Tyr Ser Trp Arg Lys Lys Asn Asp Cys Thr Lys Ile Lys Ala
        675                 680                 685

ata cga cta agt ctt caa gtt gtt aat agg gag att cga gaa gaa aac      3132
Ile Arg Leu Ser Leu Gln Val Val Asn Arg Glu Ile Arg Glu Glu Asn
    690                 695                 700

aaa ctc tac aaa aga act gca ctt gca ctt cat tac ctt ttg aca tat      3180
Lys Leu Tyr Lys Arg Thr Ala Leu Ala Leu His Tyr Leu Leu Thr Tyr
705                 710                 715                 720

aag cac ctt tct gcc att ctt gag gcc tta aaa cac cta gag gta gtt      3228
Lys His Leu Ser Ala Ile Leu Glu Ala Leu Lys His Leu Glu Val Val
                725                 730                 735
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act aga ttg tct cca ctt tgt tgt gag aac atg gcc cag agt gga gca       3276
Thr Arg Leu Ser Pro Leu Cys Cys Glu Asn Met Ala Gln Ser Gly Ala
            740                 745                 750

att tct aaa ata ttt gtt ttg atc cga agt tgt aat cgc agt att cct       3324
Ile Ser Lys Ile Phe Val Leu Ile Arg Ser Cys Asn Arg Ser Ile Pro
        755                 760                 765

tgt atg gaa gtc atc aga tat gct gtg caa gtc ttg ctt aat gta tct       3372
Cys Met Glu Val Ile Arg Tyr Ala Val Gln Val Leu Leu Asn Val Ser
    770                 775                 780

aag tat gag aaa act act tca gca gtt tat gat gta gaa aat tgt ata       3420
Lys Tyr Glu Lys Thr Thr Ser Ala Val Tyr Asp Val Glu Asn Cys Ile
785                 790                 795                 800

gat ata cta ttg gag ctt ttg cag ata tac cga gaa aag cct ggt aat       3468
Asp Ile Leu Leu Glu Leu Leu Gln Ile Tyr Arg Glu Lys Pro Gly Asn
                805                 810                 815

aaa gtt gca gac aaa ggc gga agc att ttt aca aaa act tgt tgt ttg       3516
Lys Val Ala Asp Lys Gly Gly Ser Ile Phe Thr Lys Thr Cys Cys Leu
            820                 825                 830

ttg gct att tta ctg aag aca aca aat aga gcc tct gat gta cga agt       3564
Leu Ala Ile Leu Leu Lys Thr Thr Asn Arg Ala Ser Asp Val Arg Ser
        835                 840                 845

agg tcc aaa gtt gtt gac cgt att tac agt ctc tac aaa ctt aca gct       3612
Arg Ser Lys Val Val Asp Arg Ile Tyr Ser Leu Tyr Lys Leu Thr Ala
    850                 855                 860

cat aaa cat aaa atg aat act gaa aga ata ctt tac aag caa aag aag       3660
His Lys His Lys Met Asn Thr Glu Arg Ile Leu Tyr Lys Gln Lys Lys
865                 870                 875                 880

aat tct tct ata agc att cct ttt atc cca gaa aca cct gta agg acc       3708
Asn Ser Ser Ile Ser Ile Pro Phe Ile Pro Glu Thr Pro Val Arg Thr
                885                 890                 895

aga ata gtt tca aga ctt aag cca gat tgg gtt ttg aga aga gat aac       3756
Arg Ile Val Ser Arg Leu Lys Pro Asp Trp Val Leu Arg Arg Asp Asn
            900                 905                 910

atg gaa gaa atc aca aat ccc ctg caa gct att caa atg gtg atg gat       3804
Met Glu Glu Ile Thr Asn Pro Leu Gln Ala Ile Gln Met Val Met Asp
        915                 920                 925

acg ctt ggc att cct tat tag ta aatgtaaaca ttttcagtat gtatagtgta        3857
Thr Leu Gly Ile Pro Tyr  *
    930                 935

aagaaatatt aaagccaatc atgagtacgt aaagtgattt ttgctctctg tgtacaactt     3917

ttaaaatctg actttgtttt aaaaaaacat aaactgttca ttacattctt catttttatc     3977

atttatagtt ttatgcatgt aataaactaa tatgtcataa aaaaaaaaaa                4027
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<213> Homo sapiens

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<222> (1335)..(2939)

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taatcaaaat gaaaatttag tacctaacaa tcgtgttcaa atacacagaa gccctgcaca 120

gaatttagtt ggagagaaca atcatgatgt tgataacagt gacctcccag tattgtccac 180

tgatcaagat gaaagtttgc tgttatttga agatgttaat acagagttcg acgatgtgag 240

tctttcaccc ttgaacagta aaagcgaatc tttacctgtg tcagacaaaa ctgctattag 300

tgaaacgcct ctggtctctc agttcttaat ttctgatgaa cttttgttgg acaataattc 360

tgaactccaa gatcaaatca cccgtgatgc taatagtttt aaatctcgtg atcagagagg 420

tgtacaggaa gaaaaagtga agaatcatga ggatattttt gattgctcta gggatttatt 480

ttctgttacc tttgatttag gattctgtag tccagattct gatgatgaaa tattggaaca 540

tacatcagat agcaatagac ctctagatga tctatatgga aggtatttgg aaattaagga 600

gataagtgat gcaaattatg tttcgaatca agcactaata ccaagagatc atagtaaaaa 660

ttttactagt ggaactgtta ttatcccatc aaatgaagat atgcagaatc caaattatgt 720

acatttgcca ctgagtgcag caaaaaatga agaattgtta tctcctggtt attctcagtt 780

ttctttacca gtgcaaaaaa aagttatgag tacaccactc tctaaatcaa acacattgaa 840

ctcattttct aagataagaa aggaaatact taagacacca gattctagta aggaaaaagt 900

aaacctacaa agattcaaag aagcattgaa ttcaactttt gattattcag aattttctct 960

agaaaagtct aaaagcagtg gtccaatgta tctgcataaa tcctgtcatt ctgttgaaga 1020

tggacaatta ttaacaagta acgaaagtga agatgacgag attttccgaa gaaaagttaa 1080

aagagcaaaa ggaaatgttt taaactctcc tgaggatcag aaaaatagtg aagttgattc 1140

tccacttcat gctgtcaaaa agcgcagatt tcctataaac agatcagaat tatcatctag 1200

tgatgagagt gagaattttc ccaaaccatg ttcacaatta gaagacttca aggtttgtaa 1260

cgggaatgcc agaagaggca tcaaagtccc aaagagacag agtcacttaa agcatgtagc 1320

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taggaagttt ttag  atg atg aag cag aac ttt ctg aag aag atg cag aat    1370
                 Met Met Lys Gln Asn Phe Leu Lys Lys Met Gln Asn
                   1               5                  10

atg ttt cat cag atg aaa atg atg agt cag aaa atg aac aag att cct     1418
Met Phe His Gln Met Lys Met Met Ser Gln Lys Met Asn Lys Ile Pro
         15                  20                  25

cat tac ttg act ttt tta aat gat gaa act caa ctt tca cag gct ata     1466
His Tyr Leu Thr Phe Leu Asn Asp Glu Thr Gln Leu Ser Gln Ala Ile
     30                  35                  40

aat gat tct gaa atg aga gct att tac atg aaa tct ttg cgt agt cca     1514
Asn Asp Ser Glu Met Arg Ala Ile Tyr Met Lys Ser Leu Arg Ser Pro
 45                  50                  55                  60

atg atg aac aat aag tac aaa atg att cat aag aca cat aaa aac ata     1562
Met Met Asn Asn Lys Tyr Lys Met Ile His Lys Thr His Lys Asn Ile
                 65                  70                  75

aac att ttc tcg cag att cct gaa caa gat gaa acc tat tta gag gat     1610
Asn Ile Phe Ser Gln Ile Pro Glu Gln Asp Glu Thr Tyr Leu Glu Asp
             80                  85                  90

agt ttt tgt gtt gat gaa gag gag tct tgc aaa ggc caa tca agt gaa     1658
Ser Phe Cys Val Asp Glu Glu Glu Ser Cys Lys Gly Gln Ser Ser Glu
         95                 100                 105

gaa gaa gtt tgt gtt gat ttt aac tta ata act gat gat tgc ttt gca     1706
Glu Glu Val Cys Val Asp Phe Asn Leu Ile Thr Asp Asp Cys Phe Ala
    110                 115                 120

aat agt aaa aag tat aaa act cga cgt gca gta atg cta aaa gaa atg     1754
Asn Ser Lys Lys Tyr Lys Thr Arg Arg Ala Val Met Leu Lys Glu Met
125                 130                 135                 140

atg gaa caa aat tgt gca cat tca aaa aaa aaa tta tcc aga att att     1802
Met Glu Gln Asn Cys Ala His Ser Lys Lys Lys Leu Ser Arg Ile Ile
                145                 150                 155

tta cca gat gat tca agt gag gag gag aac aat gta aat gat aaa aga     1850
Leu Pro Asp Asp Ser Ser Glu Glu Glu Asn Asn Val Asn Asp Lys Arg
            160                 165                 170

gaa tct aat act gcg gtt aac cca agc act gtt aag aag aac aaa caa     1898
Glu Ser Asn Thr Ala Val Asn Pro Ser Thr Val Lys Lys Asn Lys Gln
        175                 180                 185

cag gac cat tgt tta aat tca gtg cct tct gga tct tct gcg cag tcc     1946
Gln Asp His Cys Leu Asn Ser Val Pro Ser Gly Ser Ser Ala Gln Ser
    190                 195                 200

aag gtg cgt tct act cca aga gtt aat cca tta gca aag cag agc aaa     1994
Lys Val Arg Ser Thr Pro Arg Val Asn Pro Leu Ala Lys Gln Ser Lys
205                 210                 215                 220
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cag aca ttg ctg aat tta aag gat aca att tcc gaa gtc tca gac ttc     2042
Gln Thr Leu Leu Asn Leu Lys Asp Thr Ile Ser Glu Val Ser Asp Phe
                225                 230                 235

aaa cct cag aat cat aat gaa gtc cag tct acc aca cca ccc ttc act     2090
Lys Pro Gln Asn His Asn Glu Val Gln Ser Thr Thr Pro Pro Phe Thr
            240                 245                 250

act gtt gat tca cag aaa gac tgt aga aaa ttt cca gtt cca cag aag     2138
Thr Val Asp Ser Gln Lys Asp Cys Arg Lys Phe Pro Val Pro Gln Lys
        255                 260                 265

agg ttc gga cat cta gca cta atg ttt ccc atg ccc tct gcc tct gca     2186
Arg Phe Gly His Leu Ala Leu Met Phe Pro Met Pro Ser Ala Ser Ala
    270                 275                 280

aaa aga gga gct cat ggt cca cag gat ttg gca gat tac ttt gga aag     2234
Lys Arg Gly Ala His Gly Pro Gln Asp Leu Ala Asp Tyr Phe Gly Lys
285                 290                 295                 300

gaa agc tgg gat ggt agt gct ttg gag gat tct agc act tca ggg gca     2282
Glu Ser Trp Asp Gly Ser Ala Leu Glu Asp Ser Ser Thr Ser Gly Ala
                305                 310                 315

tcc tgt tcc aag tca aga cca cat tta gct ggg aca cat act tct ctt     2330
Ser Cys Ser Lys Ser Arg Pro His Leu Ala Gly Thr His Thr Ser Leu
            320                 325                 330

aga ctt ccg cag gaa gga aaa gga acc tgt att ctt gta ggt ggt cat     2378
Arg Leu Pro Gln Glu Gly Lys Gly Thr Cys Ile Leu Val Gly Gly His
        335                 340                 345

gaa atc act tct gga tta gaa gta att tct tcc cta aga gca att cat     2426
Glu Ile Thr Ser Gly Leu Glu Val Ile Ser Ser Leu Arg Ala Ile His
    350                 355                 360

ggg ttg caa gta gaa gtt tgt cct ctt aat ggc tgt gat tac atc gtg     2474
Gly Leu Gln Val Glu Val Cys Pro Leu Asn Gly Cys Asp Tyr Ile Val
365                 370                 375                 380

agt aat cgc atg gtg gtg gaa agg agg tct caa tct gag atg tta aat     2522
Ser Asn Arg Met Val Val Glu Arg Arg Ser Gln Ser Glu Met Leu Asn
                385                 390                 395

agt gtc aat aag aac aag ttc att gag cag atc cag cac ctg cag agt     2570
Ser Val Asn Lys Asn Lys Phe Ile Glu Gln Ile Gln His Leu Gln Ser
            400                 405                 410

atg ttt gaa aga ata tgt gtg att gtg gaa aag gac aga gaa aaa aca     2618
Met Phe Glu Arg Ile Cys Val Ile Val Glu Lys Asp Arg Glu Lys Thr
        415                 420                 425

gga gac aca tca agg atg ttt agg aga aca aag agc tat gac agc ctg     2666
Gly Asp Thr Ser Arg Met Phe Arg Arg Thr Lys Ser Tyr Asp Ser Leu
    430                 435                 440

ctg act acc tta att ggc gct gga atc cga att ctt ttc agt tcc tgc     2714
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Leu Thr Thr Leu Ile Gly Ala Gly Ile Arg Ile Leu Phe Ser Ser Cys
445                 450                 455                 460

caa gaa gaa acc gca gat ttg cta aag gaa ctg tct tta gtg gaa caa      2762
Gln Glu Glu Thr Ala Asp Leu Leu Lys Glu Leu Ser Leu Val Glu Gln
                465                 470                 475

aga aag aat gtt ggt att cat gtt cca aca gtg gtg aat agt aat aaa      2810
Arg Lys Asn Val Gly Ile His Val Pro Thr Val Val Asn Ser Asn Lys
            480                 485                 490

agt gag gca ctc cag ttt tat tta agt att ccc aat ata agt tat ata      2858
Ser Glu Ala Leu Gln Phe Tyr Leu Ser Ile Pro Asn Ile Ser Tyr Ile
        495                 500                 505

act gca tta aat atg tgt cac cag ttt tca tct gtg aaa agg atg gct      2906
Thr Ala Leu Asn Met Cys His Gln Phe Ser Ser Val Lys Arg Met Ala
    510                 515                 520

aac agg tat gtc tgt tgt aat att ttt aaa tga ttactttt aaaagattcg      2957
Asn Arg Tyr Val Cys Cys Asn Ile Phe Lys  *
525                 530                 535

taaaagcatt ccatagaagt ttaatgttaa aaaaatttaa gcggcatcat gcctgttaga    3017

ttattttatt cagtaaacat tttttgcctg ccaacatata ttagttactg tatgaagcta    3077

agggacatta ttcgaaaaaa aaaaaa                                         3103



     <210> 66
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     <212> DNA
     <213> Homo sapiens

     <220>
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     <222> (337)..(912)

     <400> 66
ccgtgcgacc cacgcgccgg ttaccactgg cagagcaaat atgactcaga aaccggctcc      60

tcagggttgt aacattagat gatacaggct tgggtcgtta cacatgacac cagtgccttt     120

gtttcattgg gctgggctct ctggaaggtg tgctgctgcc tgagctgctg gaaaagcact     180

gacaggtgtt tgctagaaaa gcactcctgg agcttgccac cagcttggac ttctagggac     240

tttcctctca gccaggaagg attttgatat tcatcagaaa tacctccaga agattcaagg     300

agctgtagag gtgaagtaag cctgtgaagg accagc atg gga atc cta tac tct       354
                                        Met Gly Ile Leu Tyr Ser
                                         1               5

gag ccc atc tgc caa gca gcc tat cag aat gac ttt gga caa gtg tgg       402
```

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Glu Pro Ile Cys Gln Ala Ala Tyr Gln Asn Asp Phe Gly Gln Val Trp
            10                  15                  20

cgg tgg gtg aaa gaa gac agc agc tat gcc aac gtt caa gat ggc ttt      450
Arg Trp Val Lys Glu Asp Ser Ser Tyr Ala Asn Val Gln Asp Gly Phe
        25                  30                  35

aat gga gac acg ccc ctg atc tgt gct tgc agg cga ggg cat gtg aga      498
Asn Gly Asp Thr Pro Leu Ile Cys Ala Cys Arg Arg Gly His Val Arg
    40                  45                  50

atc gtt tcc ttc ctt tta aga aga aat gct aat gtc aac ctc aaa aac      546
Ile Val Ser Phe Leu Leu Arg Arg Asn Ala Asn Val Asn Leu Lys Asn
 55                  60                  65                  70

cag aaa gag aga acc tgc ttg cat tat gct gtg aag aaa aaa ttt acc      594
Gln Lys Glu Arg Thr Cys Leu His Tyr Ala Val Lys Lys Lys Phe Thr
                75                  80                  85

ttc att gat tat cta cta att atc ctc tta atg cct gtt ctg ctt att      642
Phe Ile Asp Tyr Leu Leu Ile Ile Leu Leu Met Pro Val Leu Leu Ile
            90                  95                 100

ggg tat ttc ctc atg gta tca aag aca aag cag aat gag gct ctt gta      690
Gly Tyr Phe Leu Met Val Ser Lys Thr Lys Gln Asn Glu Ala Leu Val
        105                 110                 115

cga atg cta ctt gat gct ggc gtc gaa gtt aat gct aca gat tgt tat      738
Arg Met Leu Leu Asp Ala Gly Val Glu Val Asn Ala Thr Asp Cys Tyr
    120                 125                 130

ggc tgt acc gca tta cat tat gcc tgt gaa atg aaa aac cag tct ctt      786
Gly Cys Thr Ala Leu His Tyr Ala Cys Glu Met Lys Asn Gln Ser Leu
135                 140                 145                 150

atc cct ctg ctc ttg gaa gcc cgt gca gac ccc aca ata aag aat aag      834
Ile Pro Leu Leu Leu Glu Ala Arg Ala Asp Pro Thr Ile Lys Asn Lys
                155                 160                 165

cat ggt gag agc tca ctg gat att gca cgg aga tta aaa ttt tcc cag      882
His Gly Glu Ser Ser Leu Asp Ile Ala Arg Arg Leu Lys Phe Ser Gln
            170                 175                 180

att gaa tta atg cta agg aaa gca ttg taa t ccttgtgacc acaccgatgg      933
Ile Glu Leu Met Leu Arg Lys Ala Leu  *
        185                 190

agatacagaa aaagttaacg actggattct atcttcattt tagacttttg gtctgtgggc    993

catttaacct ggatgccacc attttatggg gataatgatg cttaccatgg ttaatgtttt   1053

ggaagagctt tttatttata gcattgttta ctcagtcaag ttcaccatgg ccgtaatcct   1113

tctaagggaa acactaaagt tgttgtagtc tccatttcag tcagaaactg atgtttcagc   1173

taggcacagt ggtacatgcc tgt                                           1196
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<211> 529
<212> DNA
<213> Homo sapiens

<220>
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<222> (209)..(403)

<400> 67
cttttgttcc ttcattcagc ggaagagaat tgtgtgctta ctgtgtgctg ggctccagtg      60

ttgcaaagtg aataatgtac tagatctctg cccttgaagg tctcactttg tgatttcagt     120

gcaaattact taatctcagt aggcctcagt tctctctttc accaaatcag gagaattatt     180

tttttaatca tcaactgtac attattat   atg caa aac ata ctg gta ggc att      232
                                 Met Gln Asn Ile Leu Val Gly Ile
                                   1               5

atg tgg acc aaa aaa tat gac agc agg tgg tcc ttc cct ttt aag aaa       280
Met Trp Thr Lys Lys Tyr Asp Ser Arg Trp Ser Phe Pro Phe Lys Lys
     10                  15                  20

cta aga tat aca cac atg aag act gct ggt ggt gca agg tgt gga gtc       328
Leu Arg Tyr Thr His Met Lys Thr Ala Gly Gly Ala Arg Cys Gly Val
 25                  30                  35                  40

att ggt gcc gtg ata gca gtg tgc agg tca gag cta gag agt cca gag       376
Ile Gly Ala Val Ile Ala Val Cys Arg Ser Glu Leu Glu Ser Pro Glu
                 45                  50                  55

aag gga ctt tgc tgt ggg ctg aag tga ccagg aagggctccg tggaggaagt       428
Lys Gly Leu Cys Cys Gly Leu Lys  *
             60                  65

ggggcccaag gatggacagg acatggatgt ggcaggaaga gggagagcct taccagatgg     488

gccagacttc cggaaccaag atgttgctgg tgggatgtgt g                         529




<210> 68
<211> 309
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (16)..(267)

<400> 68
ctggtcggga ttggg atg tcg aag aac aca gtg tcg tcg gcc cgc ttc cgg       51
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                 Met Ser Lys Asn Thr Val Ser Ser Ala Arg Phe Arg
                  1               5                  10

aag gtg gac gtg gat gaa tat gac gag aac aag ttc gtg gac gaa gaa       99
Lys Val Asp Val Asp Glu Tyr Asp Glu Asn Lys Phe Val Asp Glu Glu
        15                  20                  25

gat ggg ggc gac ggc cag gcc ggg ccc gac gag ggc gag gtg gac tcc      147
Asp Gly Gly Asp Gly Gln Ala Gly Pro Asp Glu Gly Glu Val Asp Ser
    30                  35                  40

tgc ctg cgg caa gga aac atg aca gct gcc cta cag gca gct ctg aag      195
Cys Leu Arg Gln Gly Asn Met Thr Ala Ala Leu Gln Ala Ala Leu Lys
 45                  50                  55                  60

aac ccc cct atc aac acc aag agt cag gca gtg aag gtg agt cgc aga      243
Asn Pro Pro Ile Asn Thr Lys Ser Gln Ala Val Lys Val Ser Arg Arg
                 65                  70                  75

cta caa cac agt gat ctc tgc tga tatcttattc ttagtaaaat cctctgcagt     297
Leu Gln His Ser Asp Leu Cys  *
            80

tgcaaaaaaa aa                                                        309




     <210> 69
     <211> 772
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (95)..(592)

     <400> 69
cgaacagtcc tgggttctga gcctgccatc caaggaactc aggaggagga gttgacagtc     60

tcttcgttcc taaccagtgt gggacgactt cagc    atg tct cag gcc acc aag     112
                                         Met Ser Gln Ala Thr Lys
                                          1               5

agg aag cat gtg gtg aag gag gtg cta ggg gag cac ata gtg ccc tcc      160
Arg Lys His Val Val Lys Glu Val Leu Gly Glu His Ile Val Pro Ser
            10                  15                  20

gac cag cag cag att gtc agg gta ctc agg acc cca ggg aac aat ctg      208
Asp Gln Gln Gln Ile Val Arg Val Leu Arg Thr Pro Gly Asn Asn Leu
        25                  30                  35

cat gag gtg gag aca gcc caa ggg cag cgc ttc ctg gtg agc atg ccc      256
His Glu Val Glu Thr Ala Gln Gly Gln Arg Phe Leu Val Ser Met Pro
    40                  45                  50

tcc aaa tac cgc aag aac atc tgg atc aag aga ggg gac ttt ctc att      304
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Ser Lys Tyr Arg Lys Asn Ile Trp Ile Lys Arg Gly Asp Phe Leu Ile
 55                 60                  65                  70

gtt gac ccc att gaa gag gga gaa aag gtg aag gct gaa atc tcg ttt      352
Val Asp Pro Ile Glu Glu Gly Glu Lys Val Lys Ala Glu Ile Ser Phe
                75                  80                  85

gtg ctc tgc aag gac cac gtg cgc tct ctg cag aag gag ggg ttt tgg      400
Val Leu Cys Lys Asp His Val Arg Ser Leu Gln Lys Glu Gly Phe Trp
            90                  95                  100

cct gag gcc ttc tct gaa gtg gct gag aaa cac aac aac agg aac aga      448
Pro Glu Ala Phe Ser Glu Val Ala Glu Lys His Asn Asn Arg Asn Arg
        105                 110                 115

caa act caa cca gaa ctc cca gct gag cca cag tta tca gga gag gag      496
Gln Thr Gln Pro Glu Leu Pro Ala Glu Pro Gln Leu Ser Gly Glu Glu
    120                 125                 130

tcc agc tca gaa gat gat tct gac ctg ttt gtt aac aca aac cgc aga      544
Ser Ser Ser Glu Asp Asp Ser Asp Leu Phe Val Asn Thr Asn Arg Arg
135                 140                 145                 150

cag tat cat gag agt gag gag gag agt gaa gag gag gag gca gcc tga      592
Gln Tyr His Glu Ser Glu Glu Glu Ser Glu Glu Glu Glu Ala Ala  *
                155                 160                 165

gactccagga cccaattctc cacttgctca gggactggcc cctggctctt ctgggcttgg    652

acattcccag ggtgctctgc acatcttcac ccctgcatga ggacaaagca gggctcctct    712

ctgaactgat cttttgattc agagaattaa acccctggtg ggttggtgaa aaaaaaaaaa    772



     <210> 70
     <211> 857
     <212> DNA
     <213> Homo sapiens

     <220>
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     <222> (66)..(725)

     <400> 70
cccacgcgtc cgcccacgcg tccgcaggga acgggtcttg tggctttgtc tcccgcgaag     60

aggag    atg gcg gag tcg ttg agg tct ccg cgc cgc tcc ctg tac aaa      107
         Met Ala Glu Ser Leu Arg Ser Pro Arg Arg Ser Leu Tyr Lys
           1               5                  10

ctg gtg ggc tcg ccg cct tgg aaa gag gct ttc cgg cag aga tgc ctg      155
Leu Val Gly Ser Pro Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu
 15                 20                  25                  30

gag aga atg aga aac agc cgg gac agg ctc cta aac agg tac cgc cag      203
```

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Glu Arg Met Arg Asn Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln
                 35                  40                  45

gct gga agc agt ggg cca ggg aat tct cag aac agc ttt cta gtt caa      251
Ala Gly Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln
             50                  55                  60

gag gtg atg gaa gaa gag tgg aat gct ttg cag tca gtg gag aat tgt      299
Glu Val Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys
         65                  70                  75

cca gaa gac ttg gct cag ctg gag gag ctg ata gac atg gct gtg ctg      347
Pro Glu Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu
     80                  85                  90

gag gaa att caa cag gag ctg atc aac caa gag cag tcc atc atc agc      395
Glu Glu Ile Gln Gln Glu Leu Ile Asn Gln Glu Gln Ser Ile Ile Ser
 95                 100                 105                 110

gag tat gag aag agc ttg cag ttt gat gaa aag tgt ctc agc atc atg      443
Glu Tyr Glu Lys Ser Leu Gln Phe Asp Glu Lys Cys Leu Ser Ile Met
                115                 120                 125

ctg gct gag tgg gag gca aac cca ctc atc tgt cct gta tgt aca aag      491
Leu Ala Glu Trp Glu Ala Asn Pro Leu Ile Cys Pro Val Cys Thr Lys
            130                 135                 140

tac aac ctg aga atc aca agc ggt gtg gtg gtg tgt cag tgt ggc ctg      539
Tyr Asn Leu Arg Ile Thr Ser Gly Val Val Val Cys Gln Cys Gly Leu
        145                 150                 155

tcc atc cca tct cat tct tct gag ttg aca gag cag aag ctt cgt gcc      587
Ser Ile Pro Ser His Ser Ser Glu Leu Thr Glu Gln Lys Leu Arg Ala
    160                 165                 170

tgt tta gag ggt agt ata aat gag cac agt gca cat tgt ccc cac aca      635
Cys Leu Glu Gly Ser Ile Asn Glu His Ser Ala His Cys Pro His Thr
175                 180                 185                 190

cct gaa ttt tca gtc act gga gga aca gaa gaa aag tcc agt ctt ctc      683
Pro Glu Phe Ser Val Thr Gly Gly Thr Glu Glu Lys Ser Ser Leu Leu
                195                 200                 205

atg agc tgt ctg gcc tgt gat act tgg gct gtg atc ctc tag agccagc      732
Met Ser Cys Leu Ala Cys Asp Thr Trp Ala Val Ile Leu  *
            210                 215                 220

tgggactcac atcattctat gggcgttgaa gacaactcat tcctctgagg agccttgtac    792

atacaagcct tttatttata acttattttg tattgaaact tttacaccat tctggagaaa    852

aaaaa                                                                857
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<210> 71

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<211> 1004
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (207)..(1004)

<400> 71
atttggccct cgaggccaag aattcggcac gaggttcgcc tagcggcaac tccctcctcc      60

ctgcaatcct tccttcttat tccggtttcc agagcacgtc tccaggcttc gacgtcacca     120

cgctgggacg tatgtgccga gggccgcggc gtctgacctc atggcgtaga gcctagcaac     180

agcgcaggct cccagccgag tccgtt atg gcc gct gcc gtc ccg aag agg atg      233
                             Met Ala Ala Ala Val Pro Lys Arg Met
                               1               5

agg ggg cca gca caa gcg aaa ctg ctg ccc ggg tcg gcc atc caa gcc      281
Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln Ala
 10                  15                  20                  25

ctt gtg ggg ttg gcg cgg ccg ctg gtc ttg gcg ctc ctg ctt gtg tcc      329
Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Leu Val Ser
                 30                  35                  40

gcc gct cta tcc agt gtt gta tca cgg act gat tca ccg agc cca acc      377
Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro Thr
             45                  50                  55

gta ctc aac tca cat att tct acc cca aat gtg aat gct tta aca cat      425
Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr His
         60                  65                  70

gaa aac caa acc aaa cct tct att tcc caa atc agc acc acc ctc cct      473
Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu Pro
     75                  80                  85

ccc acg acg agt acc aag aaa agt gga gga gca tct gtg gtc cct cat      521
Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro His
 90                  95                 100                 105

ccc tcg cct act cct ctg tct caa gag gaa gct gat aac aat gaa gat      569
Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu Asp
                110                 115                 120

cct agt ata gag gag gag gat ctt ctc atg ctg aac agt tct cca tcc      617
Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro Ser
            125                 130                 135

aca gcc aaa gac act cta gac aat ggc gat tat gga gaa cca gac tat      665
Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp Tyr
        140                 145                 150

gac tgg acc acg ggc ccc agg gac gac gac gag tct gat gac acc ttg      713
Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Asp Thr Leu
```

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    155                 160                 165

gaa gaa aac agg ggt tac atg gaa att gaa cag tca gtg aaa tct ttt       761
Glu Glu Asn Arg Gly Tyr Met Glu Ile Glu Gln Ser Val Lys Ser Phe
170                 175                 180                 185

aag atg cca tcc tca aat ata gaa gag gaa gac agc cat ttc ttt ttt       809
Lys Met Pro Ser Ser Asn Ile Glu Glu Glu Asp Ser His Phe Phe Phe
                190                 195                 200

cat ctt att att ttt gct ttt tgc att gct gtt gtt tac att aca tat       857
His Leu Ile Ile Phe Ala Phe Cys Ile Ala Val Val Tyr Ile Thr Tyr
            205                 210                 215

cac aac aaa agg aag att ttt ctt ctg gtt caa agc agg aaa tgg cgt       905
His Asn Lys Arg Lys Ile Phe Leu Leu Val Gln Ser Arg Lys Trp Arg
        220                 225                 230

gat ggc ctt tgt tcc aaa aca gtg gaa tac cat cgc cta gat cag aat       953
Asp Gly Leu Cys Ser Lys Thr Val Glu Tyr His Arg Leu Asp Gln Asn
    235                 240                 245

gtt aat gag gca atg cct tct ttg aag att acc aat gat tat att ttt      1001
Val Asn Glu Ala Met Pro Ser Leu Lys Ile Thr Asn Asp Tyr Ile Phe
250                 255                 260                 265

taa                                                                  1004
 *




     <210> 72
     <211> 1562
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (1244)..(1399)

     <400> 72
cttgagcagg ggttcactta ttctgagagc attagttctc ctaaaaagct ccagcataga      60

aagggaagat aaaccaaatt ctagcttgtg ttttacccac agaaggatac aggacaaagg     120

aatagtaact ggcctgtttg gatactaaaa ttgaaaataa cttttagcct cctccttatg     180

atagccgcca gagtaaatgt tgagcattac tacagaaaag ccacaaacca agaatctacc     240

tgtttggaaa gatcttttgc atctctgaag gtgcttaaag catacttagt gcctttcctt     300

ttaactggga agataaaaga agtatctgtc caagatatta atatgtaaga taacattgta     360

gacatgttct tctgataata caaggtttat tctatttgca ttaggatatt tgtggacatg     420
```

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tccatctaat ataaaggaaa gtttttaat  cattgaggca tgtagggctg agttatataa    480
```

```
tccatctaat ataaaggaaa gtttttaat cattgaggca tgtagggctg agttatataa    480

tgtagaaact tctaaagata attggatgag aatatacata ttgacctgta tattatgact    540

aatcatgact cagatcttaa tacagggatg atctcatagc atttagatat cagaaaaggt    600

tttgacctat atgtctttaa tattgtttga atacatgtat aatctttatc attcctcagt    660

gtttcatttc tcaaattctg taaaaggaat ataagaggaa agacaattca tatacaaaga    720

caacgagatt aaaaatatgc agtaggaaaa ataattactt aaggggagat tttttttaca    780

tgaaatctgg gctttggatg tgtgtgtgtg tgtgtgtgtg cacatatgca ctgtggtggg    840

agtggggcaa cttggggaat atgttacatg tgtgactttg ttttgccctg gcgaagttaa    900

tgttgttcag aaagggtaaa tgtttggaca cttgcaattg ctcatggatg aatttatatg    960

ttttagtcat agaaaaattg taccctttga tagaagcaca ttttctttcc aaagttggtt   1020

attaaccaca gaattatagc aggtattcat aacttaagtt tgaaaatcaa tagcgtctgc   1080

aaatggatta acagattaga gaatcaacag catcggaaaa taggttaatg catattgctt   1140

ctaacaagtg catgaagaaa tagaagaagc tatgtagctt tcagttctga cagaaaaggg   1200

tgaaggaggg tatcatttca agaaaaaaaa tagctatcac gca  atg gtt atc tct    1255
                                                 Met Val Ile Ser
                                                   1

gaa aat att tgt att aag atg tgt ata cat ggc cag gca tgg tgg ctc     1303
Glu Asn Ile Cys Ile Lys Met Cys Ile His Gly Gln Ala Trp Trp Leu
  5                  10                  15                  20

atg cct gta atc cca gca ctt tgg gag gca ggt gga tca cga ggt cag     1351
Met Pro Val Ile Pro Ala Leu Trp Glu Ala Gly Gly Ser Arg Gly Gln
                 25                  30                  35

gag atc aag acc atc ctg gcc aac atg gtg aaa cct cat ctc tac taa     1399
Glu Ile Lys Thr Ile Leu Ala Asn Met Val Lys Pro His Leu Tyr  *
             40                  45                  50

aaatacaaaa atgagcgggg tgtggtggcc catgcctgta gtcccagctg ctcgggagac   1459

tgaatctctt gagcctggga agcagaggtt gcagtgaact gagatcgcgt cactgcactc   1519

cagcccgggt gacagagcga gattccatct caaaaaaaaa aaa                     1562
```

<210> 73
<211> 2100
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> (1229)..(1432)

<220>
<221> misc_feature
<222> (1)...(2100)
<223> n = a,t,c or g

<400> 73
taacttggaa ctttattttt aaagtattct gaaaattttc caagaatttt aaccaccacc      60

tacttccctt aaacacacac acatttttat cttacaatta taacccctat tgcagtacaa     120

aacaagaaac aataattcta agttagccag ccaatcaaac tacttcagta aatgatcata     180

ctacagcctg gaatcactca aacaaaaaat tcttctagtt ctctttaaag atatttatcg     240

tttatttttt catgaaacca aagtaattga ttcaacaata ctaacagttc tagcatgcaa     300

caaaccatct actatctaat gtttaatctt cttaacatgt atattttcat tcctataaag     360

tttccataag aagcttgcaa tgacaataaa ggtaaataag tacagttgtc ccttggtatc     420

catggggtat tggttcctgg accgtccccc caacccacag ataccaaaaa tccaagtata     480

ctcaagtccc ttacataaaa tgacatattt gtatataacc aacgcacatc cgcctgtata     540

ctttatccct agactaatac ctaatgcaat gtaaatgcta tttaaataac tgttatactg     600

tatttttatt tgtattattt ttattttttc taatattttt gatctgcaat tggtttaatc     660

cacagatgca gagtacatgg atacagaggg ccaactgttt tgttacaggt acttcaaata     720

gcactacagt acatctttga caaaattttt acaatattcc acctttcaat atgaaacagc     780

ttaaaaaggc atgggtcaaa aataaagtat agtagtatca cttacgcaaa taaagtctca     840

gaatcataca agcacaacac tgttaggact ctccctgttt aggctgggaa aaacattata     900

caaaacattt tcttcaaata aaattacata aattgcttag aaaaatgcca aaatcaataa     960

tttcaaacat attaaggaga aaaccttgaa cattattgga aaatataaac tagttattcc    1020

ttgcttttaa cagatgagtt cttgacaagt tttgtgtaaa gcaaattctg taaaccatta    1080

tcttgcttgc actggaggaa catatctcaa ggaaacctaa gagaaagtgt tctttaaagc    1140

atgtgattct cctgtttttg ctggatgtct gtatctacat aataaacagg cacacttcta    1200

catcactggg tattttactc agactgtc   atg ttt cat ctc tgt aaa tta aac     1252
                                 Met Phe His Leu Cys Lys Leu Asn
                                   1               5

cca agt tac tta aaa atc acc tgt ggt aaa aga agc aag cag atc acc      1300
Pro Ser Tyr Leu Lys Ile Thr Cys Gly Lys Arg Ser Lys Gln Ile Thr
    10                  15                  20
```

```
ccc atc tac tat ccc tcc cgc ctc ccc cct gtc aaa aga aag ttc tca      1348
Pro Ile Tyr Tyr Pro Ser Arg Leu Pro Pro Val Lys Arg Lys Phe Ser
 25                  30                  35                  40

gtt tat gat gca aaa ctt aca att gtt cat tta tcc aca ttc tca ata      1396
Val Tyr Asp Ala Lys Leu Thr Ile Val His Leu Ser Thr Phe Ser Ile
                 45                  50                  55

gag gat ttt cca cta tat tta agt atg gca gga taa ttac ccacctgttc      1446
Glu Asp Phe Pro Leu Tyr Leu Ser Met Ala Gly  *
             60                  65

ctcttttcag cttagaaaca taacggttca ttccttttat tgctagagaa tgtcattcct   1506

gaagatttta taaacaaagg caaatatgaa ggaaaatttg taattatgaa ataagtcctt   1566

tgtagtaaag aatatttccc aaatcataac agttctattt ggaatgatac ccacaactct   1626

acaagcatct tatccctcta caggaatgac taccttatta attaaaataa aaatttaaca   1686

aggatcaaaa taaaattctt tagcaataga ctcctgcaaa aataaaaact aaaactagac   1746

ctagtcattg ccatttgatc aaacttagaa caggcttaaa taacagaacc actccattaa   1806

agaggcatag aaagaaaagt ttactaaaat aaatgtaaaa gtcttatgga gatgaagatc   1866

tctagaatag tcttaagtct atgactactg ctatcattaa tgagcaaata aatgacttga   1926

aattattccn cctggaaaag gtaaactcat acgtattatg gaaaangcct atgggcactt   1986

agaaaaatat tcctgggtaa gtaaaccatg gnaaatatag ggtacatcct aagcctctcc   2046

gccctaactt ttaaaattat tnttggagaa aggatagcac tagccgggga ggaa         2100


     <210> 74
     <211> 933
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (267)..(866)

     <400> 74
tgctttcttt ttctccaaaa ggggaggaaa ttgaaactga gtggcccacg atgggaagag     60

gggaaagccc aggggtacag gaggcctctg ggtgaaggca gaggctacca tggggttcgg    120

agcgaccttg gccgttggcc tgaccatctt agtgctgtct gtcgtcacta tcatcatctg    180

cttcacctgc tcctgctgct gcctttacaa gacgtgccgc cgaccacgtc cggttgtcac    240

caccaccaca tccaccactg tggtgc atg ccc ctt atc ctc agc ctc caa gtg     293
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```
                             Met Pro Leu Ile Leu Ser Leu Gln Val
                               1               5

tgc cgc cca gct acc cgt gga cca agc tac cag ggc tac cac acc atg      341
Cys Arg Pro Ala Thr Arg Gly Pro Ser Tyr Gln Gly Tyr His Thr Met
 10                  15                  20                  25

ccg cct cag cca ggg atg cca gca gcg acc cta ccc aat gca ggg aag      389
Pro Pro Gln Pro Gly Met Pro Ala Ala Thr Leu Pro Asn Ala Gly Lys
                 30                  35                  40

atg gcg gac att cag act gag cgt gcc tac caa aag cag ccg acc atc      437
Met Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Gln Pro Thr Ile
             45                  50                  55

ttt caa aac aag aag agg gtc ctg ctg gga gaa act ggc aag gag aag      485
Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys Glu Lys
         60                  65                  70

ctc ccg cgg tac tac aag aac atc ggt ctg ggc ttc aag aca ccc aag      533
Leu Pro Arg Tyr Tyr Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Lys
     75                  80                  85

gag gct att gag ggc acc tac att gac aag aaa tgc ccc ttc act ggt      581
Glu Ala Ile Glu Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe Thr Gly
 90                  95                 100                 105

aat gtg tcc att cga ggg cgg atc ctc tct ggc gtg gtg acc aag atg      629
Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr Lys Met
                110                 115                 120

aag atg cag agg acc att gtc atc cgc cga gac tat ctg cac tac atc      677
Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr Ile
            125                 130                 135

cgc aag tac aac cgc ttc gag aag cgc cac aag aac atg tct gta cac      725
Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val His
        140                 145                 150

ctg tcc ccc tgc ttc agg gac gtc cag atc ggt gac atc gtc aca gtg      773
Leu Ser Pro Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr Val
    155                 160                 165

ggc gag tgc cgg cct ctg agc aag aca gtg cgc ttc aac gtg ctc aag      821
Gly Glu Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys
170                 175                 180                 185

gtc acc aag gct gcc ggc acc aag aag cag ttc cag aag ttc tga ggc      869
Val Thr Lys Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe  *
                190                 195                 200

tggacatcgg cccgctcccc acaatgaaat aaagttattt tctcattccc aaaaaaaaaa    929

aaaa                                                                 933
```

```
<210> 75
<211> 3093
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (446)..(2956)

<400> 75
attcccgggt cgacgatttc gtggtgctgg accttgcggg ctgcgggtcg ctgtggagct     60

ggcgctgctg ggggcccgag tggtgctggt ggaaaagcgc accaagttct ctcgccacaa    120

cgtgctccac ctctggccct tcaccatcca cgacctgcgg gcactcggtg ctaagaagtt    180

ctacgggcgc ttctgcaccg gcaccctgga ccacatcagc atcaggcagc tccagctgct    240

tctgctgaag gtagcattgc tgctgggggt ggaaattcac tggggtgtca ctttcactgg    300

cctccagccc cctcctagga aggggagtgg ctggcgtgcc cagctccaac ccaacccccc    360

tgcccagctg gccaactatg aatttgacgt ccttatctcg gctgcaggag gtaaattcgt    420

ccctgaaggc ttcaaagttc gagaa  atg cga ggc aaa ctg gcc att ggc atc     472
                             Met Arg Gly Lys Leu Ala Ile Gly Ile
                               1               5

aca gcc aac ttt gtg aat gga cgc acc gtg gag gag aca cag gtg ccg      520
Thr Ala Asn Phe Val Asn Gly Arg Thr Val Glu Glu Thr Gln Val Pro
 10                  15                  20                  25

gag atc agt ggt gta gcc agg atc tac aac cag agc ttc ttc cag agc      568
Glu Ile Ser Gly Val Ala Arg Ile Tyr Asn Gln Ser Phe Phe Gln Ser
                 30                  35                  40

ctt ctc aaa gcc aca ggc att gat ctg gag aac att gtg tac tac aag      616
Leu Leu Lys Ala Thr Gly Ile Asp Leu Glu Asn Ile Val Tyr Tyr Lys
             45                  50                  55

gac gac acc cac tac ttt gtg atg aca gcc aag aag cag tgc ctg ctg      664
Asp Asp Thr His Tyr Phe Val Met Thr Ala Lys Lys Gln Cys Leu Leu
         60                  65                  70

cgg ctg ggg gtg ctg cgc cag gac tgg cca gac acc aat cgg ctg ctg      712
Arg Leu Gly Val Leu Arg Gln Asp Trp Pro Asp Thr Asn Arg Leu Leu
     75                  80                  85

ggc agt gcc aat gtg gtg ccc gag gct ctg cag cgc ttt acc cgg gca      760
Gly Ser Ala Asn Val Val Pro Glu Ala Leu Gln Arg Phe Thr Arg Ala
 90                  95                 100                 105

gct gct gac ttt gcc acc cat ggc aag ctc ggg aaa cta gag ttt gcc      808
Ala Ala Asp Phe Ala Thr His Gly Lys Leu Gly Lys Leu Glu Phe Ala
                110                 115                 120
```

```
cag gat gcc cat ggg cag cct gat gtc tct gcc ttt gac ttc acg agc        856
Gln Asp Ala His Gly Gln Pro Asp Val Ser Ala Phe Asp Phe Thr Ser
            125                 130                 135

atg atg cgg gca gag agt tct gct cgt gtg caa gag aag cat ggc gcc        904
Met Met Arg Ala Glu Ser Ser Ala Arg Val Gln Glu Lys His Gly Ala
        140                 145                 150

cgc ctg ctg ctg gga ctg gtg ggg gac tgc ctg gtg gag ccc ttc tgg        952
Arg Leu Leu Leu Gly Leu Val Gly Asp Cys Leu Val Glu Pro Phe Trp
    155                 160                 165

ccc ctg ggc act gga gtg gca cgg ggc ttc ctg gca gcc ttt gat gca       1000
Pro Leu Gly Thr Gly Val Ala Arg Gly Phe Leu Ala Ala Phe Asp Ala
170                 175                 180                 185

gcc tgg atg gtg aag cgg tgg gca gag ggc gct gag tcc cta gag gtg       1048
Ala Trp Met Val Lys Arg Trp Ala Glu Gly Ala Glu Ser Leu Glu Val
            190                 195                 200

ttg gct gag cgt gag agc ctg tac cag ctt ctg tca cag aca tcc cca       1096
Leu Ala Glu Arg Glu Ser Leu Tyr Gln Leu Leu Ser Gln Thr Ser Pro
            205                 210                 215

gaa aac atg cat cgc aat gtg gcc cag tat ggg ctg gac cca gcc acc       1144
Glu Asn Met His Arg Asn Val Ala Gln Tyr Gly Leu Asp Pro Ala Thr
        220                 225                 230

cgc tac ccc aac ctg aac ctc cgg gca gtg acc ccc aat cag gta cga       1192
Arg Tyr Pro Asn Leu Asn Leu Arg Ala Val Thr Pro Asn Gln Val Arg
    235                 240                 245

gac ctg tat gat gtg cta gcc aag gag cct gtg cag agg aac aac gac       1240
Asp Leu Tyr Asp Val Leu Ala Lys Glu Pro Val Gln Arg Asn Asn Asp
250                 255                 260                 265

aag aca gat aca ggg atg cca gcc acc ggg tcg gca ggc acc cag gag       1288
Lys Thr Asp Thr Gly Met Pro Ala Thr Gly Ser Ala Gly Thr Gln Glu
                270                 275                 280

gag ctg cta cgc tgg tgc cag gag cag aca gct ggg tac ccg gga gtc       1336
Glu Leu Leu Arg Trp Cys Gln Glu Gln Thr Ala Gly Tyr Pro Gly Val
            285                 290                 295

cac gtc tcc gat ttg tct tcc tcc tgg gct gat ggg cta gct ctg tgt       1384
His Val Ser Asp Leu Ser Ser Ser Trp Ala Asp Gly Leu Ala Leu Cys
        300                 305                 310

gcc ctg gtg tac cgg ctg cag cct ggc ctg ctg gaa ccc tca gag ctg       1432
Ala Leu Val Tyr Arg Leu Gln Pro Gly Leu Leu Glu Pro Ser Glu Leu
    315                 320                 325

cag ggg ctg gga gct ctg gaa gca act gct tgg gca cta aag gtg gca       1480
Gln Gly Leu Gly Ala Leu Glu Ala Thr Ala Trp Ala Leu Lys Val Ala
330                 335                 340                 345

gag aat gag ctg ggc atc aca ccg gtg gtg tct gca cag gcc gtg gta       1528
```

```
Glu Asn Glu Leu Gly Ile Thr Pro Val Val Ser Ala Gln Ala Val Val
                350                 355                 360

gca ggg agt gac cca ctg ggc ctc att gcc tac ctc agc cac ttc cac      1576
Ala Gly Ser Asp Pro Leu Gly Leu Ile Ala Tyr Leu Ser His Phe His
            365                 370                 375

agt gcc ttc aag agc atg gcc cac agc cca ggc cct gtc agc cag gcc      1624
Ser Ala Phe Lys Ser Met Ala His Ser Pro Gly Pro Val Ser Gln Ala
        380                 385                 390

tcc cca ggg acc tcc agt gct gta tta ttc ctt agt aaa ctt cag agg      1672
Ser Pro Gly Thr Ser Ser Ala Val Leu Phe Leu Ser Lys Leu Gln Arg
    395                 400                 405

acc ctg cag cga tcc cgg gcc aag gaa aat gca gag gat gct ggt ggc      1720
Thr Leu Gln Arg Ser Arg Ala Lys Glu Asn Ala Glu Asp Ala Gly Gly
410                 415                 420                 425

aag aag ctg cgc ttg gag atg gag gcc gag acc cca agt act gag gtg      1768
Lys Lys Leu Arg Leu Glu Met Glu Ala Glu Thr Pro Ser Thr Glu Val
                430                 435                 440

cca cct gac cca gag cct ggt gta ccc ctg aca ccc cca tcc caa cac      1816
Pro Pro Asp Pro Glu Pro Gly Val Pro Leu Thr Pro Pro Ser Gln His
            445                 450                 455

cag gag gcc ggt gct ggg gac ctg tgt gca ctt tgt ggg gaa cac ctc      1864
Gln Glu Ala Gly Ala Gly Asp Leu Cys Ala Leu Cys Gly Glu His Leu
        460                 465                 470

tat gtc ctg gaa cgc ctc tgt gtc aac ggc cat ttc ttc cac cgg agc      1912
Tyr Val Leu Glu Arg Leu Cys Val Asn Gly His Phe Phe His Arg Ser
    475                 480                 485

tgc ttc cgc tgc cat acc tgt gag gcc aca ctg tgg cca ggt ggc tac      1960
Cys Phe Arg Cys His Thr Cys Glu Ala Thr Leu Trp Pro Gly Gly Tyr
490                 495                 500                 505

gag cag cac cca gga gat gga cat tcc tac tgc ctc cag cac ctg ccc      2008
Glu Gln His Pro Gly Asp Gly His Ser Tyr Cys Leu Gln His Leu Pro
                510                 515                 520

cag aca gac cac aaa gag gaa ggc agc gat aga ggc cct gag agt ccg      2056
Gln Thr Asp His Lys Glu Glu Gly Ser Asp Arg Gly Pro Glu Ser Pro
            525                 530                 535

gag ctc ccc aca cca agt gag aat agc atg cca cca ggc ctc tca act      2104
Glu Leu Pro Thr Pro Ser Glu Asn Ser Met Pro Pro Gly Leu Ser Thr
        540                 545                 550

ccc aca gcc tcg cag gag ggg gcc ggt cct gtt cca gat ccc agc cag      2152
Pro Thr Ala Ser Gln Glu Gly Ala Gly Pro Val Pro Asp Pro Ser Gln
    555                 560                 565

ccc acc cgt cgg cag atc cgc ctc tcc agc ccg gag cgc cag cgg ttg      2200
Pro Thr Arg Arg Gln Ile Arg Leu Ser Ser Pro Glu Arg Gln Arg Leu
```

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570                 575                 580                 585

tcc tcc ctt aac ctt acc cct gac ccg gaa atg gag cct cca ccc aag      2248
Ser Ser Leu Asn Leu Thr Pro Asp Pro Glu Met Glu Pro Pro Pro Lys
                590                 595                 600

cct ccc cgc agc tgc tcc gcc ttg gcc cgc cac gcc ctg gag agc agc      2296
Pro Pro Arg Ser Cys Ser Ala Leu Ala Arg His Ala Leu Glu Ser Ser
            605                 610                 615

ttt gtg ggc tgg ggc ctg cca gtc cag agc cct caa gct ctt gtg gcc      2344
Phe Val Gly Trp Gly Leu Pro Val Gln Ser Pro Gln Ala Leu Val Ala
        620                 625                 630

atg gag aag gag gaa aaa gag agt ccc ttc tcc agt gaa gag gaa gaa      2392
Met Glu Lys Glu Glu Lys Glu Ser Pro Phe Ser Ser Glu Glu Glu Glu
    635                 640                 645

gaa gat gtg cct ttg gac tca gat gtg gaa cag gcc ctg cag acc ttt      2440
Glu Asp Val Pro Leu Asp Ser Asp Val Glu Gln Ala Leu Gln Thr Phe
650                 655                 660                 665

gcc aag acc tca ggc acc atg aat aac tac cca aca tgg cgt cgg act      2488
Ala Lys Thr Ser Gly Thr Met Asn Asn Tyr Pro Thr Trp Arg Arg Thr
                670                 675                 680

ctg ctg cgc cgt gcg aag gag gag gag atg aag agg ttc tgc aag gcc      2536
Leu Leu Arg Arg Ala Lys Glu Glu Glu Met Lys Arg Phe Cys Lys Ala
            685                 690                 695

cag acc atc caa cgg cga cta aat gag att gag gct gcc ttg agg gag      2584
Gln Thr Ile Gln Arg Arg Leu Asn Glu Ile Glu Ala Ala Leu Arg Glu
        700                 705                 710

cta gag gcc gag ggc gtg aag ctg gag ctg gcc ttg agg cgc cag agc      2632
Leu Glu Ala Glu Gly Val Lys Leu Glu Leu Ala Leu Arg Arg Gln Ser
    715                 720                 725

agt tcc cca gaa cag caa aag aaa cta tgg gta gga cag ctg cta cag      2680
Ser Ser Pro Glu Gln Gln Lys Lys Leu Trp Val Gly Gln Leu Leu Gln
730                 735                 740                 745

ctc gtt gac aag aaa aac agc ctg gtg gct gag gag gcc gag ctc atg      2728
Leu Val Asp Lys Lys Asn Ser Leu Val Ala Glu Glu Ala Glu Leu Met
                750                 755                 760

atc acg gtg cag gaa ttg aat ctg gag gag aaa cag tgg cag ctg gac      2776
Ile Thr Val Gln Glu Leu Asn Leu Glu Glu Lys Gln Trp Gln Leu Asp
            765                 770                 775

cag gag cta cga ggc tac atg aac cgg gaa gaa aac cta aag aca gct      2824
Gln Glu Leu Arg Gly Tyr Met Asn Arg Glu Glu Asn Leu Lys Thr Ala
        780                 785                 790

gct gat cgg cag gct gag gac cag gtc ctg agg aag ctg gtg gat ttg      2872
Ala Asp Arg Gln Ala Glu Asp Gln Val Leu Arg Lys Leu Val Asp Leu
    795                 800                 805
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gtc aac cag aga gat gcc ctc atc cgc ttc cag gag gag cgc agg ctc      2920
Val Asn Gln Arg Asp Ala Leu Ile Arg Phe Gln Glu Glu Arg Arg Leu
810                 815                 820                 825

agc gag ctg gcc ttg ggg aca ggg gcc cag ggc tag acga gggtgggccg      2970
Ser Glu Leu Ala Leu Gly Thr Gly Ala Gln Gly  *
                830                 835

tctgctttcg ttcccacaaa gaaagcacct caccccagca cagtgccacc cctgttcatc    3030

tgggctgcct ggcagagagc cttgctgttt acaattaaaa tgtttctgcc aaaaaaaaaa    3090

aaa                                                                  3093
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```
<210> 76
<211> 1110
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (179)..(961)

<400> 76
gctggagaac aactatctat tcgatgatga agatacccca ccaaacccaa aaaaagagat      60

ctctcgagga tccgaattcg cggccgcgtc gacgtgggct tgtgggtctt tgagacccga     120

aaattgagag cgttttcgca ctccagcggc tgctcctggc ggctctgcgg ccgtcacc       178
atg cca cag aat gaa tat att gaa tta cac cgt aaa cgc tat gga tac       226
Met Pro Gln Asn Glu Tyr Ile Glu Leu His Arg Lys Arg Tyr Gly Tyr
 1               5                  10                  15

cgt ttg gat tac cat gag aaa aag aga aag aag gaa agt cga gag gct       274
Arg Leu Asp Tyr His Glu Lys Lys Arg Lys Lys Glu Ser Arg Glu Ala
            20                  25                  30

cat gaa cgt tca aag aag gca aag aaa atg att ggt ctg aag gct aag       322
His Glu Arg Ser Lys Lys Ala Lys Lys Met Ile Gly Leu Lys Ala Lys
        35                  40                  45

ctt tac cat aaa cag cgt cat gct gag aaa ata caa atg aaa aag act       370
Leu Tyr His Lys Gln Arg His Ala Glu Lys Ile Gln Met Lys Lys Thr
    50                  55                  60

atc aag atg cat gaa aag aga aac acc aaa caa aag aat gat gaa aag       418
Ile Lys Met His Glu Lys Arg Asn Thr Lys Gln Lys Asn Asp Glu Lys
65                  70                  75                  80

aca cca cag gga gca gta cct gcc tat ctg ctg gac aga gag gga caa       466
Thr Pro Gln Gly Ala Val Pro Ala Tyr Leu Leu Asp Arg Glu Gly Gln
                85                  90                  95
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tct cga gct aaa gta ctt tcc aat atg att aaa cag aaa aga aaa gag      514
Ser Arg Ala Lys Val Leu Ser Asn Met Ile Lys Gln Lys Arg Lys Glu
            100                 105                 110

aag gcg gga aaa tgg gaa gtc cct ctg cct aaa gta cgt gcc cag gga      562
Lys Ala Gly Lys Trp Glu Val Pro Leu Pro Lys Val Arg Ala Gln Gly
        115                 120                 125

gaa aca gaa gta tta aaa gtt att cga aca gga aag aga aag aag aag      610
Glu Thr Glu Val Leu Lys Val Ile Arg Thr Gly Lys Arg Lys Lys Lys
    130                 135                 140

gca tgg aag aga atg gtt act aaa gtg tgc ttt gtt gga gat ggc ttt      658
Ala Trp Lys Arg Met Val Thr Lys Val Cys Phe Val Gly Asp Gly Phe
145                 150                 155                 160

aca aga aaa cca cct aaa tat gaa aga ttc atc agg cca atg ggc ttg      706
Thr Arg Lys Pro Pro Lys Tyr Glu Arg Phe Ile Arg Pro Met Gly Leu
                165                 170                 175

cgt ttc aag aaa gcc cat gta aca cat cct gaa ctg aaa gcc acc ttt      754
Arg Phe Lys Lys Ala His Val Thr His Pro Glu Leu Lys Ala Thr Phe
            180                 185                 190

tgc cta cca ata ctt ggt gta aag aag aat ccc tca tcc cca ctg tat      802
Cys Leu Pro Ile Leu Gly Val Lys Lys Asn Pro Ser Ser Pro Leu Tyr
        195                 200                 205

aca act ttg ggt gtt att acc aaa ggt act gtc att gaa gta aat gtg      850
Thr Thr Leu Gly Val Ile Thr Lys Gly Thr Val Ile Glu Val Asn Val
    210                 215                 220

agc gaa ttg ggc ctt gtg aca caa gga ggc aaa gtt att tgg gga aaa      898
Ser Glu Leu Gly Leu Val Thr Gln Gly Gly Lys Val Ile Trp Gly Lys
225                 230                 235                 240

tat gcc cag gtt acc aac aat cct gaa aat gat gga tgt ata aat gca      946
Tyr Ala Gln Val Thr Asn Asn Pro Glu Asn Asp Gly Cys Ile Asn Ala
                245                 250                 255

gtc tta ctg gtt tga cagcaatttc atatataatt attgaggact acacaccaat     1001
Val Leu Leu Val  *
            260

tgaagaaact gccattactg tgatgtttct gaatactacc aaacagccat acatgtctgc    1061

aatgaagaga tttattaaat tgtaaacatt aaagtggaaa aaaaaaaaa                1110
```

<210> 77
<211> 1835
<212> DNA
<213> Homo sapiens

<220>

```
<221> CDS
<222> (29)..(1714)

<400> 77
acgagcctgc gttttccggc cagaggac  atg atg cag ggg gag gca cac cct       52
                                Met Met Gln Gly Glu Ala His Pro
                                 1               5

agt gct tcc ctt att gac aga acc atc aag atg aga aaa gaa aca gag      100
Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg Lys Glu Thr Glu
    10                  15                  20

gct agg aaa gtg gtc tta gcc tgg gga ctc cta aat gta tct atg gct      148
Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn Val Ser Met Ala
25                  30                  35                  40

gga atg ata tat act gaa atg act gga aaa ttg att agt tca tac tac      196
Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile Ser Ser Tyr Tyr
                45                  50                  55

aat gtg aca tac tgg ccc ctc tgg tat att gag ctt gcc ctt gca tct      244
Asn Val Thr Tyr Trp Pro Leu Trp Tyr Ile Glu Leu Ala Leu Ala Ser
            60                  65                  70

ctc ttc agc ctt aat gcc tta ttt gat ttt tgg aga tat ttc aaa tat      292
Leu Phe Ser Leu Asn Ala Leu Phe Asp Phe Trp Arg Tyr Phe Lys Tyr
        75                  80                  85

act gtg gca cca aca agt ctg gtt gtt agt cct gga cag caa aca ctt      340
Thr Val Ala Pro Thr Ser Leu Val Val Ser Pro Gly Gln Gln Thr Leu
    90                  95                  100

tta ggg ttg aaa aca gct gtt gta cag act acg cct cca cat gat ctg      388
Leu Gly Leu Lys Thr Ala Val Val Gln Thr Thr Pro Pro His Asp Leu
105                 110                 115                 120

gca gca acc caa atc cct ccc gct cca cct tcc cct tca att cag ggt      436
Ala Ala Thr Gln Ile Pro Pro Ala Pro Pro Ser Pro Ser Ile Gln Gly
                125                 130                 135

cag agt gtg ttg agt tat agc cct tct cgt tcg ccc agt acc agt ccc      484
Gln Ser Val Leu Ser Tyr Ser Pro Ser Arg Ser Pro Ser Thr Ser Pro
            140                 145                 150

aag ttc acc acc agc tgt atg act ggt tac agc cct cag ctg caa ggt      532
Lys Phe Thr Thr Ser Cys Met Thr Gly Tyr Ser Pro Gln Leu Gln Gly
        155                 160                 165

ctg tcc tca ggt ggc agt ggt tct tat agc cct gga gtg acc tac tcg      580
Leu Ser Ser Gly Gly Ser Gly Ser Tyr Ser Pro Gly Val Thr Tyr Ser
    170                 175                 180

ccc gtc agt ggt tat aat aag ttg gcg agc ttt agc ccc tct cct cct      628
Pro Val Ser Gly Tyr Asn Lys Leu Ala Ser Phe Ser Pro Ser Pro Pro
185                 190                 195                 200

tct ccg tac cct acc act gtt gga cca gtg gag agc agt gga ttg aga      676
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Ser Pro Tyr Pro Thr Thr Val Gly Pro Val Glu Ser Ser Gly Leu Arg
                205                 210                 215

tct cgc tac cgt tct tca cct acc gtc tac aac tca cct act gac aaa       724
Ser Arg Tyr Arg Ser Ser Pro Thr Val Tyr Asn Ser Pro Thr Asp Lys
            220                 225                 230

gaa gac tac atg acc gac cta cga act ttg gat act ttt ctc aga agt       772
Glu Asp Tyr Met Thr Asp Leu Arg Thr Leu Asp Thr Phe Leu Arg Ser
        235                 240                 245

gaa gag gag aaa cag cat agg gtt aag ctg ggg agc cca gat tct acc       820
Glu Glu Glu Lys Gln His Arg Val Lys Leu Gly Ser Pro Asp Ser Thr
    250                 255                 260

tct cct tcc agc agt cct act ttc tgg aac tat agt cgt tct atg ggg       868
Ser Pro Ser Ser Ser Pro Thr Phe Trp Asn Tyr Ser Arg Ser Met Gly
265                 270                 275                 280

gat tat gca caa act tta aag aag ttt cag tat cag ctt gcc tgt agg       916
Asp Tyr Ala Gln Thr Leu Lys Lys Phe Gln Tyr Gln Leu Ala Cys Arg
                285                 290                 295

tct cag gcc cca tgt gct aac aaa gat gaa gcc gat ctc agc tct aaa       964
Ser Gln Ala Pro Cys Ala Asn Lys Asp Glu Ala Asp Leu Ser Ser Lys
            300                 305                 310

caa gcc gca gaa gag gtc tgg gca aga gtg gct atg aat aga caa ctt      1012
Gln Ala Ala Glu Glu Val Trp Ala Arg Val Ala Met Asn Arg Gln Leu
        315                 320                 325

ctt gat cat atg gat tca tgg aca gct aaa ttt aga aat tgg atc aat      1060
Leu Asp His Met Asp Ser Trp Thr Ala Lys Phe Arg Asn Trp Ile Asn
    330                 335                 340

gag aca ata tta gtg cca ctt gtt caa gag att gag tct gtc agc aca      1108
Glu Thr Ile Leu Val Pro Leu Val Gln Glu Ile Glu Ser Val Ser Thr
345                 350                 355                 360

cag atg aga cga atg ggt tgt cca gag cta cag ata gga gag gct agt      1156
Gln Met Arg Arg Met Gly Cys Pro Glu Leu Gln Ile Gly Glu Ala Ser
                365                 370                 375

att act agc ttg aaa caa gct gcc ctg gtt aaa gcg cct ctc att ccg      1204
Ile Thr Ser Leu Lys Gln Ala Ala Leu Val Lys Ala Pro Leu Ile Pro
            380                 385                 390

act ttg aac aca atc gtt cag tat cta gac ctt act cca aat cag gaa      1252
Thr Leu Asn Thr Ile Val Gln Tyr Leu Asp Leu Thr Pro Asn Gln Glu
        395                 400                 405

tac ttg ttt gaa agg atc aaa gaa cta tct cag gga ggt tgt atg agc      1300
Tyr Leu Phe Glu Arg Ile Lys Glu Leu Ser Gln Gly Gly Cys Met Ser
    410                 415                 420

tca ttt cga tgg aac aga ggt ggc gac ttc aaa gga cga aag tgg gat      1348
Ser Phe Arg Trp Asn Arg Gly Gly Asp Phe Lys Gly Arg Lys Trp Asp
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425                 430                 435                 440

aca gac ctg ccc acc gat tct gct atc atc atg cat gta ttt tgc acc      1396
Thr Asp Leu Pro Thr Asp Ser Ala Ile Ile Met His Val Phe Cys Thr
                445                 450                 455

tac ctt gat tcc aga tta cct cca cat ccg aag tat ccc gac gga aaa      1444
Tyr Leu Asp Ser Arg Leu Pro Pro His Pro Lys Tyr Pro Asp Gly Lys
            460                 465                 470

act ttt act tct cag cac ttt gtt cag aca cca aat aaa cca gat gtt      1492
Thr Phe Thr Ser Gln His Phe Val Gln Thr Pro Asn Lys Pro Asp Val
        475                 480                 485

aca aat gag aat gtt ttt tgc att tat cag agt gct atc aac cct ccc      1540
Thr Asn Glu Asn Val Phe Cys Ile Tyr Gln Ser Ala Ile Asn Pro Pro
    490                 495                 500

cat tat gag ctc atc tac cag cgt cat gta tac aac ctg cca aag ggc      1588
His Tyr Glu Leu Ile Tyr Gln Arg His Val Tyr Asn Leu Pro Lys Gly
505                 510                 515                 520

aga aat aat atg ttt cat aca ttg ttg atg ttt ctc tac atc ata aag      1636
Arg Asn Asn Met Phe His Thr Leu Leu Met Phe Leu Tyr Ile Ile Lys
                525                 530                 535

acc aaa gag tca gga atg ctt ggg aga gtt aat ctt ggt cta tct ggt      1684
Thr Lys Glu Ser Gly Met Leu Gly Arg Val Asn Leu Gly Leu Ser Gly
            540                 545                 550

gtg aat ata ttg tgg atc ttt ggc gag tag c aagtcatata tttaattctg      1735
Val Asn Ile Leu Trp Ile Phe Gly Glu  *
        555                 560

acatttagac tatttcactg aaccagaagt cgaaactaaa catctctgag ccactgactc   1795

ttctgaaata aaatacacat gggtgtaaaa aaaaaaaaaa                          1835



    <210> 78
    <211> 1029
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (428)..(817)

    <400> 78
ccctgattat aactggatat tgggtagcat ccagttaaag tatcagtaga gcttggatgt     60

atcaaagaaa atattttatt caagttccca aaacaaactt gaggagttat gctgggtttg    120

aattgaagaa aaaaggccaa gttaaaatag gaaaacaaat ggttttcatt tggtggcagt    180
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tgaaatcaaa gtatacatgt gtatacattc taatccgtca tctatcccat gtggcatttt    240

ccaaggtttt aagagtctac caggccaaac cctttgccac tttcactgct tttgctttgc    300

ttttcccctt tcttttctct cgctttgcct tcagcctttt tctttgcctt tggttcatcc    360

atattgggta ctgtccatgc tggtcggcgt gagcgtgagg tgtgggtgtt cgtttctcag    420

gtaaaac  atg gct aaa agc tta cgg agt aag tgg aaa aga aag atg cgt     469
         Met Ala Lys Ser Leu Arg Ser Lys Trp Lys Arg Lys Met Arg
           1               5                  10

gct gaa aag aga aaa aag aat gcc cca aag gag gcc agc agg ctt aaa      517
Ala Glu Lys Arg Lys Lys Asn Ala Pro Lys Glu Ala Ser Arg Leu Lys
 15                  20                  25                  30

agt att ctc aaa cta gac ggt gat gtt tta atg aaa gat gtt caa gag      565
Ser Ile Leu Lys Leu Asp Gly Asp Val Leu Met Lys Asp Val Gln Glu
                 35                  40                  45

ata gca act gtg gtg gta ccc aaa ccc aaa cat tgc caa gag aaa atg      613
Ile Ala Thr Val Val Val Pro Lys Pro Lys His Cys Gln Glu Lys Met
             50                  55                  60

caa tgt gag gta aaa gat gaa aaa gat gac atg aaa atg gag act gat      661
Gln Cys Glu Val Lys Asp Glu Lys Asp Asp Met Lys Met Glu Thr Asp
         65                  70                  75

att aag aga aac aaa aag act ctt cta gac cag cat gga cag tac cca      709
Ile Lys Arg Asn Lys Lys Thr Leu Leu Asp Gln His Gly Gln Tyr Pro
     80                  85                  90

ata tgg atg aac caa agg caa aga aaa agg ctg aag gca aag cga gag      757
Ile Trp Met Asn Gln Arg Gln Arg Lys Arg Leu Lys Ala Lys Arg Glu
 95                 100                 105                 110

aaa aga aag ggg aaa agc aaa gca aaa gca gtg aaa gtg gca aag ggt      805
Lys Arg Lys Gly Lys Ser Lys Ala Lys Ala Val Lys Val Ala Lys Gly
                115                 120                 125

ttg gcc tgg tag act cttaaaacct tggaaaatgc cacatgggat agatgacgga      860
Leu Ala Trp  *
        130

ttagaatgta tacacatgta tactttgatt tcaactgcca ccaaatgaaa accatttgtt    920

ttcctatttt aacttggcct tttttcttca attcaaaccc agcataactc ctcaagtttg    980

ttttgggaac ttgaataaaa tattttcttt gatacaaaaa aaaaaaaaa               1029
```

<210> 79
<211> 5476
<212> DNA
<213> Homo sapiens

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     <220>
     <221> CDS
     <222> (188)..(5149)

     <400> 79
ggcccctgct cggataaagg tgggaggctc aggtgtcaat gtcaatgcaa agggcttgga      60

cttgggtggc agaggagggg tccaagttcc agcagtggac atttcatctt ctcttggggg     120

tagggcagta gaggtacagg gcccatctct ggagagtggt gatcatggca aaattaaatt     180

tcccacc  atg aaa gtg ccg aaa ttt ggt gtc tca aca ggg cgt gag ggc     229
         Met Lys Val Pro Lys Phe Gly Val Ser Thr Gly Arg Glu Gly
           1               5                  10

cag aca cca aag gca ggg ctg agg gtt tct gca cct gaa gtc tct gtg      277
Gln Thr Pro Lys Ala Gly Leu Arg Val Ser Ala Pro Glu Val Ser Val
 15                 20                  25                  30

ggg cac aag ggc ggc aag cca ggc ttg act atc caa gcc cct cag ctg      325
Gly His Lys Gly Gly Lys Pro Gly Leu Thr Ile Gln Ala Pro Gln Leu
                 35                  40                  45

gaa gtc agt gtg ccc tct gcc aat att gag ggc ctt gag ggg aag ctg      373
Glu Val Ser Val Pro Ser Ala Asn Ile Glu Gly Leu Glu Gly Lys Leu
             50                  55                  60

aag ggc ccc caa atc act ggg cca tca ctt gag ggt gac cta ggc ctg      421
Lys Gly Pro Gln Ile Thr Gly Pro Ser Leu Glu Gly Asp Leu Gly Leu
         65                  70                  75

aaa ggt gcc aag cca cag ggg cac att ggg gtg gat gcc tct gct ccc      469
Lys Gly Ala Lys Pro Gln Gly His Ile Gly Val Asp Ala Ser Ala Pro
     80                  85                  90

caa att ggg ggt agc atc act ggc ccc agt gtg gaa gtt cag gcc cct      517
Gln Ile Gly Gly Ser Ile Thr Gly Pro Ser Val Glu Val Gln Ala Pro
 95                 100                 105                 110

gac att gat gtt cag ggg cct ggg agc aaa ctg aat gtg ccc aag atg      565
Asp Ile Asp Val Gln Gly Pro Gly Ser Lys Leu Asn Val Pro Lys Met
                115                 120                 125

aaa gtc ccc aag ttc tct gta tca ggt gca aag gga gag gaa act ggg      613
Lys Val Pro Lys Phe Ser Val Ser Gly Ala Lys Gly Glu Glu Thr Gly
            130                 135                 140

att gat gtg aca ctg cct aca ggt gaa gtg act gtt cct ggg gtc tct      661
Ile Asp Val Thr Leu Pro Thr Gly Glu Val Thr Val Pro Gly Val Ser
        145                 150                 155

ggg gat gtc agc ctg cct gag att gct act ggt ggg ctg gaa gga aag      709
Gly Asp Val Ser Leu Pro Glu Ile Ala Thr Gly Gly Leu Glu Gly Lys
    160                 165                 170

atg aaa ggt act aaa gtg aag act cct gaa atg att att cag aaa cct      757
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Met Lys Gly Thr Lys Val Lys Thr Pro Glu Met Ile Ile Gln Lys Pro
175                 180                 185                 190

aaa atc tcc atg cag gat gtg gat ctg agc ctt ggg tct cct aaa ctg         805
Lys Ile Ser Met Gln Asp Val Asp Leu Ser Leu Gly Ser Pro Lys Leu
                195                 200                 205

aaa gga gat att aag gtt tct gct cct ggg gtg caa ggt gat gtt aaa         853
Lys Gly Asp Ile Lys Val Ser Ala Pro Gly Val Gln Gly Asp Val Lys
            210                 215                 220

ggc cct caa gtg gca ctt aaa ggc tcc aga gtg gac ata gag aca cca         901
Gly Pro Gln Val Ala Leu Lys Gly Ser Arg Val Asp Ile Glu Thr Pro
        225                 230                 235

aac cta gag gga acc ttg aca ggc cct agg ctt ggc agt cct tcc ggg         949
Asn Leu Glu Gly Thr Leu Thr Gly Pro Arg Leu Gly Ser Pro Ser Gly
    240                 245                 250

aaa acc gga acc tgt agg atc tct atg tca gaa gta gac tta aat gtg         997
Lys Thr Gly Thr Cys Arg Ile Ser Met Ser Glu Val Asp Leu Asn Val
255                 260                 265                 270

gcc gca cct aaa gtg aaa ggg ggt gta gat gtc aca ctc ccc aga gta        1045
Ala Ala Pro Lys Val Lys Gly Gly Val Asp Val Thr Leu Pro Arg Val
                275                 280                 285

gaa ggg aaa gtc aaa gtc cct gaa gtt gat gtc aga ggc ccc aaa gtg        1093
Glu Gly Lys Val Lys Val Pro Glu Val Asp Val Arg Gly Pro Lys Val
            290                 295                 300

gat gtc agt gcc cca gat gtc gaa gcg cat ggc cca gaa tgg aac ctg        1141
Asp Val Ser Ala Pro Asp Val Glu Ala His Gly Pro Glu Trp Asn Leu
        305                 310                 315

aaa atg ccc aag atg aaa atg ccc acg ttc agc act cca gga gcc aaa        1189
Lys Met Pro Lys Met Lys Met Pro Thr Phe Ser Thr Pro Gly Ala Lys
    320                 325                 330

ggg gaa ggt cca gat gtt cat atg act cta ccc aaa gga gat atc agt        1237
Gly Glu Gly Pro Asp Val His Met Thr Leu Pro Lys Gly Asp Ile Ser
335                 340                 345                 350

att tca ggg ccc aag gtc aat gtg gaa gcc cca gat gtc aac ttg gag        1285
Ile Ser Gly Pro Lys Val Asn Val Glu Ala Pro Asp Val Asn Leu Glu
                355                 360                 365

ggt ctg ggg gga aaa ctt aaa ggc ccc gat gtt aag ctg cct gat atg        1333
Gly Leu Gly Gly Lys Leu Lys Gly Pro Asp Val Lys Leu Pro Asp Met
            370                 375                 380

agt gtc aag aca cca aag atc tcc atg cct gat gta gat ttg cac gtg        1381
Ser Val Lys Thr Pro Lys Ile Ser Met Pro Asp Val Asp Leu His Val
        385                 390                 395

aaa ggt aca aag gtg aag gga gag tat gat gta act gta cca aag ctg        1429
Lys Gly Thr Lys Val Lys Gly Glu Tyr Asp Val Thr Val Pro Lys Leu
```

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    400                 405                 410

gaa gga gaa ctc aaa ggc cca aaa gtg gac att gat gcc cca gat gtg     1477
Glu Gly Glu Leu Lys Gly Pro Lys Val Asp Ile Asp Ala Pro Asp Val
415                 420                 425                 430

gat gtt cat ggc cca gac tgg cac ttg aag atg ccc aag atg aaa atg     1525
Asp Val His Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met
                435                 440                 445

ccc aaa ttc agt gtg cca ggg ttc aaa gca gag ggc cca gaa gtg gat     1573
Pro Lys Phe Ser Val Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp
            450                 455                 460

gtg aac ctg ccc aag gct gat gtg gac att tcc ggg ccc aag ata gat     1621
Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Ile Asp
        465                 470                 475

gtt act gct cct gat gtg agc att gag gaa cca gaa ggg aaa ttg aaa     1669
Val Thr Ala Pro Asp Val Ser Ile Glu Glu Pro Glu Gly Lys Leu Lys
    480                 485                 490

ggg ccc aag ttt aag atg cct gag atg aac atc aaa gtc ccc aag atc     1717
Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Val Pro Lys Ile
495                 500                 505                 510

tcc atg cct gat gtg gac tta cat ctg aaa ggc cct aac gta aag gga     1765
Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Asn Val Lys Gly
                515                 520                 525

gaa tat gat gtc aca atg cca aag gtt gaa agt gag att aaa gtt cct     1813
Glu Tyr Asp Val Thr Met Pro Lys Val Glu Ser Glu Ile Lys Val Pro
            530                 535                 540

gat gtt gaa ctt aaa agt gcc aaa atg gac att gat gtc cca gat gtg     1861
Asp Val Glu Leu Lys Ser Ala Lys Met Asp Ile Asp Val Pro Asp Val
        545                 550                 555

gag gtt caa ggc cca gac tgg cac ctg aag atg ccc aag atg aaa atg     1909
Glu Val Gln Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met
    560                 565                 570

ccc aag ttc agc atg cct ggc ttc aaa gca gag ggc cca gaa gtg gat     1957
Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp
575                 580                 585                 590

gtg aac ctg ccc aag gct gat gtg gac atc tca gga ccc aag gtg ggt     2005
Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Val Gly
                595                 600                 605

gtt gaa gtt cca gat gtg aat att gaa gga cct gaa gga aag ctg aag     2053
Val Glu Val Pro Asp Val Asn Ile Glu Gly Pro Glu Gly Lys Leu Lys
            610                 615                 620

ggc ccc aag ttc aag atg cca gag atg aat atc aag gcc ccc aag atc     2101
Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Ala Pro Lys Ile
        625                 630                 635
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tcc atg cct gat gtg gac ttg cat atg aaa ggt cct aaa gta aag gga      2149
Ser Met Pro Asp Val Asp Leu His Met Lys Gly Pro Lys Val Lys Gly
    640                 645                 650

gaa tat gat atg aca gtg cca aag ctg gaa ggg gac ctg aaa ggc cca      2197
Glu Tyr Asp Met Thr Val Pro Lys Leu Glu Gly Asp Leu Lys Gly Pro
655                 660                 665                 670

aaa gta gat gtc agt gcc cca gat gtt gaa atg cag ggt cct gac tgg      2245
Lys Val Asp Val Ser Ala Pro Asp Val Glu Met Gln Gly Pro Asp Trp
                675                 680                 685

aac ttg aag atg cca aag att aaa atg ccc aaa ttt agc atg ccc agc      2293
Asn Leu Lys Met Pro Lys Ile Lys Met Pro Lys Phe Ser Met Pro Ser
            690                 695                 700

ctc aaa gga gag ggg cca gaa ttt gat gtg aac ctg tcc aaa gcg aat      2341
Leu Lys Gly Glu Gly Pro Glu Phe Asp Val Asn Leu Ser Lys Ala Asn
        705                 710                 715

gtg gac att tct gca cca aaa gta gat act aat gct cca gat ctg agc      2389
Val Asp Ile Ser Ala Pro Lys Val Asp Thr Asn Ala Pro Asp Leu Ser
    720                 725                 730

ctt gaa gga cct gaa ggg aag ttg aaa ggc ccg aag ttt aag atg cct      2437
Leu Glu Gly Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro
735                 740                 745                 750

gag atg cac ttc aga gct cct aag atg cct ttg cca gat gtt gac ctg      2485
Glu Met His Phe Arg Ala Pro Lys Met Pro Leu Pro Asp Val Asp Leu
                755                 760                 765

gat ctt aaa gga ccc aaa atg aaa gga aat gta gat atc tct gca cca      2533
Asp Leu Lys Gly Pro Lys Met Lys Gly Asn Val Asp Ile Ser Ala Pro
            770                 775                 780

aag ata gag ggt gaa atg cag gtt cca gat gtg gac atc aga ggt ccc      2581
Lys Ile Glu Gly Glu Met Gln Val Pro Asp Val Asp Ile Arg Gly Pro
        785                 790                 795

aag gta gat att aaa gca cca gat gtg gaa ggc caa ggc ctg gac tgg      2629
Lys Val Asp Ile Lys Ala Pro Asp Val Glu Gly Gln Gly Leu Asp Trp
    800                 805                 810

agc ctg aaa ata ccc aag atg aaa atg ccc aag ttc agc atg ccc agc      2677
Ser Leu Lys Ile Pro Lys Met Lys Met Pro Lys Phe Ser Met Pro Ser
815                 820                 825                 830

ctc aaa ggc gag ggc cca gaa gtg gat gtg aac ttg cct aag gct gac      2725
Leu Lys Gly Glu Gly Pro Glu Val Asp Val Asn Leu Pro Lys Ala Asp
                835                 840                 845

gtt gat gtc tca gga ccc aag gtg gac atc gaa gcc cca gat gtg agc      2773
Val Asp Val Ser Gly Pro Lys Val Asp Ile Glu Ala Pro Asp Val Ser
            850                 855                 860
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 ctc gaa ggt cca gaa ggg aag ctg aag ggt ccc aag ttt aag atg cct      2821
 Leu Glu Gly Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro
         865                 870                 875

 gag atg cat ttc aag acc ccc aag atc tcc atg cct gat gtg gac tta      2869
 Glu Met His Phe Lys Thr Pro Lys Ile Ser Met Pro Asp Val Asp Leu
     880                 885                 890

 cac ttg aaa ggc ccc aaa gtc aaa ggg gat gtg gat gtg tct gtg ccc      2917
 His Leu Lys Gly Pro Lys Val Lys Gly Asp Val Asp Val Ser Val Pro
 895                 900                 905                 910

 aag gta gaa ggt gaa atg aaa gtg cca gat gtt gaa atc aaa gga ccc      2965
 Lys Val Glu Gly Glu Met Lys Val Pro Asp Val Glu Ile Lys Gly Pro
                 915                 920                 925

 aaa atg gac att gat gcc cca gat gtg gag gtt caa ggc cca gac tgg      3013
 Lys Met Asp Ile Asp Ala Pro Asp Val Glu Val Gln Gly Pro Asp Trp
             930                 935                 940

 cac ctg aag atg ccc aag atg aaa atg ccc aag ttt agc atg cct ggc      3061
 His Leu Lys Met Pro Lys Met Lys Met Pro Lys Phe Ser Met Pro Gly
         945                 950                 955

 ttc aaa gga gag ggc cga gaa gtg gat gtg aac ctg ccc aag gct gac      3109
 Phe Lys Gly Glu Gly Arg Glu Val Asp Val Asn Leu Pro Lys Ala Asp
     960                 965                 970

 att gat gtc tca gga ccc aag gtg gat gtt gaa gtc cca gat gtg agc      3157
 Ile Asp Val Ser Gly Pro Lys Val Asp Val Glu Val Pro Asp Val Ser
 975                 980                 985                 990

 ctt gag ggc ccg gaa gga aag ctg aag ggt ccc aag ttt aag atg cct      3205
 Leu Glu Gly Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro
                 995                1000                1005

 gag atg cac ttc aag gcc ccc aag atc tcc atg cct gat gtg gac ctg      3253
 Glu Met His Phe Lys Ala Pro Lys Ile Ser Met Pro Asp Val Asp Leu
            1010                1015                1020

 aat ctt aag ggg cca aaa ttg aag gga gat gtg gat gtg tcc ttg cct      3301
 Asn Leu Lys Gly Pro Lys Leu Lys Gly Asp Val Asp Val Ser Leu Pro
        1025                1030                1035

 gag gta gaa ggt gaa atg aaa gtg cca gat gtt gac att aaa ggg ccc      3349
 Glu Val Glu Gly Glu Met Lys Val Pro Asp Val Asp Ile Lys Gly Pro
    1040                1045                1050

 aaa gtt gac att agt gct cca gat gtg gat gtt cat ggc cca gat tgg      3397
 Lys Val Asp Ile Ser Ala Pro Asp Val Asp Val His Gly Pro Asp Trp
1055                1060                1065                1070

 cac ctg aag atg ccc aag gtg aaa atg ccc aag ttc agc atg ccc ggc      3445
 His Leu Lys Met Pro Lys Val Lys Met Pro Lys Phe Ser Met Pro Gly
                1075                1080                1085

 ttc aaa gga gag ggc cct gaa gtg gat gtg aag ctg ccc aaa gct gac      3493
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Phe Lys Gly Glu Gly Pro Glu Val Asp Val Lys Leu Pro Lys Ala Asp
            1090                1095                1100

gtt gat gtc tca gga ccc aaa atg gat gct gaa gtt cca gat gtg aat      3541
Val Asp Val Ser Gly Pro Lys Met Asp Ala Glu Val Pro Asp Val Asn
        1105                1110                1115

att gaa ggt cca gac gca aaa cta aaa ggt ccc aaa ttc aag atg cca      3589
Ile Glu Gly Pro Asp Ala Lys Leu Lys Gly Pro Lys Phe Lys Met Pro
    1120                1125                1130

gaa atg agt ata aag cct cag aag ata tcc ata cca gat gtt ggt ttg      3637
Glu Met Ser Ile Lys Pro Gln Lys Ile Ser Ile Pro Asp Val Gly Leu
1135                1140                1145                1150

cat ttg aaa ggt cct aaa atg aaa gga gat tat gat gta aca gtt cca      3685
His Leu Lys Gly Pro Lys Met Lys Gly Asp Tyr Asp Val Thr Val Pro
                1155                1160                1165

aaa gta gaa gga gag ata aaa gct cct gat gtt gac atc aaa ggc ccc      3733
Lys Val Glu Gly Glu Ile Lys Ala Pro Asp Val Asp Ile Lys Gly Pro
            1170                1175                1180

aaa gtt gat att aat gca cca gat gtg gag gtt cat ggc cca gac tgg      3781
Lys Val Asp Ile Asn Ala Pro Asp Val Glu Val His Gly Pro Asp Trp
        1185                1190                1195

cac ctg aag atg ccc aag gta aaa atg ccc aag ttc agc atg cct ggc      3829
His Leu Lys Met Pro Lys Val Lys Met Pro Lys Phe Ser Met Pro Gly
    1200                1205                1210

ttt aaa gga gag ggc cca gag gtg gat atg aac ctg ccc aag gct gac      3877
Phe Lys Gly Glu Gly Pro Glu Val Asp Met Asn Leu Pro Lys Ala Asp
1215                1220                1225                1230

ctt ggt gtt tca gga ccc aag gtg gac att gat gtt cca gat gtg aat      3925
Leu Gly Val Ser Gly Pro Lys Val Asp Ile Asp Val Pro Asp Val Asn
                1235                1240                1245

ctt gaa gct cca gag ggg aaa cta aaa ggc cct aag ttc aag atg cca      3973
Leu Glu Ala Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro
            1250                1255                1260

agc atg aat ata cag acg cac aaa atc tct atg cct gat gtt gga ctt      4021
Ser Met Asn Ile Gln Thr His Lys Ile Ser Met Pro Asp Val Gly Leu
        1265                1270                1275

aat ttg aaa gcc cct aaa ctg aaa act gat gta gat gtt tcc ctt ccc      4069
Asn Leu Lys Ala Pro Lys Leu Lys Thr Asp Val Asp Val Ser Leu Pro
    1280                1285                1290

aaa gtg gaa gga gac ttg aag ggt cct gaa att gat gtg aaa gcc cct      4117
Lys Val Glu Gly Asp Leu Lys Gly Pro Glu Ile Asp Val Lys Ala Pro
1295                1300                1305                1310

aag atg gat gtg aat gtt ggt gat att gat att gaa ggt cca gaa ggg      4165
Lys Met Asp Val Asn Val Gly Asp Ile Asp Ile Glu Gly Pro Glu Gly
```

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                1315                1320                1325

aag ttg aag ggc ccc aag ttt aag atg cct gag atg cat ttc aag gcc      4213
Lys Leu Lys Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Ala
            1330                1335                1340

ccc aag atc tcc atg ccc gat gtg gac tta cac ttg aaa ggc ccc aaa      4261
Pro Lys Ile Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Lys
        1345                1350                1355

gtc aaa ggg gat atg gat gtg tct gtg ccc aag gta gaa ggt gaa atg      4309
Val Lys Gly Asp Met Asp Val Ser Val Pro Lys Val Glu Gly Glu Met
    1360                1365                1370

aaa gtg cca gat gtt gac att aaa ggg ccc aaa gtg gac att gat gcc      4357
Lys Val Pro Asp Val Asp Ile Lys Gly Pro Lys Val Asp Ile Asp Ala
1375                1380                1385                1390

cca gat gtg gag gtt cac gac cca gat tgg cac ctg aaa atg ccc aag      4405
Pro Asp Val Glu Val His Asp Pro Asp Trp His Leu Lys Met Pro Lys
                1395                1400                1405

atg aaa atg ccc aag ttc agt atg cct ggc ttc aaa gca gag ggc cct      4453
Met Lys Met Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro
            1410                1415                1420

gaa gtg gat gtg aat ctc cga aag gct gac att gat gtg tct gga ccc      4501
Glu Val Asp Val Asn Leu Arg Lys Ala Asp Ile Asp Val Ser Gly Pro
        1425                1430                1435

agt gtg gac act gat gct cct gat ttg gat att gag gga cca gaa gga      4549
Ser Val Asp Thr Asp Ala Pro Asp Leu Asp Ile Glu Gly Pro Glu Gly
    1440                1445                1450

aag ttg aaa ggc tcc aaa ttt aag atg ccc aag ttg aat ata aaa gct      4597
Lys Leu Lys Gly Ser Lys Phe Lys Met Pro Lys Leu Asn Ile Lys Ala
1455                1460                1465                1470

ccc aag gtc tcc atg cca gat gtg gac ttg aat ttg aag gga ccc aaa      4645
Pro Lys Val Ser Met Pro Asp Val Asp Leu Asn Leu Lys Gly Pro Lys
                1475                1480                1485

ctg aag gga gag ata gat gct tct gtg cca gaa ctg gaa ggt gat ctc      4693
Leu Lys Gly Glu Ile Asp Ala Ser Val Pro Glu Leu Glu Gly Asp Leu
            1490                1495                1500

aga ggg ccg caa gtt gat gtc aaa ggt cct ctt gtg gaa gcg gag gtg      4741
Arg Gly Pro Gln Val Asp Val Lys Gly Pro Leu Val Glu Ala Glu Val
        1505                1510                1515

ccc gat gtt gat ctg gag tgt cct gat gca aag ctg aag ggc ccc aag      4789
Pro Asp Val Asp Leu Glu Cys Pro Asp Ala Lys Leu Lys Gly Pro Lys
    1520                1525                1530

ctt aag atg cct gag atg cac ttc aag gcc ccc aag atc tcc atg cct      4837
Leu Lys Met Pro Glu Met His Phe Lys Ala Pro Lys Ile Ser Met Pro
1535                1540                1545                1550
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 gat gtg gac tta cac ttg aaa ggc ccc aaa gtc aaa ggg gat gtg gat     4885
 Asp Val Asp Leu His Leu Lys Gly Pro Lys Val Lys Gly Asp Val Asp
                1555                1560                1565

 gtg tct ttg cca aaa ttg gag gga gat tta aca ggc ccc agt gtg gat     4933
 Val Ser Leu Pro Lys Leu Glu Gly Asp Leu Thr Gly Pro Ser Val Asp
            1570                1575                1580

 gtg gag gtg cct gat gtt gag ctg gag tgt cct gat gca aag ttg aaa     4981
 Val Glu Val Pro Asp Val Glu Leu Glu Cys Pro Asp Ala Lys Leu Lys
        1585                1590                1595

 ggg ccc aag ttt aag atg cct gag atg cac ttc aag acc ccc aag atc     5029
 Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Thr Pro Lys Ile
    1600                1605                1610

 tcc atg cct gat gtg aac tta aac ttg aaa ggc ccc aaa gtc aaa ggg     5077
 Ser Met Pro Asp Val Asn Leu Asn Leu Lys Gly Pro Lys Val Lys Gly
1615                1620                1625                1630

 gat atg gat gtg tct gtt ccc aaa att gga ggg aga ttt aac agg ccc     5125
 Asp Met Asp Val Ser Val Pro Lys Ile Gly Gly Arg Phe Asn Arg Pro
                1635                1640                1645

 cag tgt gga tgt gga ggt gcc tga tgttgagctg gctgtcgttg ttctgagggc    5179
 Gln Cys Gly Cys Gly Gly Ala  *
            1650

 ggcatcactc tggggtcagt ctctcccctg tcctttgagg acatacagac ctcacctatt   5239

 gtttaagtgt ttgaaccagc cccgaaccca agcaacacca gagtcctcct tacatttctt   5299

 cagtgagcaa accttacgca ccgtgaactt gggagtcaaa ccagctgtgc ccctcactag   5359

 ccgggtaagc gcagggaggt atcgtgccac actgagcatc agttccccaa tccgaatcag   5419

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tgtgccagcc gggctctggc aggctcctgg cagc    atg gca gtg aag ctt ggg     112
                                         Met Ala Val Lys Leu Gly
                                           1               5
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acc ctc ctg ctg gcc ctt gcc ctg ggc ctg gcc cag cca gcc tct gcc      160
Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu Ala Gln Pro Ala Ser Ala
            10                  15                  20

cgc cgg aag ctg ctg gtg ttt ctg ctg gat ggt ttt cgc tca gac tac      208
Arg Arg Lys Leu Leu Val Phe Leu Leu Asp Gly Phe Arg Ser Asp Tyr
        25                  30                  35

atc agt gat gag gcg ctg gag tca ttg cct ggt ttc aaa gag att gtg      256
Ile Ser Asp Glu Ala Leu Glu Ser Leu Pro Gly Phe Lys Glu Ile Val
    40                  45                  50

agc agg gga gta aaa gtg gat tac ttg act cca gac ttc cct agt ctc      304
Ser Arg Gly Val Lys Val Asp Tyr Leu Thr Pro Asp Phe Pro Ser Leu
55                  60                  65                  70

tcg tat ccc aat tat tat acc cta atg act ggc cgc cat tgt gaa gtc      352
Ser Tyr Pro Asn Tyr Tyr Thr Leu Met Thr Gly Arg His Cys Glu Val
                75                  80                  85

cat cag atg atc ggg aac tac atg tgg gac ccc acc acc aac aag tcc      400
His Gln Met Ile Gly Asn Tyr Met Trp Asp Pro Thr Thr Asn Lys Ser
            90                  95                  100

ttt gac att ggc gtc aac aaa gac agc cta atg cct ctc tgg tgg aat      448
Phe Asp Ile Gly Val Asn Lys Asp Ser Leu Met Pro Leu Trp Trp Asn
        105                 110                 115

gga tca gaa cct ctg tgg gtc act ctg acc aag gcc aaa agg aag gtc      496
Gly Ser Glu Pro Leu Trp Val Thr Leu Thr Lys Ala Lys Arg Lys Val
    120                 125                 130

tac atg tac tac tgg cca ggc tgt gag gtt gag att ctg ggt gtc aga      544
Tyr Met Tyr Tyr Trp Pro Gly Cys Glu Val Glu Ile Leu Gly Val Arg
135                 140                 145                 150

ccc acc tac tgc cta gaa tat aaa aat gtc cca acg gat atc aat ttt      592
Pro Thr Tyr Cys Leu Glu Tyr Lys Asn Val Pro Thr Asp Ile Asn Phe
                155                 160                 165

gcc aat gca gtc agc gat gct ctt gac tcc ttc aag agt ggc cgg gcc      640
Ala Asn Ala Val Ser Asp Ala Leu Asp Ser Phe Lys Ser Gly Arg Ala
            170                 175                 180

gac ctg gca gcc ata tac cat gag cgc att gac gtg gaa ggc cac cac      688
Asp Leu Ala Ala Ile Tyr His Glu Arg Ile Asp Val Glu Gly His His
        185                 190                 195

tac ggg cct gca tct ccg cag agg aaa gat gcc ctc aag gct gta gac      736
Tyr Gly Pro Ala Ser Pro Gln Arg Lys Asp Ala Leu Lys Ala Val Asp
    200                 205                 210

act gtc ctg aag tac atg acc aag tgg atc cag gag cgg ggc ctg cag      784
Thr Val Leu Lys Tyr Met Thr Lys Trp Ile Gln Glu Arg Gly Leu Gln
215                 220                 225                 230
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gac cgc ctg aac gtc att att ttc tcg gat cac gga atg acc gac att       832
Asp Arg Leu Asn Val Ile Ile Phe Ser Asp His Gly Met Thr Asp Ile
                235                 240                 245

ttc tgg atg gac aaa gtg att gag ctg aat aag tac atc agc ctg aat       880
Phe Trp Met Asp Lys Val Ile Glu Leu Asn Lys Tyr Ile Ser Leu Asn
            250                 255                 260

gac ctg cag caa gtg aag gac cgc ggg cct gtt gtg agc ctt tgg ccg       928
Asp Leu Gln Gln Val Lys Asp Arg Gly Pro Val Val Ser Leu Trp Pro
        265                 270                 275

gcc cct ggg aaa cac tct gag ata tat aac aaa ctg agc aca gtg gaa       976
Ala Pro Gly Lys His Ser Glu Ile Tyr Asn Lys Leu Ser Thr Val Glu
    280                 285                 290

cac atg act gtc tac gag aaa gaa gcc atc cca agc agg ttc tat tac      1024
His Met Thr Val Tyr Glu Lys Glu Ala Ile Pro Ser Arg Phe Tyr Tyr
295                 300                 305                 310

aag aaa gga aag ttt gtc tct cct ttg act tta gtg gct gat gaa ggc      1072
Lys Lys Gly Lys Phe Val Ser Pro Leu Thr Leu Val Ala Asp Glu Gly
                315                 320                 325

tgg ttc ata act gag aat cga gag atg ctt ccg ttt tgg atg aac agc      1120
Trp Phe Ile Thr Glu Asn Arg Glu Met Leu Pro Phe Trp Met Asn Ser
            330                 335                 340

acc ggc agg cgg gaa ggt tgg cag cgt gga tgg cac ggc tac gac aac      1168
Thr Gly Arg Arg Glu Gly Trp Gln Arg Gly Trp His Gly Tyr Asp Asn
        345                 350                 355

gag ctc atg gac atg cgg ggc atc ttc ctg gcc ttc gga cct ggt agg      1216
Glu Leu Met Asp Met Arg Gly Ile Phe Leu Ala Phe Gly Pro Gly Arg
    360                 365                 370

cga gga aat gac cag atg ctc tca gac ccc att ccc aag gaa gtg tct      1264
Arg Gly Asn Asp Gln Met Leu Ser Asp Pro Ile Pro Lys Glu Val Ser
375                 380                 385                 390

gta agg ggg gct acg ggt gcc agg aga ggc tgc agg gat ttc ctt aca      1312
Val Arg Gly Ala Thr Gly Ala Arg Arg Gly Cys Arg Asp Phe Leu Thr
                395                 400                 405

gac cct ctt tat gag cca agc aga gca aac cca gcc ggt ctc cat gaa      1360
Asp Pro Leu Tyr Glu Pro Ser Arg Ala Asn Pro Ala Gly Leu His Glu
            410                 415                 420

aca tct ttt gct ggc ttc ctt tca aat gct tct tgg gtt tgg caa atg      1408
Thr Ser Phe Ala Gly Phe Leu Ser Asn Ala Ser Trp Val Trp Gln Met
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caccctcaag cttcaggtga gctgagcttc taacactacc atcaaagcaa ctggaacccc     180

ttgaatttga tttctggaga cgcgagcata atccttttgc aaacatctca acgctggctc     240

tccaggtgga gcacc atg gaa ggc gac tgt ctg agc tgc atg aag tat ctg      291
                 Met Glu Gly Asp Cys Leu Ser Cys Met Lys Tyr Leu
                 1               5                   10

atg ttt gta ttc aat ttc ttc ata ttt ctg ggc ggg gcc tgc ctg ctg       339
Met Phe Val Phe Asn Phe Phe Ile Phe Leu Gly Gly Ala Cys Leu Leu
        15                  20                  25

gcc atc ggc atc tgg gtc atg gtg gac ccc acc ggc ttc cgg gag atc       387
Ala Ile Gly Ile Trp Val Met Val Asp Pro Thr Gly Phe Arg Glu Ile
    30                  35                  40

gtg gct gcc aat cct ctg ctc ctc acg ggc gcc tac atc ctc ctg gcc       435
Val Ala Ala Asn Pro Leu Leu Leu Thr Gly Ala Tyr Ile Leu Leu Ala
45                  50                  55                  60

atg ggg ggc ctg ctc ttt ctg ctc ggc ttc ctg ggc tgc tgc ggg gcc       483
Met Gly Gly Leu Leu Phe Leu Leu Gly Phe Leu Gly Cys Cys Gly Ala
                65                  70                  75

gtc cgt gag aac aag tgt ctg ctg cta ttt ttc ttc ctg ttc atc ctg       531
Val Arg Glu Asn Lys Cys Leu Leu Leu Phe Phe Phe Leu Phe Ile Leu
            80                  85                  90

atc atc ttc ctg gca gag ctc tca gca gcc atc ctg gcc ttc atc ttc       579
Ile Ile Phe Leu Ala Glu Leu Ser Ala Ala Ile Leu Ala Phe Ile Phe
        95                  100                 105

agg gaa aat ctc acc cga gaa ttc ttc acc aag gag ctc acc aag cac       627
Arg Glu Asn Leu Thr Arg Glu Phe Phe Thr Lys Glu Leu Thr Lys His
    110                 115                 120

tac cag ggc aat aac gac aca gac gtc ttc tct gcc acc tgg aac tcg       675
Tyr Gln Gly Asn Asn Asp Thr Asp Val Phe Ser Ala Thr Trp Asn Ser
125                 130                 135                 140
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gtc atg atc aca ttt ggt tgc tgc ggg gtc aac ggg cct gaa gac ttt      723
Val Met Ile Thr Phe Gly Cys Cys Gly Val Asn Gly Pro Glu Asp Phe
                145                 150                 155

aag ttt gca tct gtg ttt cga ctc ctg acc ctg gat agt gaa gag gtg      771
Lys Phe Ala Ser Val Phe Arg Leu Leu Thr Leu Asp Ser Glu Glu Val
            160                 165                 170

ccg gag gcc tgc tgc cgg agg gaa ccc caa agt cgg gac ggg gtc ctg      819
Pro Glu Ala Cys Cys Arg Arg Glu Pro Gln Ser Arg Asp Gly Val Leu
        175                 180                 185

ctg agc cgg gag gag tgc ctc ctg gga agg agc cta ttc cta aac aag      867
Leu Ser Arg Glu Glu Cys Leu Leu Gly Arg Ser Leu Phe Leu Asn Lys
    190                 195                 200

cag ggc tgt tac acg gtg atc ctc aac acc ttc gag acc tac gtc tac      915
Gln Gly Cys Tyr Thr Val Ile Leu Asn Thr Phe Glu Thr Tyr Val Tyr
205                 210                 215                 220

ttg gcc gga gcc ctt gcc atc ggg gta ctg gcc atc gag ctt ttc gcc      963
Leu Ala Gly Ala Leu Ala Ile Gly Val Leu Ala Ile Glu Leu Phe Ala
                225                 230                 235

atg atc ttt gcc atg tgc ctc ttc cgg ggc atc cag tag agggtatggc      1012
Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile Gln  *
            240                 245

ctgaagcctg aagactcgcc ccacccacca ctgcccagca cccaatgtcc tcccgtgccc   1072

ctccccgctg tcctcttggc cccaggggag aagatgaggc catcagagat ggccaggaga   1132

agggccaggg gaatagagct attttttttaa caaaacaaaa tgaagacaaa aatatggact   1192

gatgtatcct cgcctggact cagggcaggt gccgtgggtt ctccagagac cccagcacct   1252

ggcccaggat agcaaggctg ctctagagac aaaggaacac aaggccaggc cactatgggc   1312

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    <222> (264)..(1508)

    <400> 82
gctggacacc tgcggtaccg gtccggaatt cccgggtcga cccacgcgtc cgaccactga     60
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gacgagcggg agcgcggagc agcagcctct gctgccctga ctttttaaga aatctcaatg     120

aactatttgt agagaatcac tgatccggcc tgcaagcatt ttgcacggca aaaatatcga     180

tcagtgttaa gtgaagatca cattttatat gcgatcttga cttttttgtc ttacattata     240

tttttataga ttttgttata aac    atg gtg ctg gga aag gtg aag agt ttg       290
                            Met Val Leu Gly Lys Val Lys Ser Leu
                              1               5

aca ata agc ttt gac tgt ctt aat gac agc aat gtc cct gtg tat tct       338
Thr Ile Ser Phe Asp Cys Leu Asn Asp Ser Asn Val Pro Val Tyr Ser
 10                  15                  20                  25

agt ggg gat acc gtc tca gga agg gta aat tta gaa gtt act ggg gaa       386
Ser Gly Asp Thr Val Ser Gly Arg Val Asn Leu Glu Val Thr Gly Glu
                 30                  35                  40

atc aga gta aaa tct ctt aaa att cat gca aga gga cat gcg aaa gta       434
Ile Arg Val Lys Ser Leu Lys Ile His Ala Arg Gly His Ala Lys Val
             45                  50                  55

cgc tgg act gaa tct aga aac gcc ggc tcc aat act gcc tat aca cag       482
Arg Trp Thr Glu Ser Arg Asn Ala Gly Ser Asn Thr Ala Tyr Thr Gln
         60                  65                  70

aat tac act gaa gaa gta gag tat ttc aac cat aaa gac atc tta att       530
Asn Tyr Thr Glu Glu Val Glu Tyr Phe Asn His Lys Asp Ile Leu Ile
     75                  80                  85

ggg cac gaa aga gat gat gat aat tcc gaa gaa ggc ttc cac act att       578
Gly His Glu Arg Asp Asp Asp Asn Ser Glu Glu Gly Phe His Thr Ile
 90                  95                 100                 105

cat tca gga agg cat gaa tat gca ttc agc ttc gag ctt cca cag aca       626
His Ser Gly Arg His Glu Tyr Ala Phe Ser Phe Glu Leu Pro Gln Thr
                110                 115                 120

cca ctc gct acc tca ttc gaa ggc cga cat ggc agt gtg cgc tat tgg       674
Pro Leu Ala Thr Ser Phe Glu Gly Arg His Gly Ser Val Arg Tyr Trp
            125                 130                 135

gtg aaa gcc gaa ttg cac agg cct tgg cta cta cca gta aaa tta aag       722
Val Lys Ala Glu Leu His Arg Pro Trp Leu Leu Pro Val Lys Leu Lys
        140                 145                 150

aag gaa ttt aca gtc ttt gag cat ata gat atc aac act cct tca tta       770
Lys Glu Phe Thr Val Phe Glu His Ile Asp Ile Asn Thr Pro Ser Leu
    155                 160                 165

ctg tca ccc caa gca ggc aca aaa gaa aag aca ctc tgt tgc tgg ttc       818
Leu Ser Pro Gln Ala Gly Thr Lys Glu Lys Thr Leu Cys Cys Trp Phe
170                 175                 180                 185

tgt acc tca ggc cca ata tcc tta agt gcc aaa att gaa agg aag ggc       866
Cys Thr Ser Gly Pro Ile Ser Leu Ser Ala Lys Ile Glu Arg Lys Gly
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                190                 195                 200

tat acc cca ggt gaa tca att cag ata ttt gct gag att gag aac tgc          914
Tyr Thr Pro Gly Glu Ser Ile Gln Ile Phe Ala Glu Ile Glu Asn Cys
            205                 210                 215

tct tcc cga atg gtg gtg cca aag gca gcc att tac caa aca cag gcc          962
Ser Ser Arg Met Val Val Pro Lys Ala Ala Ile Tyr Gln Thr Gln Ala
        220                 225                 230

ttc tat gcc aaa ggg aaa atg aag gaa gta aaa cag ctt gtg gct aac         1010
Phe Tyr Ala Lys Gly Lys Met Lys Glu Val Lys Gln Leu Val Ala Asn
    235                 240                 245

ttg cgt ggg gaa tcc tta tca tct gga aag aca gag acg tgg aat ggc         1058
Leu Arg Gly Glu Ser Leu Ser Ser Gly Lys Thr Glu Thr Trp Asn Gly
250                 255                 260                 265

aag ttg ctg aaa att cca cca gtt tct ccc tct atc ctc gac tgt agt         1106
Lys Leu Leu Lys Ile Pro Pro Val Ser Pro Ser Ile Leu Asp Cys Ser
                270                 275                 280

ata atc cgc gtg gaa tat tca cta atg gta tat gtg gat att cct gga         1154
Ile Ile Arg Val Glu Tyr Ser Leu Met Val Tyr Val Asp Ile Pro Gly
            285                 290                 295

gct atg gat tta ttt ctt aat ttg cca ctt gtc atc ggt acc att cct         1202
Ala Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro
        300                 305                 310

cta cat cca ttt ggt agc aga acc tca agt gta agc agt cag tgt agc         1250
Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser
    315                 320                 325

atg aat atg aac tgg ctc agt tta tca ctt cct gaa aga cct gaa gca         1298
Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu Arg Pro Glu Ala
330                 335                 340                 345

cca ccc agc tat gca gaa gtg gta aca gag gaa caa agg cgg aac aat         1346
Pro Pro Ser Tyr Ala Glu Val Val Thr Glu Glu Gln Arg Arg Asn Asn
                350                 355                 360

ctt gca cca gtg agt gct tgt gat gac ttt gag aga gcc ctt caa gga         1394
Leu Ala Pro Val Ser Ala Cys Asp Asp Phe Glu Arg Ala Leu Gln Gly
            365                 370                 375

cca ctg ttt gca tat atc cag gag ttt cga ttc ttg cct cca cct ctt         1442
Pro Leu Phe Ala Tyr Ile Gln Glu Phe Arg Phe Leu Pro Pro Pro Leu
        380                 385                 390

tat tca gag att gat cca aat cct gat cag tca gca gat gat aga cca         1490
Tyr Ser Glu Ile Asp Pro Asn Pro Asp Gln Ser Ala Asp Asp Arg Pro
    395                 400                 405

tcc tgc ccc tct cgt tga aggaac acttggttga atcaagttga tgtgggttcc         1544
Ser Cys Pro Ser Arg  *
410                 415
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gaactgtatc tcttccggct gaggacagag aagtatcttg gagacacgtt tcagaggaag   1604

tggaattact tttgcccaga aaaatggcga atacatgaaa caaccagtga tcatgcttta   1664

gaagcctaca gcaacattct gagactgctc caacatgctt gaagatctaa gcttttctct   1724

tttaaaactg gcacatactc agagcagtct tcttagccta tggtcgtacg tgtcaagaca   1784

tcacgttgta aagagggatg atttccttct tttgatttga aaatttgcac atgctc       1840



      <210> 83
      <211> 800
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (509)..(685)

      <400> 83
gcacgaggga accgattttt tttatccaat gtgaattata aatgagataa tccacagtta     60

ttcattgtgg agttgttgag actatgaaag actcattgtc tttgtattca gctcttaaat    120

agtgtaacta tatccccacc tctgcttgct ttctttccct cccctccaat gataaagaaa    180

atgataaatt ttctgttgtg cattcaattc ttattttaaa taagactaag tataggcatt    240

gtacctgaca ttgctacgtt tctaccagtg tttcaattta aagtgctagt gtttaaaaac    300

attttcaagg gataaggcct tctgtacttt gcttatttga agaatcagtg gtaggagcag    360

tgaagtaaat tctatggagt acatttctaa aataccacat ttctgaaatc ataaataagt    420

ttattcaggt tctaaccctt tgctgtacac aagcagacag aaatgcatct gttacataaa    480

tgagaaaaag ctattatgct gatggagc   atg ctt ttt aaa tcc ttt aaa aac     532
                                 Met Leu Phe Lys Ser Phe Lys Asn
                                 1               5

act cac cat ata aac ttg cat ttg agc ttg tgt gtt ctt ttg tta atg      580
Thr His His Ile Asn Leu His Leu Ser Leu Cys Val Leu Leu Leu Met
    10                  15                  20

tgt aga gtt ctc ctt tct cga aat tgc cag tgt gta ctt ggc tta act      628
Cys Arg Val Leu Leu Ser Arg Asn Cys Gln Cys Val Leu Gly Leu Thr
25                  30                  35                  40

caa gaa cag ttt ctt ctg gat tcc tta ttt gat tta ttt aac cta att      676
Gln Glu Gln Phe Leu Leu Asp Ser Leu Phe Asp Leu Phe Asn Leu Ile
                45                  50                  55

ata ttc taa tattgca aatattacca taagtgggta aaagtaaaat tcctcttctg      732
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```
Ile Phe  *


aaaatgggtc ctggggtttt agatttttaa attccataaa aaacattctt aattttcaac    792

tcaaaaaa                                                             800




     <210> 84
     <211> 2885
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (585)..(1370)

     <400> 84
ccatgtaggg aattccccaa agcagggctt gccatacctg gacccсgagg agcctgcttg     60

ctggaaaggc tctcctgtct gatgtgcagg aggcagaatg ccaaactgac tcttcaaggg    120

gcaactgcag gggctcgaga ccagccagca gtatctcatc cttcgataca ggggatatac    180

tgtacagtcc tttttctaga agtgagacat acaagattac tctacaagag gaagattcca    240

ggggctcaaa aacgcaaagg tttgcacttt gagagcccct tggaatgttg acaactcagg    300

atctaaaaca aagttctgtg ttaatgagtt acagaattca cgtggaagtc aatgtcactt    360

tataatcgat aataatactg agtgaggaac actatgcagg aagaaacctt ccgtagaaag    420

acaggcaggg aaaagcttag gctgacctta aacttaccta atagagcaag cctgagatag    480

actgccaaaa tggccaaata agagactcta tgaaataaca gtcttgtaac tgtagtaatc    540

ataaggaaat tttctccttg aaatcacgat accaaatagg aaaa atg atc tac aag      596
                                                 Met Ile Tyr Lys
                                                 1

tgc ccc atg tgt agg gaa ttt ttc tct gag aga gca gat ctt ttt atg      644
Cys Pro Met Cys Arg Glu Phe Phe Ser Glu Arg Ala Asp Leu Phe Met
5                   10                  15                  20

cat cag aaa att cac aca gct gag aag ccc cat aaa tgt gac aag tgt      692
His Gln Lys Ile His Thr Ala Glu Lys Pro His Lys Cys Asp Lys Cys
                25                  30                  35

gat aag ggt ttc ttt cat ata tca gaa ctt cat att cat tgg aga gac      740
Asp Lys Gly Phe Phe His Ile Ser Glu Leu His Ile His Trp Arg Asp
            40                  45                  50

cat aca gga gag aag gtc tat aaa tgt gat gat tgt ggt aag gat ttt      788
His Thr Gly Glu Lys Val Tyr Lys Cys Asp Asp Cys Gly Lys Asp Phe
        55                  60                  65
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agc act aca aca aaa ctt aat aga cat aag aaa atc cac aca gtg gag      836
Ser Thr Thr Thr Lys Leu Asn Arg His Lys Lys Ile His Thr Val Glu
     70                  75                  80

aag ccc tat aaa tgt tac gag tgt ggc aaa gcc ttc aat tgg agc tcc      884
Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe Asn Trp Ser Ser
 85                  90                  95                 100

cat ctt caa att cat atg aga gtt cat aca ggt gag aaa ccg tat gtc      932
His Leu Gln Ile His Met Arg Val His Thr Gly Glu Lys Pro Tyr Val
                105                 110                 115

tgt agt gag tgt gga agg ggc ttt agt aat agt tca aac ctt tgc atg      980
Cys Ser Glu Cys Gly Arg Gly Phe Ser Asn Ser Ser Asn Leu Cys Met
            120                 125                 130

cat cag aga gtc cac acc gga gag aag ccc ttt aaa tgt gaa gag tgt     1028
His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys Cys Glu Glu Cys
        135                 140                 145

ggg aag gcc ttc agg cac acc tcc agc ctc tgc atg cat caa aga gtc     1076
Gly Lys Ala Phe Arg His Thr Ser Ser Leu Cys Met His Gln Arg Val
    150                 155                 160

cac aca gga gag aaa ccc tat aaa tgt tat gag tgt ggg aag gcg ttc     1124
His Thr Gly Glu Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe
165                 170                 175                 180

agt cag agt tcg agc ctc tgc atc cac cag aga gtc cac act gga gag     1172
Ser Gln Ser Ser Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu
                185                 190                 195

aaa ccc tat aga tgt tgt gga tgt ggg aag gcc ttc agt cag agt tcg     1220
Lys Pro Tyr Arg Cys Cys Gly Cys Gly Lys Ala Phe Ser Gln Ser Ser
            200                 205                 210

agc ctg tgc atc cac cag aga gtc cac aca gga gag aaa cct ttc aaa     1268
Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys
        215                 220                 225

tgt gat gag tgc gga aag gcc ttc agt cag agt acg agc ctc tgc atc     1316
Cys Asp Glu Cys Gly Lys Ala Phe Ser Gln Ser Thr Ser Leu Cys Ile
    230                 235                 240

cac cag aga gtc cac aca aag gag aga aac cat ctc aaa ata tca gtt     1364
His Gln Arg Val His Thr Lys Glu Arg Asn His Leu Lys Ile Ser Val
245                 250                 255                 260

ata taa aacgttttgc taagagttta aaatcttaaa acccataagt gccactagga      1420
Ile  *


aggaaaccct gtatatacct acattgaccc aagaaatatt tacgcaatcc ctagcagaac   1480

attgtttctg aggaggcata tgtgagattg atttgttggt tcatgccaag tgtgttccac   1540
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aggttgactt tgaatgtgga cctctgagca tccacgcagg atggctctca ggtcccagtc 1600

acagacgtcg cttcctggga ttccagcacg atgcctccat agttgaaaga ctacacaaaa 1660

agccacaatc attgcccggc ctcctgagtc accttctatc tatactttgc ttaaaagcta 1720

tcccagatac tccccttga ggagctcatg cccttccttc ctctttattc gagcatactg 1780

gcaatgcatt ggaaaacaga cagctcccac taagatcacg ttctggtatt tctgaggtta 1840

acacttgatt tagcccctac atatctttcc atatatccta ttatttctga atatatgtcc 1900

tcaaaatccc cataaatatc catcccttcc tagatggcat taactttcat tttagatttt 1960

aggtgactca taattcccat tcacttagcc tatcagaaaa gtcattggca gacatatatg 2020

tccttgaacc ttttttattt gtgtggattc tgctcatcac tgtctctgtt agacttattt 2080

tgtagtggct gcatcacata tttttcactt gaatttttt ggaaatagct gaatgtaaat 2140

agcagggagg aagaagcaag caaagtgaga gcttttcttc atccagaatt gccctctggg 2200

ctcctttggt aacagatgga gctccttcct agctagggag accttatgag aagtggatgg 2260

taggaggagt cactaatgtt tcaatctcta tttctgtaat cttgggcaat aatgcatagg 2320

agttcttgat accccttcat tgattactgt gtatcagttc tttgttaggc atgaacgtct 2380

ttattaatcc atcattcttt tcttcattca acaaatatgt attgaacacc tcctatatgc 2440

caggcactgt gctaggtgct gggaatacca ctgatgagac agacaaggtc cctactcttg 2500

tggagtttac ttctggtgga ggagacagat gataagtaaa caaataaata atgtagtttg 2560

agatagtgat taagtgctat gaagaaaata aactagggtg atgattttag tggtggggtg 2620

gggtgggggt ggggttacat tagctagtgg tcagggaggc ctttccgcgg tgggatgttg 2680

agctgaggcc ggaggagaag tagcagtcgc tggcagagca cacaggctgc tctgggggat 2740

gagctggtgc gtttaaggaa caggccagca ctggcattcg caagcagtgg ggaaggggag 2800

agatgccgag gtggtcagta tcctgacttt cagaggcctt tttttgtttg ttttaatttt 2860

tgctagattg atattaaaaa aaaaa 2885

<210> 85
<211> 1685
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (66)..(1382)

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<400> 85
cccacgcgtc cgttcttttc tgccgggtaa tggctgcttc caagacccag ggggctgtcg        60

cccga    atg cag gaa gac cgt gat ggg agc tgc agc aca gtc ggg ggt        107
         Met Gln Glu Asp Arg Asp Gly Ser Cys Ser Thr Val Gly Gly
           1               5                  10

gta ggt tat ggg gac agt aag gat tgt atc ctg gag ccg ctt tcc ctg         155
Val Gly Tyr Gly Asp Ser Lys Asp Cys Ile Leu Glu Pro Leu Ser Leu
 15                  20                  25                  30

cca gaa agt cca ggt ggc acc acc act tta gaa ggt tct cca tct gtg         203
Pro Glu Ser Pro Gly Gly Thr Thr Thr Leu Glu Gly Ser Pro Ser Val
                 35                  40                  45

cct tgt att ttc tgt gaa gaa cat ttt cct gtg gct gaa caa gac aaa         251
Pro Cys Ile Phe Cys Glu Glu His Phe Pro Val Ala Glu Gln Asp Lys
             50                  55                  60

ctt ctg aag cac atg att att gag cat aag att gtc ata gct gat gtc         299
Leu Leu Lys His Met Ile Ile Glu His Lys Ile Val Ile Ala Asp Val
         65                  70                  75

aag ttg gtt gct gat ttc caa agg tac att tta tat tgg agg aaa agg         347
Lys Leu Val Ala Asp Phe Gln Arg Tyr Ile Leu Tyr Trp Arg Lys Arg
     80                  85                  90

ttc act gaa cag ccc atc aca gat ttt tgt agt gta ata aga att aat         395
Phe Thr Glu Gln Pro Ile Thr Asp Phe Cys Ser Val Ile Arg Ile Asn
 95                 100                 105                 110

tcc act gct cca ttt gaa gaa caa gag aat tat ttt ttg tta tgt gac         443
Ser Thr Ala Pro Phe Glu Glu Gln Glu Asn Tyr Phe Leu Leu Cys Asp
                115                 120                 125

gtt tta cca gaa gat aga att ctt aga gaa gag ctt cag aaa cag aga         491
Val Leu Pro Glu Asp Arg Ile Leu Arg Glu Glu Leu Gln Lys Gln Arg
            130                 135                 140

ctg aga gaa att ctg gaa caa cag cag caa gaa cga aat gat acc aat         539
Leu Arg Glu Ile Leu Glu Gln Gln Gln Gln Glu Arg Asn Asp Thr Asn
        145                 150                 155

ttt cat ggc gtt tgt atg ttt tgc aat gaa gaa ttc ctt gga aac aga         587
Phe His Gly Val Cys Met Phe Cys Asn Glu Glu Phe Leu Gly Asn Arg
    160                 165                 170

tct gtt att ttg aac cac atg gcc aga gaa cat gct ttc aac att gga         635
Ser Val Ile Leu Asn His Met Ala Arg Glu His Ala Phe Asn Ile Gly
175                 180                 185                 190

ttg cca gac aac att gta aac tgc aat gaa ttt ttg tgt aca tta cag         683
Leu Pro Asp Asn Ile Val Asn Cys Asn Glu Phe Leu Cys Thr Leu Gln
                195                 200                 205

aaa aag ctt gac aat ttg cag tgc ttg tac tgt gag aag acc ttc agg         731
```

```
Lys Lys Leu Asp Asn Leu Gln Cys Leu Tyr Cys Glu Lys Thr Phe Arg
            210                 215                 220

gac aaa aat aca ctt aaa gat cac atg agg aaa aaa cag cat cgt aag       779
Asp Lys Asn Thr Leu Lys Asp His Met Arg Lys Lys Gln His Arg Lys
    225                 230                 235

att aat cct aag aac aga gaa tat gac aga ttt tat gtc atc aat tat       827
Ile Asn Pro Lys Asn Arg Glu Tyr Asp Arg Phe Tyr Val Ile Asn Tyr
    240                 245                 250

ttg gaa ctt gga aaa tcg tgg gaa gaa gtt cag ttg gaa gat gat cgg       875
Leu Glu Leu Gly Lys Ser Trp Glu Glu Val Gln Leu Glu Asp Asp Arg
255                 260                 265                 270

gag ttg ctg gac cat cag gaa gat gac tgg tct gat tgg gaa gaa cac       923
Glu Leu Leu Asp His Gln Glu Asp Asp Trp Ser Asp Trp Glu Glu His
                275                 280                 285

cct gcc tct gca gtc tgc tta ttt tgt gaa aag caa gca gaa aca att       971
Pro Ala Ser Ala Val Cys Leu Phe Cys Glu Lys Gln Ala Glu Thr Ile
            290                 295                 300

gag aag ttg tat gtc cac atg gag gat gca cac gaa ttt gat ctt ctc      1019
Glu Lys Leu Tyr Val His Met Glu Asp Ala His Glu Phe Asp Leu Leu
        305                 310                 315

aaa ata aag tca gaa ctt gga tta aat ttc tat cag caa gtg aaa ctg      1067
Lys Ile Lys Ser Glu Leu Gly Leu Asn Phe Tyr Gln Gln Val Lys Leu
    320                 325                 330

gtc aat ttt att cgg agg caa gtt cac caa tgc aga tgt tat ggc tgc      1115
Val Asn Phe Ile Arg Arg Gln Val His Gln Cys Arg Cys Tyr Gly Cys
335                 340                 345                 350

cat gtg aag ttc aaa tcc aaa gca gac tta aga act cac atg gaa gaa      1163
His Val Lys Phe Lys Ser Lys Ala Asp Leu Arg Thr His Met Glu Glu
                355                 360                 365

act aaa cac act tcg ctg ctc ccc gat aga aag acg tgg gat caa ctg      1211
Thr Lys His Thr Ser Leu Leu Pro Asp Arg Lys Thr Trp Asp Gln Leu
            370                 375                 380

gag tat tat ttt cca acc tat gaa aat gac act ctc ctg tgt aca cta      1259
Glu Tyr Tyr Phe Pro Thr Tyr Glu Asn Asp Thr Leu Leu Cys Thr Leu
        385                 390                 395

tct gac agt gaa agt gac ctg aca gct cag gaa caa aat gaa aat gtt      1307
Ser Asp Ser Glu Ser Asp Leu Thr Ala Gln Glu Gln Asn Glu Asn Val
    400                 405                 410

ccc atc atc agt gaa gat aca tct aaa ctg tat gct ttg aaa caa agc      1355
Pro Ile Ile Ser Glu Asp Thr Ser Lys Leu Tyr Ala Leu Lys Gln Ser
415                 420                 425                 430

agt att ttg aac cag ttg cta cta taa gagta cttgaaaacc tagaagaaac      1407
Ser Ile Leu Asn Gln Leu Leu Leu  *
```

```
                435

taccacagaa gcaatttttc atgtttttct cctatgagac agatatgaaa gaacaattta   1467

aatttgaaca tcaacaaaag attggtcctt ggtgaaataa acttttcaaa aatgaatgtt   1527

cttttcaaaa aataaagtag aaaaatgcac ttactaagaa catgaaaaaa aatgaagtag   1587

gaaaataaga tgaagacttt gtattttggc tgtaaagttt tattgtgtga tcatcttaaa   1647

ttatctcact tcattaaact cataattata tatagaaa                           1685



      <210> 86
      <211> 1094
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (59)..(595)

      <400> 86
atttcgtggc ttgccgggcg gccccaggcg gctgggcacg caccccaaga aggagccc       58
atg gag gcg ctg aac acg gcg cag ggc gcg cgc gac ttc atc tac agc      106
Met Glu Ala Leu Asn Thr Ala Gln Gly Ala Arg Asp Phe Ile Tyr Ser
1               5                   10                  15

ctg cac tcc acg gag agg agc tgc ctg ctc aaa gag ctg cac cgc ttc      154
Leu His Ser Thr Glu Arg Ser Cys Leu Leu Lys Glu Leu His Arg Phe
            20                  25                  30

gag tct att gcc att gcc caa gaa aaa ttg gaa gct cca cca ccc acc      202
Glu Ser Ile Ala Ile Ala Gln Glu Lys Leu Glu Ala Pro Pro Pro Thr
        35                  40                  45

cca gga cag ctg aga tat gta ttc atc cac aat gcg ata cct ttc ata      250
Pro Gly Gln Leu Arg Tyr Val Phe Ile His Asn Ala Ile Pro Phe Ile
    50                  55                  60

ggg ttt ggc ttt ttg gat aat gca att atg att gtt gct gga acc cat      298
Gly Phe Gly Phe Leu Asp Asn Ala Ile Met Ile Val Ala Gly Thr His
65                  70                  75                  80

att gaa atg tct att gga att att ttg gga att tca act atg gca gct      346
Ile Glu Met Ser Ile Gly Ile Ile Leu Gly Ile Ser Thr Met Ala Ala
                85                  90                  95

gct gct ttg gga aat ctt gtg tca gat cta gct gga ctt gga ctt gca      394
Ala Ala Leu Gly Asn Leu Val Ser Asp Leu Ala Gly Leu Gly Leu Ala
            100                 105                 110

ggc tac gtt gaa gca ttg gct tcc agg tta ggc ctg tca att cct gat      442
Gly Tyr Val Glu Ala Leu Ala Ser Arg Leu Gly Leu Ser Ile Pro Asp
        115                 120                 125
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ctc aca cca aag caa gtt gac atg tgg caa aca cgt ctt agt aca cat      490
Leu Thr Pro Lys Gln Val Asp Met Trp Gln Thr Arg Leu Ser Thr His
    130                 135                 140

ttg ggc aaa gct gtt ggg gtg act att ggc tgc att cta gga atg ttt      538
Leu Gly Lys Ala Val Gly Val Thr Ile Gly Cys Ile Leu Gly Met Phe
145                 150                 155                 160

cct tta att ttc ttt gga gga ggt gaa gaa gat gaa aaa ctg gaa acg      586
Pro Leu Ile Phe Phe Gly Gly Gly Glu Glu Asp Glu Lys Leu Glu Thr
                165                 170                 175

aaa agt taa tcctctt agaataccta taaaaagatg taaactaatg tacctcagta      642
Lys Ser  *


attaaatatg ctgtcacaac atttaggaat taagacagta acagtataga tatgggatca    702

aataatttag catgtattat ggaaaacact aacttattgt ggcttgatct tcttaggaca    762

tctttttaa aaagctgttt agtatcattt tgtgtatatt gttgaaatgc tttttcatca     822

atagcagtca acattttatc ctttcttttt atattcataa tgttatttaa gtgtcattga    882

tgtactgtat tgacttgggg tttgcttatt tgttacttaa catgtgtaca tgcatgaaag    942

catttttcgt tgttccctga tagttacatt tcaaccttgg gatttttcca aattacttaa   1002

gatgtttaat gtcagttaaa gattttttta ccctcttttt gggaacatca attttgtact   1062

gttatgcagt aaacatttat aataatataa aa                                1094



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      <222> (272)..(1024)

      <400> 87
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gaaacccacg aggggacgcg gccgaggagg gtcgctgtcc acccgggggc gtgggagtga    120

ggtaccagat tcagcccatt tggccccgac gcctctgttc tcggaatccg ggtgctgcgg    180

attgaggtcc cggttcctaa cggtgggatc ggtgtcctcg ggatgagatt tggcgtttcc    240

tcggggcttt ggtgggatcg gtgtcctcag g   atg aga ttt agg gtt tcc tcg      292
                                     Met Arg Phe Arg Val Ser Ser
                                      1               5
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ggg ctt tcg gga cgc ggc cga gga ggg tcg ctg tcc acc cgg ggg cgt        340
Gly Leu Ser Gly Arg Gly Arg Gly Gly Ser Leu Ser Thr Arg Gly Arg
         10                  15                  20

ggg agt gag gta cca gat tca gcc cat ttg gcc ccg acg cct ctg ttc        388
Gly Ser Glu Val Pro Asp Ser Ala His Leu Ala Pro Thr Pro Leu Phe
     25                  30                  35

tcg gaa tcc ggg tgc tgc gga ttg agg tcc cgg ttc cta acg gac tgc        436
Ser Glu Ser Gly Cys Cys Gly Leu Arg Ser Arg Phe Leu Thr Asp Cys
 40                  45                  50                  55

aag atg gag gaa ggc ggg aac cta gga ggc ctg att aag atg gtc cat        484
Lys Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His
                 60                  65                  70

cta ctg gtc ttg tca ggt gcc tgg ggc atg caa atg tgg gtg acc ttc        532
Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe
             75                  80                  85

gtc tca ggc ttc ctg ctt ttc cga agc ctt ccc cga cat acc ttc gga        580
Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly
         90                  95                 100

cta gtg cag agc aaa ctc ttc ccc ttc tac ttc cac atc tcc atg ggc        628
Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly
    105                 110                 115

tgt gcc ttc atc aac ctc tgc atc ttg gct tca cag cat gct tgg gct        676
Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala
120                 125                 130                 135

cag ctc aca ttc tgg gag gcc agc cag ctt tac ctg ctg ttc ctg agc        724
Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser
                140                 145                 150

ctt acg ctg gcc act gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca        772
Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr
            155                 160                 165

gct gcc atg tgg gcc ctg caa acc gtg gag aag gag cga ggc ctg ggt        820
Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly
        170                 175                 180

ggg gag gta cca ggc agc cac cag ggt ccc gat ccc tac cgc cag ctg        868
Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu
    185                 190                 195

cga gag aag gac ccc aag tac agt gct ctc cgc aca gaa ttt ctt ccg        916
Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Thr Glu Phe Leu Pro
200                 205                 210                 215

cta cat ggg ctg tcc tct ctt tgc aat ctg ggc tgc gtc ctg agc aat        964
Leu His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn
                220                 225                 230
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ggg ctc tgt ctc gct ggc ttg ccc tgg gaa tta gga gct cta gct ggg     1012
Gly Leu Cys Leu Ala Gly Leu Pro Trp Glu Leu Gly Ala Leu Ala Gly
            235                 240                 245

cct ggt gta taa tgctctccga aaaaaaaaaa aa                            1046
Pro Gly Val  *
        250




     <210> 88
     <211> 4797
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (19)..(1830)

     <400> 88
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                     Met Ala Val Ala Val His Asn Glu Leu Ile Ile
                       1               5                 10

tct gct ata ttc cat aca att aga ttt gtt ctt gcc tca aga ctt cag       99
Ser Ala Ile Phe His Thr Ile Arg Phe Val Leu Ala Ser Arg Leu Gln
             15                  20                  25

tct gat tgg atg ttg atg ctg tat ttt gca cat act cat ttg act gtg      147
Ser Asp Trp Met Leu Met Leu Tyr Phe Ala His Thr His Leu Thr Val
         30                  35                  40

aca gtc acc att ggg ttg ctt ttg att cca aag ttt tca cat tca agc      195
Thr Val Thr Ile Gly Leu Leu Leu Ile Pro Lys Phe Ser His Ser Ser
     45                  50                  55

aat aac cca cga gat gat att gct aca gaa gca tat gag gat gag cta      243
Asn Asn Pro Arg Asp Asp Ile Ala Thr Glu Ala Tyr Glu Asp Glu Leu
 60                  65                  70                  75

gac atg ggc cga tct gga tcc tac ctg aac agc agt atc aat tca gcc      291
Asp Met Gly Arg Ser Gly Ser Tyr Leu Asn Ser Ser Ile Asn Ser Ala
                 80                  85                  90

tgg agt gag cac agc ttg gat cca gag gac att cgg gac gag ctg aaa      339
Trp Ser Glu His Ser Leu Asp Pro Glu Asp Ile Arg Asp Glu Leu Lys
             95                 100                 105

aaa ctc tat gcc caa ctg gaa ata tat aaa aga aag aag atg atc aca      387
Lys Leu Tyr Ala Gln Leu Glu Ile Tyr Lys Arg Lys Lys Met Ile Thr
        110                 115                 120

aac aac ccc cac ctc cag aaa aag cgg tgc tcg aag aag ggc cta ggt      435
Asn Asn Pro His Leu Gln Lys Lys Arg Cys Ser Lys Lys Gly Leu Gly
    125                 130                 135
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cgt tcc atc atg aga cgc att acg gag atc cca gag aca gtc agc cgg        483
Arg Ser Ile Met Arg Arg Ile Thr Glu Ile Pro Glu Thr Val Ser Arg
140                 145                 150                 155

cag tgc tct aaa gag gac aag gag ggc gcc gac cat ggc aca gcc aaa        531
Gln Cys Ser Lys Glu Asp Lys Glu Gly Ala Asp His Gly Thr Ala Lys
                160                 165                 170

ggc act gcc ctc atc agg aag aac ccc cca gag tct tca ggg aac aca        579
Gly Thr Ala Leu Ile Arg Lys Asn Pro Pro Glu Ser Ser Gly Asn Thr
            175                 180                 185

ggg aaa tcc aag gag gag acc ctg aaa aac cga gtc ttc tca ctc aag        627
Gly Lys Ser Lys Glu Glu Thr Leu Lys Asn Arg Val Phe Ser Leu Lys
        190                 195                 200

aaa tcc cac agc act tat gac cac gtg aga gac caa acg gaa gag tcc        675
Lys Ser His Ser Thr Tyr Asp His Val Arg Asp Gln Thr Glu Glu Ser
    205                 210                 215

agt agc cta ccc aca gaa agc caa gag gag gag aca aca gaa aat tcc        723
Ser Ser Leu Pro Thr Glu Ser Gln Glu Glu Glu Thr Thr Glu Asn Ser
220                 225                 230                 235

aca ctg gaa tcc ctg tcg ggt aaa aaa cta aca caa aaa cta aaa gaa        771
Thr Leu Glu Ser Leu Ser Gly Lys Lys Leu Thr Gln Lys Leu Lys Glu
                240                 245                 250

gac agc gag gct gag tcc acg gag tcg gtg ccg ttg gtg tgc aag tca        819
Asp Ser Glu Ala Glu Ser Thr Glu Ser Val Pro Leu Val Cys Lys Ser
            255                 260                 265

gca agc gct cac aac ctc agc tca gag aag aaa act ggg cac cca cga        867
Ala Ser Ala His Asn Leu Ser Ser Glu Lys Lys Thr Gly His Pro Arg
        270                 275                 280

aca tcg atg tta cag aag tct ctc agt gtc ata gca agc gcc aag gag        915
Thr Ser Met Leu Gln Lys Ser Leu Ser Val Ile Ala Ser Ala Lys Glu
    285                 290                 295

aag act ctt gga tta gct ggg aaa acc caa aca gca ggt gtg gaa gaa        963
Lys Thr Leu Gly Leu Ala Gly Lys Thr Gln Thr Ala Gly Val Glu Glu
300                 305                 310                 315

cgc act aaa tcc cag aaa cct ttg cca aaa gat aaa gag aca aac aga       1011
Arg Thr Lys Ser Gln Lys Pro Leu Pro Lys Asp Lys Glu Thr Asn Arg
                320                 325                 330

aat cac tca aat tct gat aac aca gag act aaa gat cct gcc ccc caa       1059
Asn His Ser Asn Ser Asp Asn Thr Glu Thr Lys Asp Pro Ala Pro Gln
            335                 340                 345

aac tca aat cct gcg gag gag cca aga aag cct cag aaa tct ggg att       1107
Asn Ser Asn Pro Ala Glu Glu Pro Arg Lys Pro Gln Lys Ser Gly Ile
        350                 355                 360
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atg aaa caa caa agg gtc aac ccc acc act gcc aat tct gac ctg aac      1155
Met Lys Gln Gln Arg Val Asn Pro Thr Thr Ala Asn Ser Asp Leu Asn
    365                 370                 375

cca ggc acc acc cag atg aag gac aac ttt gac att ggg gag gtg tgt      1203
Pro Gly Thr Thr Gln Met Lys Asp Asn Phe Asp Ile Gly Glu Val Cys
380                 385                 390                 395

cct tgg gag gtt tat gac ctg acc cct ggt cct gtg cct tca gaa tca      1251
Pro Trp Glu Val Tyr Asp Leu Thr Pro Gly Pro Val Pro Ser Glu Ser
                400                 405                 410

aaa gtt caa aag cac gta tct att gtg gct tct gaa atg gag aaa aac      1299
Lys Val Gln Lys His Val Ser Ile Val Ala Ser Glu Met Glu Lys Asn
            415                 420                 425

ccc act ttt tcc tta aag gag aaa tct cac cac aag cct aag gca gct      1347
Pro Thr Phe Ser Leu Lys Glu Lys Ser His His Lys Pro Lys Ala Ala
        430                 435                 440

gag gtt tgt cag caa tcc aat cag aag cgc ata gat aag gct gaa gta      1395
Glu Val Cys Gln Gln Ser Asn Gln Lys Arg Ile Asp Lys Ala Glu Val
    445                 450                 455

tgc ctt tgg gag agc caa ggc cag tcc att ttg gaa gat gag aag ctt      1443
Cys Leu Trp Glu Ser Gln Gly Gln Ser Ile Leu Glu Asp Glu Lys Leu
460                 465                 470                 475

ttg att tcc aag act cca gtt ctc cca gag agg gca aaa gag gag aac      1491
Leu Ile Ser Lys Thr Pro Val Leu Pro Glu Arg Ala Lys Glu Glu Asn
                480                 485                 490

gga ggt cag cct cgt gca gcc aat gtg tgt gct ggg cag agc gaa gaa      1539
Gly Gly Gln Pro Arg Ala Ala Asn Val Cys Ala Gly Gln Ser Glu Glu
            495                 500                 505

ctg ccc ccc aaa gct gta gca tca aaa aca gag aat gaa aat ctc aac      1587
Leu Pro Pro Lys Ala Val Ala Ser Lys Thr Glu Asn Glu Asn Leu Asn
        510                 515                 520

caa ata gga cac cag gaa aaa aag aca tct tct tct gag gag aat gtg      1635
Gln Ile Gly His Gln Glu Lys Lys Thr Ser Ser Ser Glu Glu Asn Val
    525                 530                 535

cgt ggc tcc tat aac tca agt aat aac ttc cag caa cct tta aca tca      1683
Arg Gly Ser Tyr Asn Ser Ser Asn Asn Phe Gln Gln Pro Leu Thr Ser
540                 545                 550                 555

cga gca gag gtt tgt cct tgg gag ttt gag acc cca gct caa cca aat      1731
Arg Ala Glu Val Cys Pro Trp Glu Phe Glu Thr Pro Ala Gln Pro Asn
                560                 565                 570

gct gga aga agt gta gct tta cct gcc tct tct gct cta agt gca aat      1779
Ala Gly Arg Ser Val Ala Leu Pro Ala Ser Ser Ala Leu Ser Ala Asn
            575                 580                 585

aag ata gca ggg cct agg aaa gaa gag gtc tgg gat agt ttt aaa gtg      1827
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Lys Ile Ala Gly Pro Arg Lys Glu Glu Val Trp Asp Ser Phe Lys Val
        590                 595                 600

tag catc tccaggaaga agaggaaaag gagggaaccc cggattggat atgagacaga     1884
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agatataaga atcaaatatt cccaaggagg atttgtcaat caaggaaaac atgacagatg   1944

gtgaggtaaa gtcaaaggca tgggtagaag aggaccaggg gggcaagagc aacaacgtca   2004

taatggagaa gtcagacttt ggtcaagaaa gtccttccct tggtaacact aggaaaatct   2064

ttccatttca gcatgtttaa ggaaaatagc ccacaatgtc tgccctgatc aatatgtatc   2124

catgggactt tgaagatcct aagccaggta aaccaggaga cacagaagac gtaccagatt   2184

tgcaaagaaa gaaaaggtat aagacatata taactgaaat tctaagtagc tgaccgagaa   2244

gaacttactt tacctattta accttgatag cactgctaac ttaatgcatc ccaaaaatat   2304

cttttatatt aatgattgct ctcattttct tataaatgta tgtttcagta tatcgttgtg   2364

tctcatattc aagcattcca gattgtataa tttttgcaaa taactttggt attatgtgac   2424

acaacacatt tatgcaatct gcagctattc aattgttatt gcaccttaca gaatacctgc   2484

tatctatcaa ctttagttga ttcttgaagt acagtaagct ttctctggct tgggaagcca   2544

taactgttac tataaaaact tttagttttg gctgtggttt atatattgtg actttgaatt   2604

tgactctatt atttcacatc atggtttgtt atactgtctt aatcagggtt ttttatacaa   2664

gttgagttac ttgttttgca cttcttgtta ggactcagaa gctttattaa tattggagat   2724

caagtggtcc tacttagtca tatgtctcaa taagttaagg acaacttatc cgttgtttat   2784

tcaaagtcag agatagataa cgccttcatt ccaattaatt gtccctttta actctttcag   2844

tatttcctac ttagcagcat ttccaaagga agaagctaag agtgagaaaa atataccgtg   2904

cattattatt actattggaa agggaagact ctagggatga cataagaatt atagcagtac   2964

tataaaccca ggaagtttgc ctttcaaaaa aaaacacagg tagctcctga tagcactttc   3024

aagggattat ttttttaaag agaaaaatta tggtagcatc aagatcattg tatggatata   3084

tttttattat gtgtactgaa aatacagtat tttaaaatac cttaaagtat ttattctcat   3144

aaactcttat tcattgcttc agctacaggt agaacttgct gggctcaaat cccaaagagg   3204

ttttataacc ttatttattc aaaacctata aggtggtatg gaatcttcat tctcccaagc   3264

actggaaaat gtctaagtcc tgcaaattgc cattgtgagc cacttgctcg acatgtaaca   3324

tgtaaggtcc atttgcaaag caaagcagcc cccaaagcat attttataaa gcttattgca   3384
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ttccacactg atctcttggc atgggaatcc taagctgccg actaagccct accgacatga 3444

tcatgcagtg agattccaaa gctcagtctc atttcattta aagaagaatc actcagaaat 3504

agaaccgaga cttccctttt tctccctgta aacacccaag tatcaactgc ttatttggcc 3564

aggacactcc cagcacaaat aactattttt tatgtcacaa gcagcaagga ggacatgcta 3624

gggtgataaa agatggagaa acaggatcag agggtggata tagggctgtt cttagagagt 3684

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ttttttttat tcaggagtaa gcaagcactt cactgttttc acaaagctgt gcgcaaatct 3804

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catagaaagt gaataaacac ttttaaggtc gcaaacattt gctaggttgt ccttctcaat 4344

gcatgtgcag gctgcatcct gtccttgttt ttaagccagg gtttataaat aagtagattt 4404

ataccaatct taatagaatt gtatatttta tgcaagaatt aaatgcttta caacatgaag 4464

tataactcaa cccattgtaa actttggtgg caatatggat ttgaaactcg acagttctct 4524

tgtatttgct tcctaggttt ctgcatgcaa gttatgacag gtaggactga aaaaacactg 4584

ccttttgact tctagcattt agcaaccgag agtcgtagag tcaataaagc tgtaagtgtc 4644

ttcacttaat ctgtggttct cctaaaacta ttatctgaaa cctacagcat cccaccatga 4704

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caataaaaca tatttatatg aaaaaaaaaa aaa 4797

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<222> (250)..(2664)

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accgagaccg gagatgtttt caagcccggc tccggcggct ttacaggcgg ctgcagcggc     120

gacgaagaca acgacagcga cggctacgcc gaagcactcg ttccgggggt gaagcctcct     180

gcgccggcct tgcctcggat ccaggatgag aagactgata aaagaagaag ctagctgaac     240

agctgtaaa atg ccc aaa tct ggg ttc aca aaa cca att cag agt gaa         288
          Met Pro Lys Ser Gly Phe Thr Lys Pro Ile Gln Ser Glu
          1               5                   10

aat tct gac agt gac agc aat atg gta gag aaa cca tat gga aga aag       336
Asn Ser Asp Ser Asp Ser Asn Met Val Glu Lys Pro Tyr Gly Arg Lys
    15                  20                  25

agt aaa gac aag att gca tcc tac agc aaa act cca aaa att gaa cga       384
Ser Lys Asp Lys Ile Ala Ser Tyr Ser Lys Thr Pro Lys Ile Glu Arg
30                  35                  40                  45

agt gat gtg agc aag gag atg aaa gag aaa tca tcc atg aaa cgt aaa       432
Ser Asp Val Ser Lys Glu Met Lys Glu Lys Ser Ser Met Lys Arg Lys
                50                  55                  60

ctt cct ttt act att agc cca tca aga aat gaa gaa cga gat tca gac       480
Leu Pro Phe Thr Ile Ser Pro Ser Arg Asn Glu Glu Arg Asp Ser Asp
            65                  70                  75

aca gag aaa gaa ggt cca gaa aag aag aag aca aaa aag gaa gct gga       528
Thr Glu Lys Glu Gly Pro Glu Lys Lys Lys Thr Lys Lys Glu Ala Gly
        80                  85                  90

aat aag aaa tcc aca cca gtt agc att ctt ttt ggt tat cca ctc tct       576
Asn Lys Lys Ser Thr Pro Val Ser Ile Leu Phe Gly Tyr Pro Leu Ser
    95                  100                 105

gag cga aaa cag atg gca ctt ctt atg cag atg aca gca aga gac aac       624
Glu Arg Lys Gln Met Ala Leu Leu Met Gln Met Thr Ala Arg Asp Asn
110                 115                 120                 125

agt cca gat tcc aca cca aat cat cca tca caa aca acg cct gcc caa       672
Ser Pro Asp Ser Thr Pro Asn His Pro Ser Gln Thr Thr Pro Ala Gln
                130                 135                 140

aag aaa act ccc agt tct tca tct cga cag aaa gat aaa gtt aat aaa       720
Lys Lys Thr Pro Ser Ser Ser Ser Arg Gln Lys Asp Lys Val Asn Lys
            145                 150                 155

aga aat gaa cgt ggt gaa act cct tta cac atg gct gct att cga gga       768
Arg Asn Glu Arg Gly Glu Thr Pro Leu His Met Ala Ala Ile Arg Gly
        160                 165                 170

gat gtg aaa caa gtt aaa gaa tta ata agt tta ggg gca aat gtg aat       816
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Asp Val Lys Gln Val Lys Glu Leu Ile Ser Leu Gly Ala Asn Val Asn
    175                 180                 185

gtg aaa gat ttt gca ggt tgg aca cca ctg cat gaa gct tgc aat gtt      864
Val Lys Asp Phe Ala Gly Trp Thr Pro Leu His Glu Ala Cys Asn Val
190                 195                 200                 205

gga tat tac gat gtt gct aag ata ctt ata gca gct gga gca gat gtt      912
Gly Tyr Tyr Asp Val Ala Lys Ile Leu Ile Ala Ala Gly Ala Asp Val
                210                 215                 220

aac aca caa gga tta gat gat gac act cca ctc cat gat tct gct agt      960
Asn Thr Gln Gly Leu Asp Asp Asp Thr Pro Leu His Asp Ser Ala Ser
            225                 230                 235

agt ggg cac aga gat ata gta aag ctg tta ctt cgt cac ggt gga aat     1008
Ser Gly His Arg Asp Ile Val Lys Leu Leu Leu Arg His Gly Gly Asn
        240                 245                 250

cca ttt caa gct aat aaa cat ggg gag cgt cca gtg gat gta gca gaa     1056
Pro Phe Gln Ala Asn Lys His Gly Glu Arg Pro Val Asp Val Ala Glu
    255                 260                 265

aca gag gag ttg gag ttg cta cta aaa aga gag gtg cct tta tct gat     1104
Thr Glu Glu Leu Glu Leu Leu Leu Lys Arg Glu Val Pro Leu Ser Asp
270                 275                 280                 285

gat gat gaa agt tac aca gat tcc gaa gag gct caa tct gta aat cct     1152
Asp Asp Glu Ser Tyr Thr Asp Ser Glu Glu Ala Gln Ser Val Asn Pro
                290                 295                 300

tct agt gtt gat gaa aat att gac tct gaa aca gag aaa gac tct ctc     1200
Ser Ser Val Asp Glu Asn Ile Asp Ser Glu Thr Glu Lys Asp Ser Leu
            305                 310                 315

atc tgt gaa agt aaa cag ata ctt ccc agt aaa aca cct ctt cca tct     1248
Ile Cys Glu Ser Lys Gln Ile Leu Pro Ser Lys Thr Pro Leu Pro Ser
        320                 325                 330

gcc ctt gat gag tat gag ttc aaa gat gat gat gat gaa gaa att aat     1296
Ala Leu Asp Glu Tyr Glu Phe Lys Asp Asp Asp Asp Glu Glu Ile Asn
    335                 340                 345

aag atg att gat gat agg cat att ctt agg aaa gaa caa cga aaa gaa     1344
Lys Met Ile Asp Asp Arg His Ile Leu Arg Lys Glu Gln Arg Lys Glu
350                 355                 360                 365

aat gaa cct gaa gca gaa aaa act cat tta ttt gca aaa cag gag aaa     1392
Asn Glu Pro Glu Ala Glu Lys Thr His Leu Phe Ala Lys Gln Glu Lys
                370                 375                 380

gcc ttc tat cct aaa tca ttt aaa agt aaa aaa caa aag cca tct agg     1440
Ala Phe Tyr Pro Lys Ser Phe Lys Ser Lys Lys Gln Lys Pro Ser Arg
            385                 390                 395

gtc tta tat tca agt act gaa agt tct gat gaa gaa gct ctt cag aat     1488
Val Leu Tyr Ser Ser Thr Glu Ser Ser Asp Glu Glu Ala Leu Gln Asn
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        400                 405                 410

aaa aag att tct act tca tgt tcc gtc atc cct gaa aca tca aat tct       1536
Lys Lys Ile Ser Thr Ser Cys Ser Val Ile Pro Glu Thr Ser Asn Ser
    415                 420                 425

gat atg caa acc aaa aag gaa tat gta gtt tca ggt gaa cac aaa cag       1584
Asp Met Gln Thr Lys Lys Glu Tyr Val Val Ser Gly Glu His Lys Gln
430                 435                 440                 445

aaa ggc aaa gtt aaa aga aaa ttg aaa aat cag aat aaa aat aaa gag       1632
Lys Gly Lys Val Lys Arg Lys Leu Lys Asn Gln Asn Lys Asn Lys Glu
                450                 455                 460

aac caa gag cta aag caa gaa aag gaa gga aaa gaa aat aca aga ata       1680
Asn Gln Glu Leu Lys Gln Glu Lys Glu Gly Lys Glu Asn Thr Arg Ile
            465                 470                 475

aca aac ttg aca gta aat act gga cta gat tgt tca gaa aag acc aga       1728
Thr Asn Leu Thr Val Asn Thr Gly Leu Asp Cys Ser Glu Lys Thr Arg
        480                 485                 490

gag gag ggg aac ttt agg aaa tct ttt agc cca aaa gat gat act tca       1776
Glu Glu Gly Asn Phe Arg Lys Ser Phe Ser Pro Lys Asp Asp Thr Ser
    495                 500                 505

tta cat tta ttt cat att tcc act ggt aaa tct ccc aaa cat tct tgt       1824
Leu His Leu Phe His Ile Ser Thr Gly Lys Ser Pro Lys His Ser Cys
510                 515                 520                 525

gga tta agt gaa aaa cag tca aca cca cta aaa caa gaa cat act aaa       1872
Gly Leu Ser Glu Lys Gln Ser Thr Pro Leu Lys Gln Glu His Thr Lys
                530                 535                 540

aca tgt tta tca cca gga agt tct gaa atg tca tta cag cct gat ctt       1920
Thr Cys Leu Ser Pro Gly Ser Ser Glu Met Ser Leu Gln Pro Asp Leu
            545                 550                 555

gtt cgg tat gat aat aca gaa tct gaa ttc ttg cca gaa agt tca agt       1968
Val Arg Tyr Asp Asn Thr Glu Ser Glu Phe Leu Pro Glu Ser Ser Ser
        560                 565                 570

gta aaa tct tgt aag cat aag gaa aaa agc aaa cat cag aaa gat ttc       2016
Val Lys Ser Cys Lys His Lys Glu Lys Ser Lys His Gln Lys Asp Phe
    575                 580                 585

cac tta gaa ttt ggt gaa aaa tca aat gcc aaa ata aag gat gaa gat       2064
His Leu Glu Phe Gly Glu Lys Ser Asn Ala Lys Ile Lys Asp Glu Asp
590                 595                 600                 605

cat agt cca aca ttt gaa aat tca gat tgc aca ctg aaa aaa atg gat       2112
His Ser Pro Thr Phe Glu Asn Ser Asp Cys Thr Leu Lys Lys Met Asp
                610                 615                 620

aaa gaa ggt aaa aca tta aaa aaa cat aaa ttg aag cat aaa gag agg       2160
Lys Glu Gly Lys Thr Leu Lys Lys His Lys Leu Lys His Lys Glu Arg
            625                 630                 635
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gaa aaa gaa aag cat aaa aaa gaa att gaa ggt gaa aag gaa aaa tac      2208
Glu Lys Glu Lys His Lys Lys Glu Ile Glu Gly Glu Lys Glu Lys Tyr
        640                 645                 650

aaa act aag gat agt gcc aaa gaa ctg cag agg agt gtg gaa ttt gat      2256
Lys Thr Lys Asp Ser Ala Lys Glu Leu Gln Arg Ser Val Glu Phe Asp
    655                 660                 665

aga gaa ttt tgg aaa gag aat ttt ttt aaa agt gat gaa act gaa gat      2304
Arg Glu Phe Trp Lys Glu Asn Phe Phe Lys Ser Asp Glu Thr Glu Asp
670                 675                 680                 685

ctc ttt tta aat atg gaa cat gaa tcc tta aca tta gaa aaa aaa tca      2352
Leu Phe Leu Asn Met Glu His Glu Ser Leu Thr Leu Glu Lys Lys Ser
                690                 695                 700

aaa ttg gaa aaa aac atc aaa gat gat aaa tca acc aag gaa aag cat      2400
Lys Leu Glu Lys Asn Ile Lys Asp Asp Lys Ser Thr Lys Glu Lys His
            705                 710                 715

gtg tca aaa gag agg aac ttt aaa gag gaa cga gac aag att aaa aag      2448
Val Ser Lys Glu Arg Asn Phe Lys Glu Glu Arg Asp Lys Ile Lys Lys
        720                 725                 730

gaa agc gag aaa tct ttt agg gag gaa aaa ata aaa gat cta aaa gaa      2496
Glu Ser Glu Lys Ser Phe Arg Glu Glu Lys Ile Lys Asp Leu Lys Glu
    735                 740                 745

gag aga gaa aac ata ccc aca gat aaa gac tca gaa ttt act tct ttg      2544
Glu Arg Glu Asn Ile Pro Thr Asp Lys Asp Ser Glu Phe Thr Ser Leu
750                 755                 760                 765

ggt atg agt gcc att gag gaa tct ata ggg ctt cat tta gtg gaa aag      2592
Gly Met Ser Ala Ile Glu Glu Ser Ile Gly Leu His Leu Val Glu Lys
                770                 775                 780

gaa ata gac att gaa aaa caa gaa aag cat ata aag gaa aat aaa aaa      2640
Glu Ile Asp Ile Glu Lys Gln Glu Lys His Ile Lys Glu Asn Lys Lys
            785                 790                 795

aaa aaa aaa ggg cgg ccg ctc tag agtatccctc gaggggccca agcttacgcg    2694
Lys Lys Lys Gly Arg Pro Leu  *
        800                 805

tacccagctt tcttgtacaa agtggtccct atagtgagtc gtattataag ctggcgcctg   2754

cgcagctagt caacctctca cctt                                          2778


<210> 90
<211> 1070
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (727)..(876)

<220>
<221> misc_feature
<222> (1)...(1070)
<223> n = a,t,c or g

<400> 90
cggnttgaag tatttaaaca taattagaat cttaaggcca gtgtcacata ttgtaatatg      60

ccaattatgt ttaaatactt caaacagcaa atactacagt ttatctcaat gaatataata     120

accattcctg ctgggcgcag tggctcatgc ctttaatccc agtcattaag gaggctgagg     180

tgggaagatt gcttgaaacc aggagattgc ctcaggcctg ggcaacatgg tgagacctct     240

tatctcaaaa aatcaaaata aaaaattagc tgggcatggt ggctcatccc tgtagcccca     300

gcttctcaag aggctgaggt gggaggatag cttcagccta ggagacagaa gctgcagtga     360

gctatgatca caccactaca ctccagcctg gacaacagaa agagaccttg tctctaaaaa     420

caaaacaaaa caatcaaaca aaaaagtact cctgaattta agtattgatg gctatgggaa     480

ttgcttccta acctgtttga aaaatgtgtt aactgttaca tattttgaga actgcagcac     540

tcagtgaagc tttgttaaag ggaatgagga gtttaggccc cagcaggcaa accacttcac     600

agtgctagga tgaagagctc acactcaggg acttcgagag tgaatcaact actttcgtta     660

actcaatgtt aaatgagaat aacatcaacc ttggatggtt gtggtgagaa tcaaatgaaa     720

tgacat atg gga aaa cct ttg tca cat gtt aca caa ttg acg gca act        768
       Met Gly Lys Pro Leu Ser His Val Thr Gln Leu Thr Ala Thr
         1               5                  10

aca gct tta ggt aga att tca act tct aat ttt tac tac tat gca aat       816
Thr Ala Leu Gly Arg Ile Ser Thr Ser Asn Phe Tyr Tyr Tyr Ala Asn
 15                  20                  25                  30

tat cag aat att tat gat gtt aac ttt tta aaa agg ttt tta aat aga       864
Tyr Gln Asn Ile Tyr Asp Val Asn Phe Leu Lys Arg Phe Leu Asn Arg
                 35                  40                  45

aac ttt att taa ata aatgaactct tctcaacccc aaaacccagc ttctgatctt       919
Asn Phe Ile  *
             50

gactaagttc ataattactc agggaaaaac actgctggtt ccttataagc cactgtgctg     979

tacgaaatca attcatgaaa aggaaacgcc ctatttccaa gcatacctgt actagaatat    1039

attaagtata ttcacttaac atattaattt a                                   1070
```

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<210> 91
<211> 1784
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (150)..(932)

<400> 91
ggactggctg ggaagcggtc ggtcgagtgt ggcctgtgtg gactcgcatc ttgcccgaag      60

ccgggcggag gagagctcaa gctaagggtg atcagcccat gacctaaacc tccagacaaa     120

ataaaacgga aatttgcta gaatcaaga  atg atg gat cca tgt tca gtt gga      173
                                Met Met Asp Pro Cys Ser Val Gly
                                1               5

gtc cag ctt cgt act aca aat gag tgc cat aaa acc tac tat act cgc      221
Val Gln Leu Arg Thr Thr Asn Glu Cys His Lys Thr Tyr Tyr Thr Arg
    10                  15                  20

cac aca ggt ttt aag act ttg caa gaa ttg tca tca aat gat atg ctt      269
His Thr Gly Phe Lys Thr Leu Gln Glu Leu Ser Ser Asn Asp Met Leu
25                  30                  35                  40

tta ctt caa ctt aga act gga atg aca ctt tct ggg aac aat aca att      317
Leu Leu Gln Leu Arg Thr Gly Met Thr Leu Ser Gly Asn Asn Thr Ile
                45                  50                  55

tgc ttt cat cat gta aaa att tac att gac aga ttt gag gat tta cag      365
Cys Phe His His Val Lys Ile Tyr Ile Asp Arg Phe Glu Asp Leu Gln
            60                  65                  70

aag tca tgt tgt gac cca ttt aac ata cac aag aaa tta gcc aaa aaa      413
Lys Ser Cys Cys Asp Pro Phe Asn Ile His Lys Lys Leu Ala Lys Lys
        75                  80                  85

aat ttg cat gta att gac tta gat gat gcc act ttt ctg agt gct aaa      461
Asn Leu His Val Ile Asp Leu Asp Asp Ala Thr Phe Leu Ser Ala Lys
    90                  95                  100

ttt gga aga cag ctt gta cct ggt tgg aag ctt tgt cca aaa tgc aca      509
Phe Gly Arg Gln Leu Val Pro Gly Trp Lys Leu Cys Pro Lys Cys Thr
105                 110                 115                 120

cag ata atc aat gga agt gtg gat gtt gat act gaa gac cgc cag aaa      557
Gln Ile Ile Asn Gly Ser Val Asp Val Asp Thr Glu Asp Arg Gln Lys
                125                 130                 135

agg aaa cct gag tca gat gga aga act gct aaa gct ttg agg tca tta      605
Arg Lys Pro Glu Ser Asp Gly Arg Thr Ala Lys Ala Leu Arg Ser Leu
            140                 145                 150

caa ttt acg aat cca gga agg caa act gaa ttt gct cca gaa act ggt      653
```

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Gln Phe Thr Asn Pro Gly Arg Gln Thr Glu Phe Ala Pro Glu Thr Gly
        155                 160                 165

aaa aga gaa aaa aga agg ctt aca aaa aat gca acc gct ggt tca gac        701
Lys Arg Glu Lys Arg Arg Leu Thr Lys Asn Ala Thr Ala Gly Ser Asp
    170                 175                 180

aga caa gtg ata cca gca aag agt aag gtc tat gat agc cag ggt ctc        749
Arg Gln Val Ile Pro Ala Lys Ser Lys Val Tyr Asp Ser Gln Gly Leu
185                 190                 195                 200

ctg att ttt agt ggg atg gac ctc tgt gac tgc ctg gat gaa gac tgc        797
Leu Ile Phe Ser Gly Met Asp Leu Cys Asp Cys Leu Asp Glu Asp Cys
                205                 210                 215

tta gga tgt ttc tat gct tgt cct gcc tgt ggt tct acc aag tgt gga        845
Leu Gly Cys Phe Tyr Ala Cys Pro Ala Cys Gly Ser Thr Lys Cys Gly
            220                 225                 230

gct gaa tgc cgc tgt gac cgc aag tgg ctg tat gag caa att gaa att        893
Ala Glu Cys Arg Cys Asp Arg Lys Trp Leu Tyr Glu Gln Ile Glu Ile
        235                 240                 245

gaa gga gga gaa ata att cat aat aaa cat gct gga taa tctgcggtac         942
Glu Gly Gly Glu Ile Ile His Asn Lys His Ala Gly  *
    250                 255                 260

caaactatgg agcctttaaa ggtctttatt tctaaaatc tgttactcta agatacattt      1002

taagcttgat tatcatatga caaagatttt aaaaccatct cagtgtgccc taatttttca      1062

tcttgggtgc tttaagattc actatttgat ataaattcag ataggctatt tttcagtagt      1122

cagcgttaag cctgtctgga tcaatataaa caagtagggt gtaggcagtc ctctatttgc      1182

atgtttccca tgggcacaaa tttcagtgac ctagatttag tttaaatacc agtttcctta      1242

ccaggaagga aagaaaactg gtaaggaaac tgttgttgtt aaaatctagg ttaaaatttt      1302

agttagcaca ttgtaactga gtaattacat gaagtacaaa cctctctgct agctcttcag      1362

tctacaaatc gctatgtaaa taacagatat gcttcatgat tgtgaccagt catgttattt      1422

ctttcaaatt cttccagtgg tttgtccctg tgcatctgtt aattcagttc acgtacagca      1482

gagcatgtag ttatgctgtc tctctgtcat ctacttgaca ttctatagaa gtgaacactc      1542

gaaagaactg gtcaacaaag atgaaagtgc agcaaagcaa tgaaaaatga taacactgga      1602

agtgaaattt taatcaaaca taaatgaatt tgtagaagaa gtcactgacc atgggaatgt      1662

tgttcttgct gctgtgtatt cataggagct tagtgaaggc aaacttacca acacaaataa      1722

gcaaagtggt tgcaataaag acagatacgt cccagaggaa gtgatggtta aaaaaaaaaa      1782

aa                                                                    1784
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<210> 92
<211> 2559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (978)..(1451)

<400> 92
agtaaaaaat atgctggtta taaaccttag gggactaccc attgaatatg tggtccatcg      60

ttgacctaaa catcattatg tggtgcatga ctgtccgtat atgcagatta aactaccaaa     120

catttttttcc agcaaaggtg gtttttgaaa gtaacctaat gaaaccctgg ctgccatggg    180

cattttaatt ctggactgag aagaagcgac tctgcgttgt gctgttggcc caggcctgca     240

tgcctgagga ctgttggccg ttacagttcc ttgctgtggt cgccggtctc tctgtattct     300

gccactgctc tcatgtggca tttggcagaa gtactacgta gatttctgtg ctactgaaaa     360

aaataaaaac agtggttcct tttaatagcc ctgatttgag acttaggaga gggtcaagag     420

tccctacctg atttatgagg agagaagatt ttttaaaaac ctcatgtgat gctgtcatac     480

atagttcaaa gagcttccct taattcactt catttacctt tttttccatt ttcgcttgag     540

aactagagaa gtttgtgttc tgttggaacc ctctgtagaa cactttacac tcagttctga     600

tggacctttt caggggcgat tttttaaaaa ccgctctcga aagtagtctt aaaatgagag     660

cactttattg atggcttttc aggactgtgt tggtattttt catgcagtgt atttgtcagc     720

ttacattttt cagttgagct acctgatgct actgacacac atatgatttt cctatcttac     780

caggcaaata ctactgttaa cgttttaata gtaagtctac ttatgcacat tgattttact     840

ttgaaaaaag aactggttta aaaggaaaaa aaagaaacta aaattcttta aaattgtaat     900

ggcagtgaag cattttatag tttctcctcc ctcattggtt ctgaattttg gtgacaggtg     960

tatttcttaa tgcagat  atg aaa aac agt agc tcc gta tcg aat aca ttg      1010
                    Met Lys Asn Ser Ser Ser Val Ser Asn Thr Leu
                    1               5                   10

aca aat gga tgt gtc atc aat gga cat ttg gac ttc ccc tcc acg acc     1058
Thr Asn Gly Cys Val Ile Asn Gly His Leu Asp Phe Pro Ser Thr Thr
            15                  20                  25

ccg ctc agt ggg atg gaa agc agg aat ggc cag tgc ttg aca gga act     1106
Pro Leu Ser Gly Met Glu Ser Arg Asn Gly Gln Cys Leu Thr Gly Thr
        30                  35                  40
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aac gga att agc agt gga tta gcc cca gga cag ccg ttt ccg agt agc      1154
Asn Gly Ile Ser Ser Gly Leu Ala Pro Gly Gln Pro Phe Pro Ser Ser
     45                  50                  55

cag ggt tct ctc tgc att agt ggg act gag gag cca gag aag acc ctg      1202
Gln Gly Ser Leu Cys Ile Ser Gly Thr Glu Glu Pro Glu Lys Thr Leu
 60                  65                  70                  75

aga gct aac cct gag ttg tgc ggt tct ctg cac ctg aac ggg agt cca      1250
Arg Ala Asn Pro Glu Leu Cys Gly Ser Leu His Leu Asn Gly Ser Pro
                 80                  85                  90

agt agc tgc ata gcc agt agg cct tcc tgg gtg gaa gac att ggg gat      1298
Ser Ser Cys Ile Ala Ser Arg Pro Ser Trp Val Glu Asp Ile Gly Asp
             95                 100                 105

aac ctg tac tat gga cac tac cac ggg ttt ggg gac act gct gaa agc      1346
Asn Leu Tyr Tyr Gly His Tyr His Gly Phe Gly Asp Thr Ala Glu Ser
        110                 115                 120

atc cca gaa ctg aac agt gtg gtc gag cat tcc aag tcc gtg aag gtg      1394
Ile Pro Glu Leu Asn Ser Val Val Glu His Ser Lys Ser Val Lys Val
    125                 130                 135

cag gag cgg tac gac agt gcc gtg ctg ggc acc atg cac ctg cac cac      1442
Gln Glu Arg Tyr Asp Ser Ala Val Leu Gly Thr Met His Leu His His
140                 145                 150                 155

ggc tcc tag agacgct gacctggctc tcggaaacgc aggagtccct cctggtagcc      1498
Gly Ser  *


agctcagaat acccatgtag cagcaacttg aacgaatgtc acaacttgta cttttttat    1558

atacttcaac tttctgaaaa agtaaacttc gacaagttcc cagcaactgc ttgtttgtgc   1618

atgagtaggg cttactaagt gcatagatgt ttctacagtg aggtgtcctt tttataaggt   1678

gcacttttgg agtttttctg atgccaatct caacattgtc tttttaatac tgtcaccaga   1738

tattgccatt tttctttttg ttaaaagatt atatgatcaa gataaattgg ggtggtaaat   1798

caggtgcctg gtaatttatc tctttgcaca tgggcatcat tttaaaaagc ttgcttccac   1858

tcttttctgt agaatttgac ggaacacagc tatttcccta tgcaaggtac agccttacaa   1918

agatttctgc agtgatttgt gtgaagaaga gaatgtttgt ctttttcaat gaagctttgc   1978

agatcaccat gtggttgaag gttttagttg tggacacagt ggtccctcct taatgatgaa   2038

gatcactgcc ttgggcttca tggaaaacag gcccagcctg gggctgcgtt tggatttatt   2098

gtttttattc cacacttcct acttggtctc tggaagtttt accacatgta acagattcct   2158

ttatatgtag tgaaaatcac tatttgtaga aactgtcagg tcaaaatatt taactgactg   2218

ttgacatgta ttttcttttt tccttgtttt tgttttttgg ggttttctgc tttaagatat   2278
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ataccactat gtatatccag ttaactgaga gaattttgac tctcttaata aaactgcatt   2338

aagtttttga ttttgtagaa attagctttt gtctaggcaa ctagtggtta tactctgcaa   2398

atattgtaat gaatttttac tttttgatt tttgtaataa aaattggtgc agataaaatg   2458

tcaaatgaac aaaccagtgt tctaagagtg ttactaacat tttgttctaa aactgtcctt   2518

cacaaattga ataaaaaact ctcacactca aaaaaaaaa a                        2559



      <210> 93
      <211> 813
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (286)..(759)

      <400> 93
cggcacgagg gagctttgag gcggtctaac tacccagctt ttagtattta tgttccccaa     60

aatgtaaaaa ctgtaagtta ttcttgaaaa tgtagtccag acatttcttt gatcctggat    120

tttactgcag tttcatcatg ggtttgttga atgtgcagtc catttattgc cctgtcttgc    180

ttaaatattc ttgttgagaa cagctggagg ctttgactgg gttcctagtt ctgttttctg    240

ggaaggcaac gtggattctg ttttgtagac attaatgagc tttaa    atg gga att    294
                                                     Met Gly Ile
                                                      1

ggg gat gat gta tgt cta caa aaa aaa aaa agt tgg agc ggc cgc caa      342
Gly Asp Asp Val Cys Leu Gln Lys Lys Lys Ser Trp Ser Gly Arg Gln
    5                   10                  15

ctt agg ggc cac gtg agc cac ggc cac ggc cgc ata ggc aag cac cgg      390
Leu Arg Gly His Val Ser His Gly His Gly Arg Ile Gly Lys His Arg
 20                  25                  30                  35

aag cac ccc ggc ggc cgc ggt aat gct ggt ggt ctg cat cac cac cgg      438
Lys His Pro Gly Gly Arg Gly Asn Ala Gly Gly Leu His His His Arg
                40                  45                  50

atc aac ttc gac aaa tac cac cca ggc tac ttt ggg aaa gtt ggt atg      486
Ile Asn Phe Asp Lys Tyr His Pro Gly Tyr Phe Gly Lys Val Gly Met
            55                  60                  65

aag cat tac cac tta aag agg aac cag agc ttc tgc cca act gtc aac      534
Lys His Tyr His Leu Lys Arg Asn Gln Ser Phe Cys Pro Thr Val Asn
        70                  75                  80

ctt gac aaa ttg tgg act ttg gtc agt gaa cag aca cgg gtg aat gct      582
```

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Leu Asp Lys Leu Trp Thr Leu Val Ser Glu Gln Thr Arg Val Asn Ala
    85                  90                  95

gct aaa aac aag act ggg gct gct ccc atc att gat gtg gtg cga tcg      630
Ala Lys Asn Lys Thr Gly Ala Ala Pro Ile Ile Asp Val Val Arg Ser
100                 105                 110                 115

ggc tac tat aaa gtt ctg gga aag gga aag ctc cca aag cag cct gtc      678
Gly Tyr Tyr Lys Val Leu Gly Lys Gly Lys Leu Pro Lys Gln Pro Val
                120                 125                 130

atc gtg aag gcc aaa ttc ttc agc aga aga gct gag gag aag att aag      726
Ile Val Lys Ala Lys Phe Phe Ser Arg Arg Ala Glu Glu Lys Ile Lys
            135                 140                 145

agt gtt ggg ggg gcc tgt gtc ctg gtg gct tga agccacat ggagggagtt      777
Ser Val Gly Gly Ala Cys Val Leu Val Ala  *
        150                 155

tcattaaatg ctaactactt tttcaaaaaa aaaaaa                              813



     <210> 94
     <211> 1686
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (737)..(1003)

     <400> 94
taataaatgg tatgaatata tattttgcat actttacaat aaagaaaatt ttgaaagaaa     60

atggatctaa aactttgttt ccctccaatt tacatagtaa agtcaactgc atacagttct    120

ttccatgtgt aagttttaca tttgtatttt ctacaattaa gtaaatctaa atgttaaatt    180

ttaacacata tatccaatta tgtacacaat tacaatgtca atttataagt caagcttact    240

taacaatcat aaattacaaa aaacgcacta tgaataattt tgttctagaa gtatcacatc    300

aactcatatg atctaggtga acccaaaagt aaaaaataat gattataaat tatggtagtg    360

tctgtaaaac cctgttataa aggaggtatt cttttaaaat atgtacctta tatataaaag    420

ctcctgactc cttttaagga ccaaaattat tttcagtcta accattttca ttaaagcgct    480

tatttaaaaa gtatcacctt ataaaactga gtatataaaa tacaatgcag cccttgatag    540

ctaagaatct ttataaacgc caatgattta gtgacctgtt tatcaaacta tttctatgga    600

tgggttgatt ttttttcttc ctctaaatta agtggcccta gactaatata tttgttcagt    660

tattctgttt tcttccttac tgccatttca catctccatc agtgagttcc tcaggatttg    720
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cctttatgtt acaact    atg aaa gtc ttc aat cca att ccc tgc ttc cac      769
                     Met Lys Val Phe Asn Pro Ile Pro Cys Phe His
                       1               5                  10

aca aag gac aaa gaa agc cta aac ttt cct ttt ttc tgg gct cca ata      817
Thr Lys Asp Lys Glu Ser Leu Asn Phe Pro Phe Phe Trp Ala Pro Ile
            15                  20                  25

gga agc agc att tac aac gtg tct ggc ttg gtg gga gga aga ttg tca      865
Gly Ser Ser Ile Tyr Asn Val Ser Gly Leu Val Gly Gly Arg Leu Ser
        30                  35                  40

att gag gta tca tgt gtg ttc acc tgc ctc tct tgc cct att tct ttg      913
Ile Glu Val Ser Cys Val Phe Thr Cys Leu Ser Cys Pro Ile Ser Leu
    45                  50                  55

gtt gct ata aat ttc ctg ctt ctc aaa tat ctg gat ttt tgg cta cct      961
Val Ala Ile Asn Phe Leu Leu Leu Lys Tyr Leu Asp Phe Trp Leu Pro
60                  65                  70                  75

att tgg ctt ccg tct ttg gtg ttt ata tct gtc tgg ttt tag caggtct     1010
Ile Trp Leu Pro Ser Leu Val Phe Ile Ser Val Trp Phe  *
                80                  85

ctctgattcc tgacccacag ctcctctcct tctctaatat tcaagtatgc tgcttcccta   1070

actcctcatt ccttctcctt gaatttcact ttacaattgc gctaggttct aacatcgttg   1130

gccatagatt accacaaaac ataatttctt aaattctgca aatttctaat gtttctaatc   1190

ttggtttcct acaagatcta acactaagct tgtgttatcc tgattacagt gtatataaaa   1250

caatgcttgt ggaaaattaa cctaggagaa agcttatagg ggaaacctga tgatgaattt   1310

tattaaatta ataaccctta taacaatttc aaatgtaata ctatctggat ttgaacttca   1370

atacttttcc taagtaaaat tcttaaccat ggtagaagtt atgtttgttg atgttcactc   1430

atctataccc tccatattct cagcaaagtt ggcataaatc tgacctgaat aaacagggtt   1490

ataacattat caggcttgta aaatacttta tcaaatcaat gcatcagtta aagcaggggt   1550

ccccagccct gggctgtgtg tggcctgtta ggaatcgggc cacacagttg gtgagctgag   1610

aggcaggtga gtgagcatta ctgcctgagc tccacctctt gttagatcag tagtggcatt   1670

agattctcac tcgtgc                                                   1686


      <210> 95
      <211> 1217
      <212> DNA
      <213> Homo sapiens
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<221> CDS
<222> (353)..(472)

<400> 95
cttgcagact tttgacacaa gttctccaca aagtgtgaag agagccccag gcattcctga      60

ttggtcaatg ggagagccta actttcattg ttttcttcag tacaaagagt atccaaaagc     120

taagtttttg tattccacta ctttcagttc aataaaacct agagttgttt catctgcgcc     180

taaagtgtat ggcacaattt tcttaagaat taggggaacc aggtgcctac agttaaagga     240

acgtttcagt tcctttcatt cattcctggg tttttctttt attttctaag aaggttgaag     300

aaggatgagt gatagagaag aaagcaacac cattgatttt ttttttaag aa    atg      355
                                                            Met
                                                              1

ata tat ata tgt ata tgt ttg tgt gtg tgt gtg tgt gtg tgt gta ttc      403
Ile Tyr Ile Cys Ile Cys Leu Cys Val Cys Val Cys Val Cys Val Phe
            5                  10                  15

tgt gca tta ttt tgt cat gat ctc aat tct ctt ctt tcc acc aaa gtt      451
Cys Ala Leu Phe Cys His Asp Leu Asn Ser Leu Leu Ser Thr Lys Val
        20                  25                  30

tgt cgt aat att ttc tcc tga ag gtgcattctg gctcctttaa attagtcagt      504
Cys Arg Asn Ile Phe Ser  *
    35                  40

gttatattgt aggagactgt catggaaaaa aggactcagt ttactttcgt cattttcaca     564

ggggaacctt ttaaaacaat cttttcagca gcagatacct ttaaccctaa taatctcagg     624

ccttgatgaa aatactatat tttgtagatt atggttaaag ggggaaaatt actagttccg     684

taagataaat atgagctcca tttgacttct gatgtctggt ttagcattac ataatatgtt     744

gatcttacac tctgcttttg tccaaataaa atgcaatagt atcaatatca atttcagaaa     804

aatggactga atatgctttt ttggtgatga aatctcatgt acgatattta tagtgatgtg     864

cttttatttt ctcatgagat actaaatatt aattgtgttg tacatttgtt cttagcatat     924

attaaagttt tgaaccaaat gtgttaaagc ttacgctttg ccatgtaaat ttcccagaag     984

ttgttgagct caaatgtatc ctacatccag ctgtagaaat ttgtcagaaa ttgtttaaat    1044

tttgtatata attgtactgt ttaattctag ccattgcgct gaacagtatt tgagttacca    1104

tataatatgg ctttacacaa ggaaatgtgt ggcttttgtt ttgtattttt tcagtataga    1164

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gcttgcaatt gaacatcacc ccccaactgg aagagcctca catcctggac gaatgaccaa     180

ggcgccagga gaaagactgt gttttctccc acgctacctg ccgcccgctc ttctcttggc     240

tctctgcaaa cacctgaagc tgtgaccacc agaaagggca caggcttgct ttcctcagac     300

tacaggatca tcaatggcaa aagtggaact caggacatcc agcctggccc tctttttaat     360

aataatgctg atggagtggc cacagatata acttctacca gatccttaaa ttacaaaagc     420

actagcagcg gtcacagaga aatatcatca cctaggattc aggatgctgg acctgcttcc     480

cgagatgtcc aggccactgg cagaatcgca gatgatgctg acccaagagt agcacttgtt     540

aacgattctt tatctgatgt cacaagtacc acatcttcta gggtggatga tcatgactca     600

gaggaaattt gtcttgacca tctgtgtaag ggttgtccgc ttaatggtag ctgcagcaaa     660

gtccacttcc atctgcctta ccggtggcag     atg ctt att ggt aaa acc tgg      711
                                     Met Leu Ile Gly Lys Thr Trp
                                     1               5

acg gac ttt gag cac atg gag acg atc gag aaa ggc tac tgt aac ccc       759
Thr Asp Phe Glu His Met Glu Thr Ile Glu Lys Gly Tyr Cys Asn Pro
        10                  15                  20

gga atc cac ctc tgt tct gta gga agt tat aca atc aat ttt cgg gta       807
Gly Ile His Leu Cys Ser Val Gly Ser Tyr Thr Ile Asn Phe Arg Val
    25                  30                  35

atg agt tgt gat tcc ttt ccc atc cga cgc ctc tcc act cct tct tct       855
Met Ser Cys Asp Ser Phe Pro Ile Arg Arg Leu Ser Thr Pro Ser Ser
40                  45                  50                  55

gtc acc aag cca gcc aat tct gtc ttc acc acc aaa tgg att tgg tat       903
Val Thr Lys Pro Ala Asn Ser Val Phe Thr Thr Lys Trp Ile Trp Tyr
                60                  65                  70

tgg aag aat gaa tct ggc aca tgg att cag tat gga gaa gag aaa gac       951
Trp Lys Asn Glu Ser Gly Thr Trp Ile Gln Tyr Gly Glu Glu Lys Asp
            75                  80                  85
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aaa cgg aaa aat tca aac gtc gac tct tca tac ctg gag tct ctc tat       999
Lys Arg Lys Asn Ser Asn Val Asp Ser Ser Tyr Leu Glu Ser Leu Tyr
         90                  95                 100

caa tcc tgt ccg agg gga gtt gtg cca ttt cag gcg ggc tca cgg aac      1047
Gln Ser Cys Pro Arg Gly Val Val Pro Phe Gln Ala Gly Ser Arg Asn
    105                 110                 115

tat gag ctg agt ttc caa ggg atg att cag aca aac ata gct tcc aaa      1095
Tyr Glu Leu Ser Phe Gln Gly Met Ile Gln Thr Asn Ile Ala Ser Lys
120                 125                 130                 135

act caa aag gat gtc atc aga aga cca aca ttt gtg cct cag tgg tat      1143
Thr Gln Lys Asp Val Ile Arg Arg Pro Thr Phe Val Pro Gln Trp Tyr
            140                 145                 150

gtg cag cag atg aag aga ggg cca gag taa g tgttctgaag cagctgtttg      1194
Val Gln Gln Met Lys Arg Gly Pro Glu  *
        155                 160

ctgacagatg cttgagatgt tcatgccctg ggctcatcaa gtcactcgtg aatctggagc    1254

ctgttttcct gaaaagttcc tgtttgcatt actctgcagt ttccatttgc attatcgatg    1314

agtaagatgc ttgttaagca gcatggtgtg actgaaagga tactagatcg gaaaatgaat    1374

tttctt                                                               1380



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gctctggtaa gccaagactc cttgtgttta cctgttcatc tctgcaatct agggggtagc     180

attttgtcct gtgtccttac cggcaaaacg atgtataaat gaaagaaatt gagatggtgc     240

acgatgcaca gttgaagtga acttgcgggg tttttcagta tctacgattc atagatctgg     300

aattcgcggc cgcgtcgacg aaatatctct ttcaataatg aaagaataag aaaaagaaat     360

agaagagctg gaaacaatag gtaaagttta ggctaggcct tagacttctc ctgcattgta     420

atccttctgg tttgccacat atgcatgctg tcaggaagtt gatgaggt atg tac agg      477
                                                     Met Tyr Arg
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                                                            1

aca atg att ttc cat ttt ttg cct tta ggc acc gac tca ttg gtc act        525
Thr Met Ile Phe His Phe Leu Pro Leu Gly Thr Asp Ser Leu Val Thr
      5                  10                  15

cat ctg ctg aat gta tcc tct cag gca ata ctg ccc att gga gca cga        573
His Leu Leu Asn Val Ser Ser Gln Ala Ile Leu Pro Ile Gly Ala Arg
 20                  25                  30                  35

agc cgc caa ttt gtc aac gtg agt tga aatct ctttccccat tcaccccacc        625
Ser Arg Gln Phe Val Asn Val Ser  *
                 40

attgaatcct agagttgtcc tcctagaatt acaaagaatg gatctcatcc ctcttggaaa      685

tggtatcctt ctgatatttg aagaatctag tcatatcctt aaaatggctc acagcattcc      745

aaacttccgc cttcacctag aaatgctttt ttttttctta tctcagtcta atgtatttta      805

aactagtctt tagctcattt aaccagcccc caatgtcctc ttctgttggt tgagcacctc      865

gcagtttgaa gagcattttg tttagtgaag tcaacaaata caaagtcagt gaaagaaacc      925

ccatatcctc tctgcaagct cttagtatca catcagatat tcaagccatg cagctctttc      985

ttccttctta ttctttgtct aaacaggatc atgccatctt ccctgtgagt tgtttggaag     1045

atgagctttc gtcgacgcgg ccgcgaattc ggatcctcga gagatctctt tttttgggtt     1105

tggtggggta tcttcatcat cgaatagata gttatataca tcagcctatc aatcgccc       1163



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gaaccggacg cggacaccgc cgccccgcga gcctccagcc cctcgcctgt tgccgcgcga      120

gtcccgggcc cggagcgcta ggagcgcgcg gaaggagcc   atg gct ctg gac ggg       174
                                             Met Ala Leu Asp Gly
                                              1               5

ata agg atg cca gat ggc tgc tac gcg gac ggg acg tgg gaa ctg agt        222
Ile Arg Met Pro Asp Gly Cys Tyr Ala Asp Gly Thr Trp Glu Leu Ser
                 10                  15                  20
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gtc cat gtg acg gac ctg aac cgc gat gtc acc ctg aga gtg acc ggc      270
Val His Val Thr Asp Leu Asn Arg Asp Val Thr Leu Arg Val Thr Gly
             25                  30                  35

gag gtg cac att gga ggc gtg atg ctt aag ctg gtg gag aaa ctc gat      318
Glu Val His Ile Gly Gly Val Met Leu Lys Leu Val Glu Lys Leu Asp
         40                  45                  50

gta aaa aaa gat tgg tct gac cat gct ctc tgg tgg gaa aag aag aga      366
Val Lys Lys Asp Trp Ser Asp His Ala Leu Trp Trp Glu Lys Lys Arg
     55                  60                  65

act tgg ctt ctg aag aca cat tgg acc tta gat aag tat ggt att cag      414
Thr Trp Leu Leu Lys Thr His Trp Thr Leu Asp Lys Tyr Gly Ile Gln
 70                  75                  80                  85

gca gat gct aag ctt cag ttc acc cct cag cac aaa ctg ctc cgc ctg      462
Ala Asp Ala Lys Leu Gln Phe Thr Pro Gln His Lys Leu Leu Arg Leu
                 90                  95                 100

cag ctt ccc aac atg aag tat gtg aag gtg aaa gtg aat ttc tct gat      510
Gln Leu Pro Asn Met Lys Tyr Val Lys Val Lys Val Asn Phe Ser Asp
            105                 110                 115

aga gtc ttc aaa gct gtt tct gac atc tgt aag act ttt aat atc aga      558
Arg Val Phe Lys Ala Val Ser Asp Ile Cys Lys Thr Phe Asn Ile Arg
        120                 125                 130

cac ccc gaa gaa ctt tct ctc tta aag aaa ccc aga gat cca aca aaa      606
His Pro Glu Glu Leu Ser Leu Leu Lys Lys Pro Arg Asp Pro Thr Lys
    135                 140                 145

aaa aaa aaa aaa aag cta gat gac cag tct gaa gat gag gca ctt gaa      654
Lys Lys Lys Lys Lys Leu Asp Asp Gln Ser Glu Asp Glu Ala Leu Glu
150                 155                 160                 165

tta gag ggg cct ctt atc act cct gga tca gga agt ata tat tca agc      702
Leu Glu Gly Pro Leu Ile Thr Pro Gly Ser Gly Ser Ile Tyr Ser Ser
                170                 175                 180

cca gga ctg tat agt aaa aca atg acc ccc act tat gat gct cat gat      750
Pro Gly Leu Tyr Ser Lys Thr Met Thr Pro Thr Tyr Asp Ala His Asp
            185                 190                 195

gga agc ccc ttg tca cca act tct gct tgg ttt ggt gac agt gct ttg      798
Gly Ser Pro Leu Ser Pro Thr Ser Ala Trp Phe Gly Asp Ser Ala Leu
        200                 205                 210

tca gaa ggc aat cct ggt ata ctt gct gtc agt caa cca atc acg tca      846
Ser Glu Gly Asn Pro Gly Ile Leu Ala Val Ser Gln Pro Ile Thr Ser
    215                 220                 225

cca gaa atc ttg gca aaa atg ttc aag cct caa gct ctt ctt gat aaa      894
Pro Glu Ile Leu Ala Lys Met Phe Lys Pro Gln Ala Leu Leu Asp Lys
230                 235                 240                 245

gca aaa atc aac caa gga tgg ctt gat tcc tca aga tct ctc atg gaa      942
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Ala Lys Ile Asn Gln Gly Trp Leu Asp Ser Ser Arg Ser Leu Met Glu
                250                 255                 260

caa gat gtg aag gaa aat gag gcc ttg ctg ctc cga ttc aag tat tac         990
Gln Asp Val Lys Glu Asn Glu Ala Leu Leu Leu Arg Phe Lys Tyr Tyr
            265                 270                 275

agc ttt ttt gat ttg aat cca aag tat gat gca atc aga atc aat cag        1038
Ser Phe Phe Asp Leu Asn Pro Lys Tyr Asp Ala Ile Arg Ile Asn Gln
        280                 285                 290

ctt tac gag cag gcc aaa tgg gcc att ctc ctg gaa gag att gaa tgc        1086
Leu Tyr Glu Gln Ala Lys Trp Ala Ile Leu Leu Glu Glu Ile Glu Cys
    295                 300                 305

aca gaa gaa gaa atg atg atg ttt gca gcc ctg cag tat cat atc aat        1134
Thr Glu Glu Glu Met Met Met Phe Ala Ala Leu Gln Tyr His Ile Asn
310                 315                 320                 325

aag ctg tca atc agg aca tca gag aat cat ttg aac aac agt gac aaa        1182
Lys Leu Ser Ile Arg Thr Ser Glu Asn His Leu Asn Asn Ser Asp Lys
                330                 335                 340

gaa gtt gat gaa gtt gat gct gcc ctt tca gac ctg gag att act ctg        1230
Glu Val Asp Glu Val Asp Ala Ala Leu Ser Asp Leu Glu Ile Thr Leu
            345                 350                 355

gaa ggg ggt aaa acg tca aca att ttg ggt gac att act tcc att cct        1278
Glu Gly Gly Lys Thr Ser Thr Ile Leu Gly Asp Ile Thr Ser Ile Pro
        360                 365                 370

gaa ctt gct gac tac att aaa gtt ttc aag cca aaa aag ctg act ctg        1326
Glu Leu Ala Asp Tyr Ile Lys Val Phe Lys Pro Lys Lys Leu Thr Leu
    375                 380                 385

aaa ggt tac aaa caa tat tgg tgc acc ttc aaa gac aca tcc att tct        1374
Lys Gly Tyr Lys Gln Tyr Trp Cys Thr Phe Lys Asp Thr Ser Ile Ser
390                 395                 400                 405

tgt tat aag agc aaa gaa gaa tcc agt ggc aca cca gct cat cag atg        1422
Cys Tyr Lys Ser Lys Glu Glu Ser Ser Gly Thr Pro Ala His Gln Met
                410                 415                 420

aac ctc agg gga tgt gaa gtt acc cca gat gta aac att tca ggc caa        1470
Asn Leu Arg Gly Cys Glu Val Thr Pro Asp Val Asn Ile Ser Gly Gln
            425                 430                 435

aaa ttt aac att aaa ctc ctg att cca gtt gca gaa ggc atg aat gaa        1518
Lys Phe Asn Ile Lys Leu Leu Ile Pro Val Ala Glu Gly Met Asn Glu
        440                 445                 450

atc tgg ctt cgt tgt gac aat gaa aaa cag tat gca cac tgg atg gca        1566
Ile Trp Leu Arg Cys Asp Asn Glu Lys Gln Tyr Ala His Trp Met Ala
    455                 460                 465

gcc tgc aga tta gcc tcc aaa ggc aag acc atg gcg gac agt tct tac        1614
Ala Cys Arg Leu Ala Ser Lys Gly Lys Thr Met Ala Asp Ser Ser Tyr
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470                 475                 480                 485

aac tta gaa gtt cag aat att ctt tcc ttt ctg aag atg cag cat tta      1662
Asn Leu Glu Val Gln Asn Ile Leu Ser Phe Leu Lys Met Gln His Leu
                490                 495                 500

aac cca gat cct cag tta ata cca gag cag atc acg act gat ata act      1710
Asn Pro Asp Pro Gln Leu Ile Pro Glu Gln Ile Thr Thr Asp Ile Thr
            505                 510                 515

cct gaa tgt ttg gtg tct ccc cgc tat cta aaa aag tat aag aac aag      1758
Pro Glu Cys Leu Val Ser Pro Arg Tyr Leu Lys Lys Tyr Lys Asn Lys
        520                 525                 530

cag ata aca gcg aga atc ttg gag gcc cat cag aat gta gct cag atg      1806
Gln Ile Thr Ala Arg Ile Leu Glu Ala His Gln Asn Val Ala Gln Met
    535                 540                 545

agt cta att gaa gcc aag atg aga ttt att caa gct tgg cag tca cta      1854
Ser Leu Ile Glu Ala Lys Met Arg Phe Ile Gln Ala Trp Gln Ser Leu
550                 555                 560                 565

cct gaa ttt ggc atc act cac ttc att gca agg ttc caa ggg ggc aaa      1902
Pro Glu Phe Gly Ile Thr His Phe Ile Ala Arg Phe Gln Gly Gly Lys
                570                 575                 580

aaa gaa gaa ctt att gga att gca tac aac aga ctg att cgg atg gat      1950
Lys Glu Glu Leu Ile Gly Ile Ala Tyr Asn Arg Leu Ile Arg Met Asp
            585                 590                 595

gcc agc act gga gat gca att aaa aca tgg cgt ttc agc aac atg aaa      1998
Ala Ser Thr Gly Asp Ala Ile Lys Thr Trp Arg Phe Ser Asn Met Lys
        600                 605                 610

cag tgg aat gtc aac tgg gaa atc aaa atg gtc acc gta gag ttt gca      2046
Gln Trp Asn Val Asn Trp Glu Ile Lys Met Val Thr Val Glu Phe Ala
    615                 620                 625

gat gaa gta cga ttg tcc ttc att tgt act gaa gta gat tgc aaa gtg      2094
Asp Glu Val Arg Leu Ser Phe Ile Cys Thr Glu Val Asp Cys Lys Val
630                 635                 640                 645

gtt cat gaa ttc att ggt ggc tac ata ttt ctc tca aca cgt gca aaa      2142
Val His Glu Phe Ile Gly Gly Tyr Ile Phe Leu Ser Thr Arg Ala Lys
                650                 655                 660

gac caa aac gag agt tta gat gaa gag atg ttc tac aaa ctt acc agt      2190
Asp Gln Asn Glu Ser Leu Asp Glu Glu Met Phe Tyr Lys Leu Thr Ser
            665                 670                 675

ggt tgg gtg tga ata gaaatactgt ttaatgaaac tccacggcca taacaatatt      2245
Gly Trp Val  *
        680

taactttaaa agctgtttgt tatatgctgc ttaataaagt aagcttgaaa tttatcattt    2305

tatcatgaaa acttctttgc cttaccagac cagttaatat gtgcactaaa caagcacgac    2365
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tattaatcta tcatgttatg atataataaa cttgaatttg gcacacattc cttagggcca   2425

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aagctagcca aactgtaaga aacaagccat ctattttaaa gctatccagg gcttaaccta   2545

tatgaactct atttatcatg tctaatgcat gtgatttaat gtatgtttaa tttgatatca   2605

tgttttaaaa tatcctactt ctggtagcca tttaattcct ccccctaccc ccaaataaat   2665

caggcatgca ggaggcctga tatttagtaa tgtcattgtg tttgaccttg aaggaaaatg   2725

ctattagtcc gtcgtgcttg atttgttttt gtccttgaat aagcatgtta tgtatattgt   2785

ctcgtgtttt tatttttaca ccatattgta ttacactttt agtattcacc agcataatca   2845

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tgcattttgt gtaactaatg taaaaacaca aattttataa aattgtacag tttttttaaaa   2965

aactactcac aactagcaga tggcttaaat gtagcaatct ctgcgttaat taaatgcctt   3025

taagagatat aattaacgtg cagttttaat atctactaaa ttaagaatga cttcattatg   3085

atcatgattt gccacaatgt ccttaactct aatgcctgga ctggccatgt tctagtctgt   3145

tgcgctgtta caatctgtat tggtgctagt cagaaaattc ctagctcaca tagcccaaaa   3205

gggtgcgagg gagaggtgga ttaccagtat tgttcaataa tccatggttc aaagactgta   3265

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                                                     Met Arg Val
                                                       1

att ggg ggt tct aac cat tta gct gtt gtt ctt gat gac att att tta      103
Ile Gly Gly Ser Asn His Leu Ala Val Val Leu Asp Asp Ile Ile Leu
      5                   10                  15

gca gtt att gac tcc att ttt gtg tgg ttc att ttt att agt ttg gca      151
Ala Val Ile Asp Ser Ile Phe Val Trp Phe Ile Phe Ile Ser Leu Ala
 20                  25                  30                  35
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caa act atg aag acc cta agg cta aga aag aac act gtg aaa ttt tca      199
Gln Thr Met Lys Thr Leu Arg Leu Arg Lys Asn Thr Val Lys Phe Ser
                40                  45                  50

tta tat aga cat ttt aaa aat act ctg atc ttt gct gtg ctg gct tct      247
Leu Tyr Arg His Phe Lys Asn Thr Leu Ile Phe Ala Val Leu Ala Ser
            55                  60                  65

ata gtg ttt atg ggg tgg aca act aag aca ttt aga att gca aaa tgc      295
Ile Val Phe Met Gly Trp Thr Thr Lys Thr Phe Arg Ile Ala Lys Cys
        70                  75                  80

caa tca gat tgg atg gaa cgc tgg gtt gac gat gca ttt tgg agc ttc      343
Gln Ser Asp Trp Met Glu Arg Trp Val Asp Asp Ala Phe Trp Ser Phe
    85                  90                  95

ctt ttt tcg ctt atc ctt att gta atc atg ttt ttg tgg aga cca tca      391
Leu Phe Ser Leu Ile Leu Ile Val Ile Met Phe Leu Trp Arg Pro Ser
100                 105                 110                 115

gca aac aat cag aga tat gcc ttc atg ccc tta ata gat gat tct gat      439
Ala Asn Asn Gln Arg Tyr Ala Phe Met Pro Leu Ile Asp Asp Ser Asp
                120                 125                 130

gat gaa att gag gaa ttc atg gta act tct gaa aat tta acc gaa gga      487
Asp Glu Ile Glu Glu Phe Met Val Thr Ser Glu Asn Leu Thr Glu Gly
            135                 140                 145

ata aaa tta aga gcc tca aaa tca gtt tcc aat gga aca gct aag cct      535
Ile Lys Leu Arg Ala Ser Lys Ser Val Ser Asn Gly Thr Ala Lys Pro
        150                 155                 160

gcc act tct gag aac ttt gat gaa gat ttg aag tgg gta gaa gaa aat      583
Ala Thr Ser Glu Asn Phe Asp Glu Asp Leu Lys Trp Val Glu Glu Asn
    165                 170                 175

att ccc tct tca ttc aca gat gta gct ctt cca gtg tta gtg gat tca      631
Ile Pro Ser Ser Phe Thr Asp Val Ala Leu Pro Val Leu Val Asp Ser
180                 185                 190                 195

gat gag gaa atc atg acc aga tct gaa atg gct gaa aaa atg ttc tct      679
Asp Glu Glu Ile Met Thr Arg Ser Glu Met Ala Glu Lys Met Phe Ser
                200                 205                 210

tca gaa aag ata atg tga ttggaa cccgtataag aaatgtagtt aagcctgaag      733
Ser Glu Lys Ile Met  *
            215

gactatcctt catcaagact gaaagtgagc tttgatttga tattgcctaa aaatttttat    793

tgtgttatct tggaagtctg tgtatcaaaa tgaagaattc agatggtagg aggttctata    853

gtccttttaa agctgactct tgagtgtcag ttgaatatcc attaaattgg atttggaaat    913

aacctgagga aagtattatg ataaagatct gcacagatgc ctcttagctg ataggtggca    973
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ggcctgtggg tttgggttct ccctcttttc tctggaacat atgacaattc cagattaaag   1033

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gtgattttct ggagtatagt atatccgtgt ctctgtgtct taggtttact agatgcaata   1153

atacttctct ttgacatttg tactgaagtg atttgatatt aagtaaaaca gttaatgttt   1213

gaatataggc atatttatag gtttttccg ctcccccca acccaccctt tttaaaaaat   1273

ctatacaaag cccttgtttg agtctcatca tgcacatcaa atcatggagt taggtcttct   1333

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ttaccctcat tgtccctcac tcaggccatg tgtacatgcg atgctgctga gtgtgctggg   1453

gtgggtggtg gccacgtggc tcccccagag cacttcctaa ctggcaagct gggagaccca   1513

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                                         Met Glu Val Val Asp Glu
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acg gag gcg ctg cag cgc ttc ttc gaa ggc cac gac atc aac ggt gcc      163
Thr Glu Ala Leu Gln Arg Phe Phe Glu Gly His Asp Ile Asn Gly Ala
             10                  15                  20

ctg gag ccc tcc aac ata gac acc agc atc ctg gag gag tac atc agc      211
Leu Glu Pro Ser Asn Ile Asp Thr Ser Ile Leu Glu Glu Tyr Ile Ser
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aag gag gat gcc tcc gac ctc tgc ttc cct gac atc tct gct cca gcc      259
Lys Glu Asp Ala Ser Asp Leu Cys Phe Pro Asp Ile Ser Ala Pro Ala
     40                  45                  50

agc tcg gcc tcc tac tcc cac ggg cag cct gcg atg cct ggc tcc agc      307
Ser Ser Ala Ser Tyr Ser His Gly Gln Pro Ala Met Pro Gly Ser Ser
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ggg gtc cac cac ctg agc ccc cct ggg ggt gga ccc tcc ccg ggg cgc        355
Gly Val His His Leu Ser Pro Pro Gly Gly Gly Pro Ser Pro Gly Arg
                 75                  80                  85

cat ggt ccc ctc cca ccc ccg ggc tac ggc acc ccg ctg aac tgc aac        403
His Gly Pro Leu Pro Pro Pro Gly Tyr Gly Thr Pro Leu Asn Cys Asn
             90                  95                 100

aac aac aac ggc atg ggc gct gcc ccc aag ccc ttc ccg ggg ggc acc        451
Asn Asn Asn Gly Met Gly Ala Ala Pro Lys Pro Phe Pro Gly Gly Thr
        105                 110                 115

ggg ccc ccc atc aag gct gag ccc aag gct ccc tat gcc cca ggc aca        499
Gly Pro Pro Ile Lys Ala Glu Pro Lys Ala Pro Tyr Ala Pro Gly Thr
    120                 125                 130

ctg ccg gac tct ccc cca gac tcg ggc tcc gag gcc tac tcc ccc cag        547
Leu Pro Asp Ser Pro Pro Asp Ser Gly Ser Glu Ala Tyr Ser Pro Gln
135                 140                 145                 150

cag gtg aat gag ccc cac ctc ctg cgc acg ata acc cct gag aca ctg        595
Gln Val Asn Glu Pro His Leu Leu Arg Thr Ile Thr Pro Glu Thr Leu
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tgc cac gtg gga gtg ccc tcc cgc ctg gag cat ccg ccc cca cct cca        643
Cys His Val Gly Val Pro Ser Arg Leu Glu His Pro Pro Pro Pro Pro
            170                 175                 180

gcc cac ttg cca ggc ccc ccg cca ccc cca cca ccc cca cct cac tac        691
Ala His Leu Pro Gly Pro Pro Pro Pro Pro Pro Pro Pro Pro His Tyr
        185                 190                 195

cct gtc ctg cag cgg gat ctg tac atg aag gcc gag ccc ccg atc ccc        739
Pro Val Leu Gln Arg Asp Leu Tyr Met Lys Ala Glu Pro Pro Ile Pro
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cac tac gct gcc atg ggg cag ggg ctg gtg ccc act gat ctt cac cac        787
His Tyr Ala Ala Met Gly Gln Gly Leu Val Pro Thr Asp Leu His His
215                 220                 225                 230

acc cag cag tcc cag atg ctg cac cag ctc ctg cag cag cac gga gct        835
Thr Gln Gln Ser Gln Met Leu His Gln Leu Leu Gln Gln His Gly Ala
                235                 240                 245

gag ctc cct aca cac ccc tcc aag aag agg aag cac tct gaa tcc ccc        883
Glu Leu Pro Thr His Pro Ser Lys Lys Arg Lys His Ser Glu Ser Pro
            250                 255                 260

ccg agc acc ctc aat gcc cag atg ctg aat gga atg atc aaa cag gag        931
Pro Ser Thr Leu Asn Ala Gln Met Leu Asn Gly Met Ile Lys Gln Glu
        265                 270                 275

cct ggg acc gtg aca gcc ctg cct ctg cac ccc act cga gcc cca tcg        979
Pro Gly Thr Val Thr Ala Leu Pro Leu His Pro Thr Arg Ala Pro Ser
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cca ccc tgg cct ccc cag ggt ccg ctc tcc ccg ggc cct ggt tcc ttg       1027
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Pro Pro Trp Pro Pro Gln Gly Pro Leu Ser Pro Gly Pro Gly Ser Leu
295                 300                 305                 310

cct ctc agc att gcc cgt gtc cag aca ccg cct tgg cac ccg cca ggt      1075
Pro Leu Ser Ile Ala Arg Val Gln Thr Pro Pro Trp His Pro Pro Gly
                315                 320                 325

gcc ccc tcc cca ggc ctc ctg cag gac agt gac agc ctc agt ggc tcc      1123
Ala Pro Ser Pro Gly Leu Leu Gln Asp Ser Asp Ser Leu Ser Gly Ser
            330                 335                 340

tac ctg gac ccc aac tac cag tcc atc aag tgg cag cct cat cag cag      1171
Tyr Leu Asp Pro Asn Tyr Gln Ser Ile Lys Trp Gln Pro His Gln Gln
        345                 350                 355

aac aag tgg gcg acc ctg tac gat gct aac tac aag gag ctg ccc atg      1219
Asn Lys Trp Ala Thr Leu Tyr Asp Ala Asn Tyr Lys Glu Leu Pro Met
    360                 365                 370

ctc acc tac cgc gtg gat gcg gac aag ggc ttc aac ttt tcg gtg ggc      1267
Leu Thr Tyr Arg Val Asp Ala Asp Lys Gly Phe Asn Phe Ser Val Gly
375                 380                 385                 390

gac gac gcc ttt gtg tgc cag aag aag aac cac ttc cag gtg aca gtg      1315
Asp Asp Ala Phe Val Cys Gln Lys Lys Asn His Phe Gln Val Thr Val
                395                 400                 405

tac atc ggc atg ctg ggc gag ccc aag tac gtc aag acg ccc gag ggc      1363
Tyr Ile Gly Met Leu Gly Glu Pro Lys Tyr Val Lys Thr Pro Glu Gly
            410                 415                 420

ctc aag ccc ctc gac tgc ttc tat ctg aag ctg cac gga gtg aag ctg      1411
Leu Lys Pro Leu Asp Cys Phe Tyr Leu Lys Leu His Gly Val Lys Leu
        425                 430                 435

gag gcc ctg aac cag tcc att aac atc gag cag tcc cag tca gac cgg      1459
Glu Ala Leu Asn Gln Ser Ile Asn Ile Glu Gln Ser Gln Ser Asp Arg
    440                 445                 450

agc aag cgg ccc ttc aac ccg gtc acg gtc aat ctg ccc cct gag cag      1507
Ser Lys Arg Pro Phe Asn Pro Val Thr Val Asn Leu Pro Pro Glu Gln
455                 460                 465                 470

gtc acg aag gtg act gtg ggg cgg ctg cac ttc agc gag acc acc gct      1555
Val Thr Lys Val Thr Val Gly Arg Leu His Phe Ser Glu Thr Thr Ala
                475                 480                 485

aac aac atg cgt aag aag ggc aag ccc aac ccg gac cag agg tac ttc      1603
Asn Asn Met Arg Lys Lys Gly Lys Pro Asn Pro Asp Gln Arg Tyr Phe
            490                 495                 500

atg ctg gtg gtg gcc ctc cag gct cat gca cag aac cag aac tac acg      1651
Met Leu Val Val Ala Leu Gln Ala His Ala Gln Asn Gln Asn Tyr Thr
        505                 510                 515

ctg gcc gcc cag atc tca gag cgc atc att gtg cgg gcc tcc aac cca      1699
Leu Ala Ala Gln Ile Ser Glu Arg Ile Ile Val Arg Ala Ser Asn Pro
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    520                 525                 530

ggc cag ttc gag agc gac agc gat gtg ttg tgg cag cgg gca cag gtg      1747
Gly Gln Phe Glu Ser Asp Ser Asp Val Leu Trp Gln Arg Ala Gln Val
535                 540                 545                 550

ccc gac acc gtc ttc cac cac ggc cgc gtg ggc atc aac aca gac cgg      1795
Pro Asp Thr Val Phe His His Gly Arg Val Gly Ile Asn Thr Asp Arg
                555                 560                 565

ccg gat gag gcg ctg gtt gtg cac ggg aat gtc aag gtc atg ggc tcg      1843
Pro Asp Glu Ala Leu Val Val His Gly Asn Val Lys Val Met Gly Ser
            570                 575                 580

ctt atg cac ccc tcc gac ctg cgc gcc aag gaa cac gtg cag gag gtg      1891
Leu Met His Pro Ser Asp Leu Arg Ala Lys Glu His Val Gln Glu Val
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gac acc acc gag caa ttg aag agg atc tcg cgc atg cgg ctg gtg cac      1939
Asp Thr Thr Glu Gln Leu Lys Arg Ile Ser Arg Met Arg Leu Val His
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tac aga tac aag ccc gag ttc gcc gcc agc gcg ggc atc gag gcc acc      1987
Tyr Arg Tyr Lys Pro Glu Phe Ala Ala Ser Ala Gly Ile Glu Ala Thr
615                 620                 625                 630

gcg cca gag aca ggt gtc atc gct cag gag gtg aag gag atc ttg cct      2035
Ala Pro Glu Thr Gly Val Ile Ala Gln Glu Val Lys Glu Ile Leu Pro
                635                 640                 645

gag gct gtg aaa gac acc gga gac atg gtc ttt gcc aat ggg aaa acc      2083
Glu Ala Val Lys Asp Thr Gly Asp Met Val Phe Ala Asn Gly Lys Thr
            650                 655                 660

ata gag aac ttc ctg gtg gtg aac aag gag cgc atc ttc atg gag aac      2131
Ile Glu Asn Phe Leu Val Val Asn Lys Glu Arg Ile Phe Met Glu Asn
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gta ggg gcc gtg aag gag ctg tgc aag ctg aca gac aac ctg gag acg      2179
Val Gly Ala Val Lys Glu Leu Cys Lys Leu Thr Asp Asn Leu Glu Thr
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cgc att gat gag ctg gag cgc tgg agc cac aag ctg gcc aag ctg cgg      2227
Arg Ile Asp Glu Leu Glu Arg Trp Ser His Lys Leu Ala Lys Leu Arg
695                 700                 705                 710

cgg ctc gac agc ctc aag tcc acc ggc agc tcg ggc gcc ttc agc cat      2275
Arg Leu Asp Ser Leu Lys Ser Thr Gly Ser Ser Gly Ala Phe Ser His
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gca ggg agc cag ttc agt cgg gcg ggc agc gtc ccc cac aag aag agg      2323
Ala Gly Ser Gln Phe Ser Arg Ala Gly Ser Val Pro His Lys Lys Arg
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ccc ccc aag gtg gcc agc aag tca tcg tcc gtg gtt ccg gac cag gcc      2371
Pro Pro Lys Val Ala Ser Lys Ser Ser Ser Val Val Pro Asp Gln Ala
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Cys Ile Ser Gln Arg Phe Leu Gln Gly Thr Ile Ile Ala Leu Val Val
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gtc atg gcc ttc agc gtg gtg tcc atg tcc aca ctg tac gtg ctg agc      2467
Val Met Ala Phe Ser Val Val Ser Met Ser Thr Leu Tyr Val Leu Ser
775                 780                 785                 790

ctg cgc aca gag gag gac ctg gta gac act gat ggc agg tcc agc cag      2515
Leu Arg Thr Glu Glu Asp Leu Val Asp Thr Asp Gly Arg Ser Ser Gln
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agc ttt ggg acc acg cag ctc cga cag tcc ccc ttg acc acg ggg cta      2563
Ser Phe Gly Thr Thr Gln Leu Arg Gln Ser Pro Leu Thr Thr Gly Leu
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cca ggc ata cag ccc tct ttg ctg ctg gtg acc acc agc ctc acc agc      2611
Pro Gly Ile Gln Pro Ser Leu Leu Leu Val Thr Thr Ser Leu Thr Ser
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tcg gcc cca ggt tct gct gtc cgc acc ttg gac atg tgt tcc agc cac      2659
Ser Ala Pro Gly Ser Ala Val Arg Thr Leu Asp Met Cys Ser Ser His
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ccc tgc cct gtc atc tgc tgt tcc tca ccc act acc aac cct acc act      2707
Pro Cys Pro Val Ile Cys Cys Ser Ser Pro Thr Thr Asn Pro Thr Thr
855                 860                 865                 870

ggt cct agt ctt ggc ccc agc ttt aac cct ggc cat gtt ctc agc cca      2755
Gly Pro Ser Leu Gly Pro Ser Phe Asn Pro Gly His Val Leu Ser Pro
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agt ccc agc ccc agc acc aac cgc tca ggc ccc agc cag atg gcc ctt      2803
Ser Pro Ser Pro Ser Thr Asn Arg Ser Gly Pro Ser Gln Met Ala Leu
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ctg cca gtc acc aac atc aga gcc aag tcc tgg ggt ctt tca gtc aat      2851
Leu Pro Val Thr Asn Ile Arg Ala Lys Ser Trp Gly Leu Ser Val Asn
        905                 910                 915

ggc att ggc cac tcc aag cat cac aag agt ctg gag cct ctg gcc agc      2899
Gly Ile Gly His Ser Lys His His Lys Ser Leu Glu Pro Leu Ala Ser
    920                 925                 930

cct gca gtc ccc ttc cct ggg ggg cag ggc aaa gcc aag aac agt ccc      2947
Pro Ala Val Pro Phe Pro Gly Gly Gln Gly Lys Ala Lys Asn Ser Pro
935                 940                 945                 950

agc ctt ggt ttc cat ggc cgg gcc cgc cga ggg gcc ctc cag tcc agc      2995
Ser Leu Gly Phe His Gly Arg Ala Arg Arg Gly Ala Leu Gln Ser Ser
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gtg ggc cct gct gag ccc acc tgg gcc cag ggc cag tca gag cca gtg      3043
Val Gly Pro Ala Glu Pro Thr Trp Ala Gln Gly Gln Ser Glu Pro Val
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 tcc cag tac tgt gct cca ggg gat gcc tgc agg cct ggg aac ttc acc     3139
 Ser Gln Tyr Cys Ala Pro Gly Asp Ala Cys Arg Pro Gly Asn Phe Thr
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 tac cac atc cct gtc agt agt ggc acc cca ctg cac ctc agc ctg act     3187
 Tyr His Ile Pro Val Ser Ser Gly Thr Pro Leu His Leu Ser Leu Thr
1015                1020                1025                1030

 ctg cag atg aac tcc tcc tcc ccc gtg tct gtg gtg ctg tgc agc ctg     3235
 Leu Gln Met Asn Ser Ser Ser Pro Val Ser Val Val Leu Cys Ser Leu
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 agg tca aag gag gaa cca tgt gag gag ggg agc ctt cca cag agt ctc     3283
 Arg Ser Lys Glu Glu Pro Cys Glu Glu Gly Ser Leu Pro Gln Ser Leu
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 cac acc cac cag gac acc cag ggc acc tct cac cgg tgg cca ata acc     3331
 His Thr His Gln Asp Thr Gln Gly Thr Ser His Arg Trp Pro Ile Thr
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 atc ctg tcc ttc cgt gaa ttc acc tac cac ttc cgg gtg gca ctg ctg     3379
 Ile Leu Ser Phe Arg Glu Phe Thr Tyr His Phe Arg Val Ala Leu Leu
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 ggt cag gcc aac tgc agt tca gag gct ctc gcc cag cca gcc aca gac     3427
 Gly Gln Ala Asn Cys Ser Ser Glu Ala Leu Ala Gln Pro Ala Thr Asp
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 tac cac ttc cac ttc tac cgc ctg tgt gac tga gctgccct cctgaggcag     3478
 Tyr His Phe His Phe Tyr Arg Leu Cys Asp  *
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                                         Met Leu Thr Gln Leu Lys
                                          1               5

gca aaa tca gag ggg aag ctt gca aaa cag att tgc aaa gtt gtg ttg       163
Ala Lys Ser Glu Gly Lys Leu Ala Lys Gln Ile Cys Lys Val Val Leu
             10                  15                  20

gat cat ttt gaa aaa cag tat tcc aaa gaa ctc gga gat gcc tgg aat       211
Asp His Phe Glu Lys Gln Tyr Ser Lys Glu Leu Gly Asp Ala Trp Asn
         25                  30                  35

aca gta agg gag ata cta aca tct cca tca tgc tgg caa tat gct gtc       259
Thr Val Arg Glu Ile Leu Thr Ser Pro Ser Cys Trp Gln Tyr Ala Val
     40                  45                  50

ctg ctt aac cga ttc aat tat cct ttt gaa ctg gaa aag gat tta cat       307
Leu Leu Asn Arg Phe Asn Tyr Pro Phe Glu Leu Glu Lys Asp Leu His
 55                  60                  65                  70

ttg aag ggc tat cac aca ctc tct cag gga tct tta ccc aac tat cct       355
Leu Lys Gly Tyr His Thr Leu Ser Gln Gly Ser Leu Pro Asn Tyr Pro
                 75                  80                  85

aaa tca gtg aag tgt tac ctt agc aga act ccg ggc cga atc cct tca       403
Lys Ser Val Lys Cys Tyr Leu Ser Arg Thr Pro Gly Arg Ile Pro Ser
             90                  95                 100

gaa aga cac caa att gga aac ctg aaa aaa tat tat ctc cta aat gct       451
Glu Arg His Gln Ile Gly Asn Leu Lys Lys Tyr Tyr Leu Leu Asn Ala
        105                 110                 115

gct tct ctt ctc cca gtg ttg gct ctg gaa tta agg gat ggg gag aag       499
Ala Ser Leu Leu Pro Val Leu Ala Leu Glu Leu Arg Asp Gly Glu Lys
    120                 125                 130

gtt ctg gat ctc tgt gct gct cct gga ggg aaa tta ata gct ctg ctg       547
Val Leu Asp Leu Cys Ala Ala Pro Gly Gly Lys Leu Ile Ala Leu Leu
135                 140                 145                 150
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cag tgt gct tgt cca ggt tat ctt cat tgt aat gaa tat gat agt ctg       595
Gln Cys Ala Cys Pro Gly Tyr Leu His Cys Asn Glu Tyr Asp Ser Leu
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aga ttg agg tgg cta agg cag acg ttg gaa tct ttc atc cca cag cct       643
Arg Leu Arg Trp Leu Arg Gln Thr Leu Glu Ser Phe Ile Pro Gln Pro
            170                 175                 180

ttg ata aat gta att aaa gtg tct gaa ttg gat ggc aga aaa atg gga       691
Leu Ile Asn Val Ile Lys Val Ser Glu Leu Asp Gly Arg Lys Met Gly
        185                 190                 195

gat gcc cag cct gaa atg ttt gac aag gtg tta gtg gat gct ccg tgt       739
Asp Ala Gln Pro Glu Met Phe Asp Lys Val Leu Val Asp Ala Pro Cys
    200                 205                 210

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Ser Asn Asp Arg Ser Trp Leu Phe Ser Ser Asp Ser Gln Lys Ala Ser
215                 220                 225                 230

tgt agg ata agt caa agg agg aat ttg cct ctt cta cag ata gag ctg       835
Cys Arg Ile Ser Gln Arg Arg Asn Leu Pro Leu Leu Gln Ile Glu Leu
                235                 240                 245

tta agg tct gca att aag gcc tta cgt cct gga ggg ata ctt gta tac       883
Leu Arg Ser Ala Ile Lys Ala Leu Arg Pro Gly Gly Ile Leu Val Tyr
            250                 255                 260

tct aca tgc acg ctt tcc aag gca gaa aat caa gat gtg atc agt gaa       931
Ser Thr Cys Thr Leu Ser Lys Ala Glu Asn Gln Asp Val Ile Ser Glu
        265                 270                 275

att tta aac tcc cac ggt aac atc atg cct atg gac att aaa gga ata       979
Ile Leu Asn Ser His Gly Asn Ile Met Pro Met Asp Ile Lys Gly Ile
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gca agg act tgc tcc cac gac ttc aca ttt gct ccc act ggc cag gaa      1027
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295                 300                 305                 310

tgt ggg ctc tta gtg att cca gat aag ggc aaa gcc tgg ggc cca atg      1075
Cys Gly Leu Leu Val Ile Pro Asp Lys Gly Lys Ala Trp Gly Pro Met
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Tyr Val Ala Lys Leu Lys Lys Ser Trp Ser Thr Gly Lys Trp  *
            330                 335                 340

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actttagcat cttagaatct aggcttgagc gctacccaaa acttaatgaa tgatggctgc    1303

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tgcgtccttt ttaagcgaac attttagggc ctgggagttt gtcaagtaag gaagtctcaa     60

gcccaaagag cagcgtcctg acc    atg gtg gtt tca tta cga gcc ctt ctg     110
                             Met Val Val Ser Leu Arg Ala Leu Leu
                              1               5

ctg gct ctc agg cag aag ccc cac agc acc ggg acc att cat gag gtc      158
Leu Ala Leu Arg Gln Lys Pro His Ser Thr Gly Thr Ile His Glu Val
 10                  15                  20                  25

act gcc cag ctc atg atg tcc gtg agg ctg tcc ttt tgg cca gta gcc      206
Thr Ala Gln Leu Met Met Ser Val Arg Leu Ser Phe Trp Pro Val Ala
                 30                  35                  40

gtg tgc agc tgt gtg gca cag atg gct tcg ttc atc ctg atc aag gcc      254
Val Cys Ser Cys Val Ala Gln Met Ala Ser Phe Ile Leu Ile Lys Ala
             45                  50                  55

cca cct cag cca cag cag tcc ccc caa cct gtg ttg tcc acc cta tta      302
Pro Pro Gln Pro Gln Gln Ser Pro Gln Pro Val Leu Ser Thr Leu Leu
         60                  65                  70

ttc atg tac ctg cca ggc cct gct aga tag c accccgtggc attacataac      353
Phe Met Tyr Leu Pro Gly Pro Ala Arg  *
     75                  80

acttcatgag tggctgtgtc ttgtaatttt ggggacaggt ttctctcttt ccctctcttt    413

tttttgtcaa aagcccagag actgacaacc agctgcagtg tctaagtgtt cctcactgac    473

agggtggggc ctcaccaccc ctggagggag cagcgttggc agggagacag cctggcccag    533

tgaccctggg cccaagccag cccctccagg gctttcaggg aagcgccatc cattttcaaa    593

gatgtcaaac gtcacttctt cctgtagggc ccgagtcctg cctcctatca gggccagatc    653

atagaaggct attttctatt ctggggaacg attataactt aaatgattgt tttaataaaa    713

attctaagct ggaaaaaaaa aaaaa                                           738
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<213> Homo sapiens

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<222> (113)..(1003)

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cagcccctgg acaacccctg gcagagctgc agccacagtg ccggctgcac ct    atg      115
                                                             Met
                                                               1

cag ctc ttc aat gga gga tgc cca ccc cct cct cct gtc ctg aat ggt      163
Gln Leu Phe Asn Gly Gly Cys Pro Pro Pro Pro Pro Val Leu Asn Gly
              5                  10                  15

gag gac gtg ctt cct gac ctg aac ctc ctc cca ccc ctt caa ccg ccc      211
Glu Asp Val Leu Pro Asp Leu Asn Leu Leu Pro Pro Leu Gln Pro Pro
        20                  25                  30

ctt cca ggg ctt ctg cct tct gaa aag gag gct cct gct cca atg ggg      259
Leu Pro Gly Leu Leu Pro Ser Glu Lys Glu Ala Pro Ala Pro Met Gly
    35                  40                  45

gcc tca ctc att gca aac tta aag cag ctg cac ctg tcc ccg ccc ccg      307
Ala Ser Leu Ile Ala Asn Leu Lys Gln Leu His Leu Ser Pro Pro Pro
 50                  55                  60                  65

ccc cca cca cag gcc cca gcg gag gga cct tca gtc cag ccc ggt ccc      355
Pro Pro Pro Gln Ala Pro Ala Glu Gly Pro Ser Val Gln Pro Gly Pro
                 70                  75                  80

ctc agg ccc atg gag gaa gag ctg cca cct ccc ccg gca gaa cct gtt      403
Leu Arg Pro Met Glu Glu Glu Leu Pro Pro Pro Pro Ala Glu Pro Val
             85                  90                  95

gag aaa ggg gca tcc aca gac atc tgt gcc ttc tgc cac aag acc gtg      451
Glu Lys Gly Ala Ser Thr Asp Ile Cys Ala Phe Cys His Lys Thr Val
        100                 105                 110

ttc ccc cga gag ctg gct gtg gag gcc atg aag agg cag tac cat gcc      499
Phe Pro Arg Glu Leu Ala Val Glu Ala Met Lys Arg Gln Tyr His Ala
    115                 120                 125

cag tgc ttc acg tgc cgc acc tgc cgc cgc cag ctg gct ggg cag agc      547
Gln Cys Phe Thr Cys Arg Thr Cys Arg Arg Gln Leu Ala Gly Gln Ser
130                 135                 140                 145

ttc tac cag aag gat ggg cga ccc ctc tgc gaa ccc tgc tac cag gac      595
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Phe Tyr Gln Lys Asp Gly Arg Pro Leu Cys Glu Pro Cys Tyr Gln Asp
                150                 155                 160

aca ctg gag agg tgc ggc aag tgt ggc gag gtg gtc cgg gac cac atc       643
Thr Leu Glu Arg Cys Gly Lys Cys Gly Glu Val Val Arg Asp His Ile
            165                 170                 175

atc agg gcc ctg ggc cag gcc ttc cac ccc tcc tgc ttc acg tgt gtg       691
Ile Arg Ala Leu Gly Gln Ala Phe His Pro Ser Cys Phe Thr Cys Val
        180                 185                 190

acc tgc gcc cgg tgc att ggg gat gag agc ttt gcc ctg ggc agc cag       739
Thr Cys Ala Arg Cys Ile Gly Asp Glu Ser Phe Ala Leu Gly Ser Gln
    195                 200                 205

aac gag gtg tac tgc ctg gac gac ttc tac agg aaa ttc gcc ccc gtc       787
Asn Glu Val Tyr Cys Leu Asp Asp Phe Tyr Arg Lys Phe Ala Pro Val
210                 215                 220                 225

tgc agc atc tgt gaa aat ccc atc atc cct cgg gat ggg aaa gat gcc       835
Cys Ser Ile Cys Glu Asn Pro Ile Ile Pro Arg Asp Gly Lys Asp Ala
                230                 235                 240

ttc aaa atc gaa tgc atg gga aga aac ttc cat gaa aat tgc tac agg       883
Phe Lys Ile Glu Cys Met Gly Arg Asn Phe His Glu Asn Cys Tyr Arg
            245                 250                 255

tgt gag gac tgc agg atc ctc ctg tct gtc gag ccc acg gac caa ggc       931
Cys Glu Asp Cys Arg Ile Leu Leu Ser Val Glu Pro Thr Asp Gln Gly
        260                 265                 270

tgc tac ccc ctg aac aac cat ctc ttc tgc aag cca tgc cat gtg aag       979
Cys Tyr Pro Leu Asn Asn His Leu Phe Cys Lys Pro Cys His Val Lys
    275                 280                 285

cgg agt gct gcg ggg tgc tgc tga gagtgcccgc tgggcagtga acagaccact     1033
Arg Ser Ala Ala Gly Cys Cys  *
290                 295

agccccggct ggggcccttc cctgacttgg gttcccttcc taacctgctc ttgcacactt    1093

tccttctgag cctccatgga gaccagcctg                                     1123



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     <213> Homo sapiens

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     <400> 104
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gccgctgccg ccgccgtccg ggtctgcgcc cgccacgccg aggcccaggc ggccgcgcgg     180

caggaactgg cgctgaagac cctggggaca gatggccttt ttctcttttc ctccttggac     240

actgacgggg at    atg tac atc agc cct gag gag ttc aaa ccc att gct       288
                 Met Tyr Ile Ser Pro Glu Glu Phe Lys Pro Ile Ala
                  1               5                  10

gag aag cta aca ggg tca act ccc gcg gcc agc tac gag gag gag gag       336
Glu Lys Leu Thr Gly Ser Thr Pro Ala Ala Ser Tyr Glu Glu Glu Glu
         15                  20                  25

ttg ccc cct gac cct agc gag gag acg ctc acc ata gaa gcc cga ttc       384
Leu Pro Pro Asp Pro Ser Glu Glu Thr Leu Thr Ile Glu Ala Arg Phe
     30                  35                  40

cag cct ctg ctc ccg gag acc atg acc aag agc aaa gat ggc ttc cta       432
Gln Pro Leu Leu Pro Glu Thr Met Thr Lys Ser Lys Asp Gly Phe Leu
 45                  50                  55                  60

ggg gtc tcc cgc ctc gcc ctg tcc ggc ctc aga aac tgg aca gcc gcc       480
Gly Val Ser Arg Leu Ala Leu Ser Gly Leu Arg Asn Trp Thr Ala Ala
                 65                  70                  75

gcc tca cca agt gca gtg ttt gcc acc cgc cac ttc cag ccc ttc ctt       528
Ala Ser Pro Ser Ala Val Phe Ala Thr Arg His Phe Gln Pro Phe Leu
             80                  85                  90

ccc ccg cca ggc cag gag ctg ggt gag ccc tgg tgg atc atc ccc agt       576
Pro Pro Pro Gly Gln Glu Leu Gly Glu Pro Trp Trp Ile Ile Pro Ser
         95                 100                 105

gag ctg agc atg ttc act ggc tac ctg tcc aac aac cgc ttc tat cca       624
Glu Leu Ser Met Phe Thr Gly Tyr Leu Ser Asn Asn Arg Phe Tyr Pro
    110                 115                 120

ccg ccg ccc aag ggc aag gag gtc atc atc cac cgg ctc ctg agc atg       672
Pro Pro Pro Lys Gly Lys Glu Val Ile Ile His Arg Leu Leu Ser Met
125                 130                 135                 140

ttc cac cct cgg ccc ttt gtg aag acc cgc ttt gcc cct cag gga gct       720
Phe His Pro Arg Pro Phe Val Lys Thr Arg Phe Ala Pro Gln Gly Ala
                145                 150                 155

gtg gcc tgc ctg act gcc atc agc gac ttc tac tac act gtg atg ttc       768
Val Ala Cys Leu Thr Ala Ile Ser Asp Phe Tyr Tyr Thr Val Met Phe
            160                 165                 170

cgg atc cat gcc gag ttc cag ctc agt gag ccg ccc gac ttc ccc ttt       816
Arg Ile His Ala Glu Phe Gln Leu Ser Glu Pro Pro Asp Phe Pro Phe
        175                 180                 185

tgg ttc tcc cct gct cag ttc acc ggc cac atc atc ctc tcc aaa gac       864
Trp Phe Ser Pro Ala Gln Phe Thr Gly His Ile Ile Leu Ser Lys Asp
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    190                 195                 200

gcc acc cac gtc cgc gac ttc cgg ctc ttc gtg ccc aac cac agg tct      912
Ala Thr His Val Arg Asp Phe Arg Leu Phe Val Pro Asn His Arg Ser
205                 210                 215                 220

ctg aat gtg gac atg gag tgg ctt tac ggg gcc agt gaa agc agc aac      960
Leu Asn Val Asp Met Glu Trp Leu Tyr Gly Ala Ser Glu Ser Ser Asn
                225                 230                 235

atg gag gtg gac atc ggc tac ata ccc cag atg gag ctg gag gcc acg     1008
Met Glu Val Asp Ile Gly Tyr Ile Pro Gln Met Glu Leu Glu Ala Thr
            240                 245                 250

ggc ccc tct gtg ccc tcc gtg atc ctg gat gag gat ggc agc atg atc     1056
Gly Pro Ser Val Pro Ser Val Ile Leu Asp Glu Asp Gly Ser Met Ile
        255                 260                 265

gac agc cac ctg ccc tca ggg gag ccc ctg cag ttt gtg ttt gag gag     1104
Asp Ser His Leu Pro Ser Gly Glu Pro Leu Gln Phe Val Phe Glu Glu
    270                 275                 280

atc aag tgg cag cag gag ctg agc tgg gag gag gct gcc cgg cgc ctg     1152
Ile Lys Trp Gln Gln Glu Leu Ser Trp Glu Glu Ala Ala Arg Arg Leu
285                 290                 295                 300

gag gtg gcc atg tac ccc ttc aag aag gtc tcc tac ttg ccg ttc act     1200
Glu Val Ala Met Tyr Pro Phe Lys Lys Val Ser Tyr Leu Pro Phe Thr
                305                 310                 315

gag gcc ttc gac cga gcc aag gct gag aac aag ctg gtg cac tca atc     1248
Glu Ala Phe Asp Arg Ala Lys Ala Glu Asn Lys Leu Val His Ser Ile
            320                 325                 330

ctg ctg tgg ggg gcc ctg gat gac cag tcc tgc tga ggtt cagggcggac     1298
Leu Leu Trp Gly Ala Leu Asp Asp Gln Ser Cys  *
        335                 340

tctccgggag actgtcctgg aaagttcgcc catcctcacc ctgctcaacg agagcttcat   1358

cagcacctgg tccctggtga aggagctgga ggaactgcag aacaaacagg agaactcgtc   1418

ccaccagaag ctggctggcc tgcacctgga gaagtacagc ttccccgtgg agatgatgat   1478

ctgcctgccc aatggcaccg tggtccatca catcaatgcc aactacttct tggacatcac   1538

ctccgtgaag cccgaggaaa tcgagagcaa tctcttcagc ttctcatcca cctttgaaga   1598

cccgtccacg gccacctaca tgcagttcct gaaggaggga ctccggcgtg gcctgcccct   1658

cctccagccc tagagtgcct ggacgggatc tgatgcacag gcccccacgc ctcagagcca   1718

gagtggtcct cagcccattt cagactgcag atgccgccca ctcccacccc actcctaggc   1778

tgccttggag ggtacaagat ccactgaggg tggccaccac agccttggct ccatggtggc   1838

gggtagacaa gggatgcctg ggctgactgg gcagaggaac ctctagctct gactgtcact   1898
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cggctctccc tacccatttg gctctggaag ctgcttggcc cccccagatc agggcctggg 1958

tgaactccct ggacctttcc tagccagccg cacagtctag gcccttgtgg ggtgaagaat 2018

ggagggagga gcaggctagg aagacggggc caccaccctc tccttgcttt cagcccttcc 2078

cacaggaaac atcaagaagc cccagccagg aggggccagg ctgccaaggc ggctcccctg 2138

tttatctaga gccttcgttc ctggccatac cccggactgc cctcctgtgc ctgatgtccc 2198

cagctggggt cagtctcaac aggagccagt cttctggagc ctctgggcag aaccctccat 2258

cagagtggaa atcagacggg accccctgca gcttccctga ccacgccact gaccagctat 2318

ctggggaagt ttactgtgaa ggggtttctg cctttagcaa tggggttcac taagggggtt 2378

cccgaggccc agggccaagg cactcccacc gcctacctta gcacagggtc tctgcaggac 2438

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ctcaggtgat ccacctgcct cagcctccca aagtgctggg attacaggcg tgagcaatcg 3458

tgcccagcct tgttcttaat tttgtatcat ccagtcatcg ctaatattac acgcaccttc 3518

tcacttaatc ctcacgacaa gcctgtgagg cagatgctca ttgttcccat cttgatgaaa 3578

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cttgagtctc agggaagtga agtgacttgc ccagggtcac tcaggtagag ttgagattca   3638

aacccacatg tggctccaaa gtctgcatct ggatttgggg gtgtttttg gcatggcacc    3698

ctcacctctc tccctgcctg ttttccccaa agtggaaagg aaggcctttc aaaccagagt   3758

gtctcactcc cctctgacct ccagaccaga tggggcatga gccagccagc tcagccaggc   3818

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tctgatgctc tctctctgcc tccccccca tcctgtcagg cacaggtgac gggggcagcc    3938

catgcgagcc cttctcctgc tgctctggga gggccagttc cacattgagc cagcctggtc   3998

ccatggaaaa tgatggcctg ggctttctga ggccttatct gatgcctctg cagttcatgt   4058

cccccaccag gcctcgaggc tcagggtggg agagggcccc gggctgccct gtcactcctc   4118

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aaaaaa                                                              4184




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                                                             Met
                                                             1

cag tgc ctg gct tct cag gcc gcc gcc agc cgg gac tgc ttt agg cgc      106
Gln Cys Leu Ala Ser Gln Ala Ala Ala Ser Arg Asp Cys Phe Arg Arg
            5                   10                  15

gaa ccc acg ctt ctg acc tgt gct ctg tct ttg cag ttc tgc acg gag      154
Glu Pro Thr Leu Leu Thr Cys Ala Leu Ser Leu Gln Phe Cys Thr Glu
        20                  25                  30

cta aac cag ccg acc ctg ccc aac atc cgc aag tgg aag ggg ccc cgg      202
Leu Asn Gln Pro Thr Leu Pro Asn Ile Arg Lys Trp Lys Gly Pro Arg
    35                  40                  45

gga tgc tgg aag gct gtt gtt gct gag aag ccc tcg aat cag ctc cag      250
Gly Cys Trp Lys Ala Val Val Ala Glu Lys Pro Ser Asn Gln Leu Gln
50                  55                  60                  65

aag gta ccc tcg tct gca aag cct ggc ctt tcc ctt cat tta att tat      298
Lys Val Pro Ser Ser Ala Lys Pro Gly Leu Ser Leu His Leu Ile Tyr
```

```
                 70                  75                  80

aca tac ttt tcc cct aat caa ggg cat tta aaa att tcc ttt gcc aat      346
Thr Tyr Phe Ser Pro Asn Gln Gly His Leu Lys Ile Ser Phe Ala Asn
                 85                  90                  95

atc ccc ggt tca att ttg tat ttc tgc cca att ttt aaa tcc ttg cca      394
Ile Pro Gly Ser Ile Leu Tyr Phe Cys Pro Ile Phe Lys Ser Leu Pro
        100                 105                 110

ttc att tcc aaa tgc cct ggt ttt cgg ttc acg ttt aga ttg gta atg      442
Phe Ile Ser Lys Cys Pro Gly Phe Arg Phe Thr Phe Arg Leu Val Met
    115                 120                 125

gac tcc tgc caa gaa gga aat gag agc ctt agg gtg ttg gga gag agg      490
Asp Ser Cys Gln Glu Gly Asn Glu Ser Leu Arg Val Leu Gly Glu Arg
130                 135                 140                 145

agg gga gaa agg caa caa atg ggt att tct gtc ctt tgt cct tct aat      538
Arg Gly Glu Arg Gln Gln Met Gly Ile Ser Val Leu Cys Pro Ser Asn
                150                 155                 160

ccc ttc gcc aca gtt ctg tct tct gcc aag ttt gtg cag agc tca tta      586
Pro Phe Ala Thr Val Leu Ser Ser Ala Lys Phe Val Gln Ser Ser Leu
            165                 170                 175

ctc gtt gac tga aaa tttcagattc accttagttc acacatgaag tatttgcttc      641
Leu Val Asp  *
        180

tagtggtaga aattatgcac ataatttcaa catagaaatg ttctattgaa atgttcagca    701

gattttggtt ttgaattttc tttcatcagt atcacccata tgagcaggta agggtaaatc    761

tctgtaaata cacgttttcc ctcatattat tattcaaggc cagatttatt caccttgcaa    821

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gggggtgtaa atggctcctg ccagctgaca gtgagtcagc acacttcaga gaaggctgga   1181

gataaagctg aatttgaatg catctagttc agggttctcc cttccagtcc acgtggaaat   1241

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cttcacaagc cttttatagt ccattcagca ctgcattcat tcaacaaatc attaatgaaa   1361

ggtggctatg taccaggcat attgtttcat gccaggtaca cactggtgag aaaaactcca   1421

tgcctgcatg ttttcactct ttgcaagaca cagtggggat cccggctgga gcctgacctg   1481
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gcccctcccg cagggagtgc acagcccg                                  1509



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cacacagtat tttatctttg attctgaata aatatttttt gtggggtttt tttttttggt     120

ggcagttgtt tgttttaaac tgaccacttg gaagaaacac cttggttatc tgtggttttc     180

atgccttgtc cctgcctcta cccccacccc ttttgagtcg ggtgactcat ttttctgtgt     240

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tgtgcctgtt gctcgccttc aggtcaccag ctgagctgcg ataggaaaat ctgaatggag     360

gcagcaaaca gccaaaacaa acattcccca cccggccctg tgcatatgaa gtctttcttc     420

ccccaactct tgaacgatga tgatattcag acgaagcatt gatgttatgg aagaaagaaa     480

gaaacaaaca aaaaatatat atatatgtcc aaaaacagac aaatccaagg gtgtgaggta     540

aacgagtgtc tgcatttaga ttccacaaaa ccaaaatcca tgttgaacaa agttaagtcc     600

gtacacagtg actttttggg tgagccgtgt gtgtctgtct gttgtgtgtg tgcctcaagc     660

cctgttttcc tgtgaagata ctttgagtgg cagccattct ctccacgtga accacacgtc     720

tggagcacag acaggcctct caaggtcatt gatcttacgc atttactgtt taccgaacaa     780

atg tct gac tgt gta ctc ggg tgt act ccg cag cat tgt cga ctg cag      828
Met Ser Asp Cys Val Leu Gly Cys Thr Pro Gln His Cys Arg Leu Gln
1               5                   10                  15

tcc cct gtg ttt gcc aga gat act gtg ctc gaa gta gag gtt tta ctc      876
Ser Pro Val Phe Ala Arg Asp Thr Val Leu Glu Val Glu Val Leu Leu
            20                  25                  30

tac tca tca ctg cga ttt gca cat tgc tcc gtg gac act cgg agg cct      924
Tyr Ser Ser Leu Arg Phe Ala His Cys Ser Val Asp Thr Arg Arg Pro
        35                  40                  45

gcg ttc tgt tcc cta taa atggaa gcgtgctctg agcctgtctg cctccctcgg      978
Ala Phe Cys Ser Leu  *
    50
```

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ctgctgctgg tcctcagtac cagcgcccgg gggtgtccac aaccacttgg gacagaagaa   1038

ggtggaattt cagacagaag cttgactggg tcttcaatga caggcttgga ctagctgtgg   1098

cccagacatc ggccctgccc agaattgcca ggaggaggct ttgcaggctc tagaggagcc   1158

gcagggcctg cctgcctctg gtgagtccaa caggcacaag caagctggcg tgtggccaga   1218

ggtagccgga gtgtgtcaca gcccctcaga tgcctttcct tccacctttt tttatttttt   1278

aagaatccca aataactcac tgaagtgtct caaaggcgaa caagttttac caaaatgaat   1338

ccttttttcag ttaacagatc aaatggatga gttctgagcc tctcaagttc ctttccccag   1398

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ggcacgagaa gacggaaatg caacctgcgg agctgggctt ggttcccagg tcacagtttg   1518

gcccccgcta caggatgctg ccctgctcag agagagattt aatagggagc tgaaggaatc   1578

gttagggggc cagggagatg tgactgaggc tggctttcca cgtgaatgag acggggtcgg   1638

tggagggttt ggtgctacag ccagtcagaa gatttgcaaa tgcgaacaca ttcctgtgtg   1698

aggcacgtta ccctttgtca gttattgtga atatgtgtat tttaagcaat aagattcagc   1758

tggtcagact tttctgggca gtctcagtga cgcatttcct gtgctgtgat tgttctgaag   1818

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aaaaaaaaaa a                                                        1889



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tagggagtcg gcggtgagaa atggacagcc cgcattgacc gaagctttgc gcatgcgttt    180

tactgctggg tgaagccgaa cctcgggagc ccaggacgcc ctcctgcaca tgcgcaggag    240

gctca atg aca gtc gag ctt tgg cta agg ctc cgg gga aag ggt cta        287
      Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu
        1               5                  10
```

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gcc atg ctg cat gtg acc cgg ggg gtc tgg ggg tcc agg gtc cga gta       335
Ala Met Leu His Val Thr Arg Gly Val Trp Gly Ser Arg Val Arg Val
 15                 20                  25                  30

tgg cca ctg ttg ccc gcg ctc ctc ggg ccc ccc cgg gcc ctc tca tcg       383
Trp Pro Leu Leu Pro Ala Leu Leu Gly Pro Pro Arg Ala Leu Ser Ser
                35                  40                  45

ctg gca gcc aaa atg ggg gag tat cgc aag atg tgg aac ccc agg gag       431
Leu Ala Ala Lys Met Gly Glu Tyr Arg Lys Met Trp Asn Pro Arg Glu
            50                  55                  60

ccc cgc gac tgg gcc cag cag tac cgc gag cgc ttc att ccc ttc tcc       479
Pro Arg Asp Trp Ala Gln Gln Tyr Arg Glu Arg Phe Ile Pro Phe Ser
        65                  70                  75

aag gag cag ctg ctc cgc ctc cta ata cag gta aca gga att cca ctc       527
Lys Glu Gln Leu Leu Arg Leu Leu Ile Gln Val Thr Gly Ile Pro Leu
    80                  85                  90

gag tcc ggc aga gaa ggc ggc ttt gga ggc gtt ctc agc cca cgt gga       575
Glu Ser Gly Arg Glu Gly Gly Phe Gly Gly Val Leu Ser Pro Arg Gly
 95                 100                 105                 110

ctt ctg cac cct gtt cca cta cca cca aat cct ggc ccg gct gca ggc       623
Leu Leu His Pro Val Pro Leu Pro Pro Asn Pro Gly Pro Ala Ala Gly
                115                 120                 125

ctt ata tga ccccatc aaccctgaca gggagaccct cgatcagcca tcactaacgg       679
Leu Ile  *


atccccagcg tctgtctaat gagcaggagg tgcttcgggc tctggagccc ctgctggccc      739

aggccaactt ctccccgctg tctgaggaca ccctggccta cgcgctggtg gtccaccacc      799

ctcaggatga ggtccaggtg acagtaaatt tggatcagcc tggttgggag tcttggctcc      859

atggcacggc cccctcctgt cattctttcc tctacctgag ctgacactct ccctacaaga      919

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gccctctcga ccctcctggg ccttgttccg ctcccctcca agcctcaaga tcactcctag     1099

gcttctccca aacccaggcc cttcctgttc tttgccctac gcccctcctt gctgctccct     1159

cgaatcttcc ccgatctcag tgtgacctca gaacacctgc ctctcccctt gcagagacct     1219

ccaggtggct ccggtcggag gtggagaact ggctcctagc caagtcaggc tgtgaggtga     1279

ccttcaacgg aactcgggcc ctggcgcatc tgcaggccct gacccccagc atgggattgt     1339

acccaccccc gggtttcccc aaactagacc cagtggctcc gatcacttcc gagcccccgc     1399
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actccaactt ccaataactg acaggtgatt atttttgctg cactgtgtgc ttaagcaaag   1579

cagccaatca aagcagctag cagttgttaa gtcttccccg ccccttcgat gaacagccaa   1639

tcaaagcgat ttagctctgc ttctgttcca tttcttagtc ccaccctcac cataaacatc   1699

caagtgtggt ttggctgagg agctgagggt gtctgccaat cacagctgct cagctctggc   1759

ttctgtaaac cgccaggtag aagagttaaa gctgcgccct cccgagacta tatatcattg   1819

tctttttcag cccgctccgg gcaaactgcc catcatgtgc accaaggccg ttagccctgc   1879

ctcctggcaa acgtccagtg acagctgctg ggttccatca actttgggca gccggttgtc   1939

gctgcaggga aggaaccaat aagaatttct aaaggaaacc tgatcttgct atcaattgct   1999

gctgcttaaa tggcaggcca actggtcagc tgctgatcag ggtgtctagg ctgaaggagt   2059

tggagacctt gtgctaggta ggtgaaccag aaaccaccct cgccaccaag actcgctccc   2119

aacctggctc ccggcaacct caggtgcctt cctcgcccag gtctttcacc ctttctacag   2179

aaactacctc ggtctggatc tccccaccac cagcagcctg tgcaatattt attggtctat   2239

caatttctcc cgtctcctgt cccaaagtaa taaatcatgt ttaataagtc tggatgaggc   2299

tactcttaac gcactgcctt tagggtaacc ctgctctgta ggagtggtta aaaaattatt   2359

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cctggaaaga ggggagggac tctagctagg tcttggggtc ccagacagag aaagctgtag   2479

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gtaacacaaa gaataaatgc ttgaggggat ggataccccc tttaccctgt gattattatg   3019

cattgcatac ctgtatcaaa gtatcccata aatatataca cctactatct acccacaaaa   3079

attaaaaaac aacaacaaaa aaccccacac cactacctca ctgatgccat aatgtttaac   3139
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catgcctttc acttaaagaa ttccaggaaa taagccaggt gtgtggctcg tgcctgtaat   3199

cccagcactt tgggaggcca aggtgggtgg atcacctgtc acctgagctc aggagttcga   3259

gaccagcctg ggcaacatgg caaaatcccg tctctactag aaatacaaaa              3309




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gttgttcatg aaataggaaa agatggacgg atcagccatt tgaatgactt gtccattcca    180

gtggatgagg aggacccttc agaagacata tttacagttt tgacagctga agaaaagcag    240

cgattggaag agctccagct gttcaaaaat aaggaaacca gtgttgccat tgaggttatc    300

gaggacacca aagagaaaag aaccatcatc catcaggcta tcaaatctct gtttccagga    360

ttagagacaa aaacagagga tagggagggg aagaaataca ttgtagccta ccacgcagct    420

gggaaaaagg ctttggcaaa tccaagaaaa cattcttggc caaaatctag gggaagttac    480

tgccacttcg tactatataa ggaaaacaaa gacaccatgg atgctattaa tgtactctcc    540

aaatacttaa gagtcaagcc aaatatattc tcctacatgg gaaccaaaga taaaagggct    600

ataacagttc aagaaattgc tgttctcaaa ataactgcac aaagacttgc ccacctgaat    660

aagtgcttg   atg aac ttt aag cta ggg aat ttc agc tat caa aaa aac      708
            Met Asn Phe Lys Leu Gly Asn Phe Ser Tyr Gln Lys Asn
             1               5                   10

cca ctg aaa ttg gga gag ctt caa gga aac cac ttc act gtt gtt ctc      756
Pro Leu Lys Leu Gly Glu Leu Gln Gly Asn His Phe Thr Val Val Leu
    15                  20                  25

aga aat ata aca gga act gat gac caa gta cag caa gct atg aac tct      804
Arg Asn Ile Thr Gly Thr Asp Asp Gln Val Gln Gln Ala Met Asn Ser
30                  35                  40                  45

ctc aag gag att gga ttt att aac tac tat gga atg caa aga ttt gga      852
Leu Lys Glu Ile Gly Phe Ile Asn Tyr Tyr Gly Met Gln Arg Phe Gly
                50                  55                  60
```

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acc aca gct gtc cct acg tat cag gtt gga aga gct ata cta caa aat          900
Thr Thr Ala Val Pro Thr Tyr Gln Val Gly Arg Ala Ile Leu Gln Asn
             65                  70                  75

tcc tgg aca gaa gtc atg gat tta ata ttg aaa ccc cgc tct gga gct          948
Ser Trp Thr Glu Val Met Asp Leu Ile Leu Lys Pro Arg Ser Gly Ala
         80                  85                  90

gaa aag ggc tac ttg gtt aaa tgc aga gaa gaa tgg gca aag acc aaa          996
Glu Lys Gly Tyr Leu Val Lys Cys Arg Glu Glu Trp Ala Lys Thr Lys
     95                 100                 105

gac cca act gct gcc ctc aga aaa cta cct gtc aaa agg tgt gtg gaa         1044
Asp Pro Thr Ala Ala Leu Arg Lys Leu Pro Val Lys Arg Cys Val Glu
110                 115                 120                 125

ggg cag ctg ctt cga gga ctt tca aaa tat gga atg aag aat ata gtc         1092
Gly Gln Leu Leu Arg Gly Leu Ser Lys Tyr Gly Met Lys Asn Ile Val
                130                 135                 140

tct gca ttt ggc ata ata ccc aga aat aat cgc tta atg tat att cat         1140
Ser Ala Phe Gly Ile Ile Pro Arg Asn Asn Arg Leu Met Tyr Ile His
            145                 150                 155

agc tac caa agc tat gtg tgg aat aac atg gta agc aag agg ata gaa         1188
Ser Tyr Gln Ser Tyr Val Trp Asn Asn Met Val Ser Lys Arg Ile Glu
        160                 165                 170

gac tat gga cta aaa cct gtt cca ggg gac ctc gtt ctc aaa gga gcc         1236
Asp Tyr Gly Leu Lys Pro Val Pro Gly Asp Leu Val Leu Lys Gly Ala
    175                 180                 185

aca gcc acc tat att gag gaa gat gat gtt aat aat tac tct atc cat         1284
Thr Ala Thr Tyr Ile Glu Glu Asp Asp Val Asn Asn Tyr Ser Ile His
190                 195                 200                 205

gat gtg gta atg ccc ttg cct ggt ttc gat gtt atc tac cca aag cat         1332
Asp Val Val Met Pro Leu Pro Gly Phe Asp Val Ile Tyr Pro Lys His
                210                 215                 220

aaa att caa gaa gcc tac agg gaa atg ctc aca gct gac aat ctt gat         1380
Lys Ile Gln Glu Ala Tyr Arg Glu Met Leu Thr Ala Asp Asn Leu Asp
            225                 230                 235

att gac aac atg aga cac aaa att cga gat tat tcc ttg tca ggg gcc         1428
Ile Asp Asn Met Arg His Lys Ile Arg Asp Tyr Ser Leu Ser Gly Ala
        240                 245                 250

tac cga aag atc att att cgt cct cag aat gtt agc tgg gaa gtc gtt         1476
Tyr Arg Lys Ile Ile Ile Arg Pro Gln Asn Val Ser Trp Glu Val Val
    255                 260                 265

gca tat gat gat ccc aaa att cca ctt ttc aac aca gat gtg gac aac         1524
Ala Tyr Asp Asp Pro Lys Ile Pro Leu Phe Asn Thr Asp Val Asp Asn
270                 275                 280                 285
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cta gaa ggg aag aca cca cca gtt ttt gct tct gaa ggc aaa tac agg      1572
Leu Glu Gly Lys Thr Pro Pro Val Phe Ala Ser Glu Gly Lys Tyr Arg
                290                 295                 300

gct ctg aaa atg gat ttt tct cta ccc cct tct act tac gcc acc atg      1620
Ala Leu Lys Met Asp Phe Ser Leu Pro Pro Ser Thr Tyr Ala Thr Met
            305                 310                 315

gcc att cga gaa gtg cta aaa atg gat acc agt atc aag aac cag acg      1668
Ala Ile Arg Glu Val Leu Lys Met Asp Thr Ser Ile Lys Asn Gln Thr
        320                 325                 330

cag ctg aat aca acc tgg ctt cgc tga gcagt accttgtcca cagattagaa      1720
Gln Leu Asn Thr Thr Trp Leu Arg  *
    335                 340

aacgtacaca agtgtttgct tcctggctcc ctgtgcattt ttgtcttagt tcagactcat    1780

atatggattt caaatctttg taataaaaat tatttgtatt tttaagtttt tattagctta    1840

aagaaataat ttgcaatatt tgtacatgta cacaaatcct gaggttctta attttagctc    1900

agaatataaa ttagtcaaaa tacacttcag gtgcttaaat cagagtaaaa tgtcagcttt    1960

acaataataa aaaaaggact ttggtttaaa gtagcaggtt taggttttgc tacattctca    2020

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tataaataca gtactcatgc tgactgaaat aataagacat ctacaaattt ataaacaaaa    2200

agtgattgtc attatcctgc ttatgtacta gattcaggca agcattatag actttttggt    2260

tgcggtggct tttgcattta tattatcaat gccttgcagg aacgttgcat tgataggccc    2320

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gcagtgcaat cctgcaattc tcaatcttgc actgcagcct cgacctccca ggctccagtg    2440

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ggattacagg catgagctgt gctggccggg tttttttttc ttgatgtaaa cgtgtacagc    2620

tgttttatta gttaaggtct aatttttact ctaggtgcct tttatgttca gaactctttc    2680

cactggactg gtatttgctc aaaaataaat aatggtagag aagaaaacta taaaaatgga    2740

caaggctttc ttctatcagt agcgtttacc ctttgtcacc agtggctttg gtatttccat    2800

gtctggcatt gcataaactt ctctggtgtg aaaggataaa tatgcctttc taaagttgta    2860

tatcaaaatt gtatcaattt ttattttcta tgatttctag aaacaaatgt aataaatatt    2920

tttaaaatct cctttctact ggttatgtaa ataaatcaaa taaatataaa aaaaaaaaa     2979
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                            Met Asp Gln Lys Leu Ser Lys Leu Val
                             1               5

gaa gag ctc aca act tca gga gaa ccc cga cta aat cct gag aaa atg      99
Glu Glu Leu Thr Thr Ser Gly Glu Pro Arg Leu Asn Pro Glu Lys Met
 10                  15                  20                  25

aag gaa ctg aag aaa att tgc aag tct tca gag gag cag ctg agc cgc     147
Lys Glu Leu Lys Lys Ile Cys Lys Ser Ser Glu Glu Gln Leu Ser Arg
                 30                  35                  40

gcc tac cgc ctc ctc ata gac ccg aac tgt agt ggc cac agc ccg cgc     195
Ala Tyr Arg Leu Leu Ile Asp Pro Asn Cys Ser Gly His Ser Pro Arg
             45                  50                  55

acc gcc cgg cac gca cct gcg gtc cgg aag ttc tcc cct gac ctt aag     243
Thr Ala Arg His Ala Pro Ala Val Arg Lys Phe Ser Pro Asp Leu Lys
         60                  65                  70

ttg ctt aag gat gta aag att agc gtg agc ttt acc gag agc tgc agg     291
Leu Leu Lys Asp Val Lys Ile Ser Val Ser Phe Thr Glu Ser Cys Arg
     75                  80                  85

agt aag gac agg aag gtg ctg tac aca gga gca gag cgc gac gtg cgg     339
Ser Lys Asp Arg Lys Val Leu Tyr Thr Gly Ala Glu Arg Asp Val Arg
 90                  95                 100                 105

gcg gag tgc ggt ctg ctc ctt agc cct gtc agt ggg gac gtg cat gct     387
Ala Glu Cys Gly Leu Leu Leu Ser Pro Val Ser Gly Asp Val His Ala
                110                 115                 120

tgt ccc ttt ggc ggg agt gtt ggt gac ggg gta ggc ata ggg ggt gag     435
Cys Pro Phe Gly Gly Ser Val Gly Asp Gly Val Gly Ile Gly Gly Glu
            125                 130                 135

agt gct gat aag aag gat gag gag aat gag ctg gat cag gaa aag aga     483
Ser Ala Asp Lys Lys Asp Glu Glu Asn Glu Leu Asp Gln Glu Lys Arg
        140                 145                 150

gtg gag tat gca gtg ctc gat gag tta gaa gat ttt act gac aat ttg     531
Val Glu Tyr Ala Val Leu Asp Glu Leu Glu Asp Phe Thr Asp Asn Leu
    155                 160                 165
```

```
gag cta gat gaa gaa gga gca ggc ggg ttc acg gct aaa gca atc gtt       579
Glu Leu Asp Glu Glu Gly Ala Gly Gly Phe Thr Ala Lys Ala Ile Val
170                 175                 180                 185

cag aga gac aga gtg gat gaa gag gcc ttg aat ttc ccc tac gag gta       627
Gln Arg Asp Arg Val Asp Glu Glu Ala Leu Asn Phe Pro Tyr Glu Val
                190                 195                 200

tgt tgg cag ccc ctc ctc tag ag ggctcttagc aaaacccaaa gagagatttg       680
Cys Trp Gln Pro Leu Leu  *
            205

ggaattgcag catcttttga aagcagggaa attaaaaaa aaaaaa                     726




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tggtggcaca caagaagagg aaatgatgag atgtgtactt tctatctctg gttaggctta     180

gtccccacta gacaaattga ttttaaatac tatgtagtga tttttaaatt ccatccacac     240

attcattacc cacacagata atcatagaaa tttgggggag tgcctagctt ctgatgaagt     300

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ggtttttttct tctggctttc ttggaggtta agctctctgt agtcataccc agttggtact    480

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ttttacagtg cagaaatgta aaatgaaaaa ggatatttcc tttcacagtg ttaccgagaa     840

gtcatgataa tttcgtttgt tcttccagat ttaggcatat acttatttaa tcaataatgt     900
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cactgagact tgcctcctct ccccccacat tgaagatgtt ctttttttcat aactatatac   1080

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aactactacc aaaaagattt caccaattta caactccatc attagtaaga atgcctgttt   1320

gcctatagtc tgccaacccct gaatccttaa aaatttttgc caatctggta ggcaaaattt   1380

ctttcttttc tttgaatatt aatgaggagg aacatctttt catgtttctt ggccatttgc   1440

atttcctatt atgaattgct tttgcccatt ttccttttt taattatgaa agtctaatga   1500

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ctaccaatca cattccactt accacagttt aacatacatc ctctagtcac ctttccgtac   1620

gaatatacat acacataaaa acacttttta cataaatagg atctcatatt ctgtagcttt   1680

ttaaaatttt ggtctcaaaa aaagataaca ggtctttaaa tttctttaat ggttgaatat   1740

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tctggagtcc agtaaggtgg atttttggat caaagggttt gttctctgtc caccttcagt   1920

cttcccaaag gccttcataa ctgtattttc accaagtgta tggagaatgt tcatttcccc   1980

atataaccat acctacactt gatagttttt atctgttggg cgaaaaagaa ccttttctta   2040

ttttgcattt ccctgattat aaaaaaaa   atg gtg aga ttg ggg tta ttt tca    2092
                                 Met Val Arg Leu Gly Leu Phe Ser
                                   1               5

tgt tta ttg gcc att tat agt tta ctg tgg att gtt tgt atc cct tac     2140
Cys Leu Leu Ala Ile Tyr Ser Leu Leu Trp Ile Val Cys Ile Pro Tyr
     10                  15                  20

ctg ctt tct att ggg tta tgt gtg gat ata ttg ttt tta ttt gtt cag     2188
Leu Leu Ser Ile Gly Leu Cys Val Asp Ile Leu Phe Leu Phe Val Gln
 25                  30                  35                  40

cat ctc ctt ccc cat ctt ctg gta aca caa cct tta ttt att tgt ggg     2236
His Leu Leu Pro His Leu Leu Val Thr Gln Pro Leu Phe Ile Cys Gly
                 45                  50                  55

gaa cct att ccc tgt ggc tta ggt gag cat gtg acc agg cct ggc ctc     2284
Glu Pro Ile Pro Cys Gly Leu Gly Glu His Val Thr Arg Pro Gly Leu
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```
                60                  65                  70

ctg agt ccc aca gct tcc tag cc acagtgataa aagaatgggt atataactta     2337
Leu Ser Pro Thr Ala Ser  *
        75

agccaggcta aggaaagccc ttaacagaac ttctgctgga actactggaa agaaggcttt   2397

atggagatcc caggaaccaa ggaccatgta agcctgaatt tgtgccatgt ggagagagtc   2457

tgtctgagga gaaactcgga tgctagcaga aatggaaaga gaactaagtt ctgatgtcat   2517

ttttctggag gccctagatc cagctgtgcc taaagcctgc cctacctccg gactttaaag   2577

ttttgtgagc caataaagtc cctttcttgt ttaagataat tgaattgagt ttttgttttg   2637

attaatatag gttatttgta ttttttttatt gatttgtaaa aaacctttgt aattttaaat   2697

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aaaa                                                                2761




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                                         Met Ser Lys Arg Asn Gln
                                          1               5

gta tcg tac gtg cgg cca gcc gag ccg gcg ttt ctg gcc cgc ttc aag     103
Val Ser Tyr Val Arg Pro Ala Glu Pro Ala Phe Leu Ala Arg Phe Lys
            10                  15                  20

gaa cgg gtc ggc tac agg gag gga ccc acc gta gag act aag aga att     151
Glu Arg Val Gly Tyr Arg Glu Gly Pro Thr Val Glu Thr Lys Arg Ile
        25                  30                  35

cag cct cag ccc cca gat gaa gat ggg gat cac agt gac aaa gaa gat     199
Gln Pro Gln Pro Pro Asp Glu Asp Gly Asp His Ser Asp Lys Glu Asp
    40                  45                  50

gaa cag cct caa gtg gtg gtt tta aaa aag gga gac ctg tca gtt gaa     247
Glu Gln Pro Gln Val Val Val Leu Lys Lys Gly Asp Leu Ser Val Glu
 55                  60                  65                  70

gaa gtc atg aaa att aaa gca gaa ata aag gct gcc aaa gca gat gaa     295
Glu Val Met Lys Ile Lys Ala Glu Ile Lys Ala Ala Lys Ala Asp Glu
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                 75                  80                  85

gaa cca act cca gcc gat gga aga atc ata tat cga aaa cca gtc aag      343
Glu Pro Thr Pro Ala Asp Gly Arg Ile Ile Tyr Arg Lys Pro Val Lys
             90                  95                 100

cat ccc tca gat gaa aaa tat tca ggt tta aca gca agc tca aaa aag      391
His Pro Ser Asp Glu Lys Tyr Ser Gly Leu Thr Ala Ser Ser Lys Lys
        105                 110                 115

aag aag cca aat gaa gat gaa gta aat cag gac tcg gtc aaa aag aac      439
Lys Lys Pro Asn Glu Asp Glu Val Asn Gln Asp Ser Val Lys Lys Asn
    120                 125                 130

tca caa aaa caa att aaa aat agt agc ctc ctt tct ttt gac aac gaa      487
Ser Gln Lys Gln Ile Lys Asn Ser Ser Leu Leu Ser Phe Asp Asn Glu
135                 140                 145                 150

gat gaa aat gag taa gtgtaaatat tttgaattta gtctactttg aaagtatatg       542
Asp Glu Asn Glu  *
                155

gagtgttcat taaaatcaca tttttcccta ttataaagat actacaagtt ctttatagaa    602

agtttaggaa atagagaaaa aaatttaata aactacatct attcatcaat acccctctga    662

cttaaaatgc caactctata gaaattagct agtattaaca ttttgttatt tcccttgtgt    722

ggttgtatat atatgtaaat tatattttta agcaaaatac atttttgtg tgtaaacaaa     782

attttataaa tacaactgta ttgcaaaaaa aaaaaaaaa                           821



     <210> 112
     <211> 573
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (152)..(457)

     <400> 112
acggaacttc ggcacgaggc tagctttctg tgtgcttagg tgcccgagct actgagggtc     60

taagtccggg cagccgaaga gtgtggtagg taacggtcct cagcgcaagg gtcatttcgt    120

cgctgggaag ggacggccct cgcccgcggt g   atg gtg gtt agc aag atg aac     172
                                     Met Val Val Ser Lys Met Asn
                                       1               5

aaa gat gcg cag atg aga gca gcg att aac caa aag ttg ata gaa act      220
Lys Asp Ala Gln Met Arg Ala Ala Ile Asn Gln Lys Leu Ile Glu Thr
         10                  15                  20
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gga gaa aga gaa cgc ctc aaa gag ttg ctg aga gct aaa tta att gaa      268
Gly Glu Arg Glu Arg Leu Lys Glu Leu Leu Arg Ala Lys Leu Ile Glu
     25                  30                  35

tgt ggc tgg aag gat cag ttg aag gca cac tgt aaa gag gta att aaa      316
Cys Gly Trp Lys Asp Gln Leu Lys Ala His Cys Lys Glu Val Ile Lys
 40                  45                  50                  55

gaa aaa gga cta gaa cac gtt act gtt gat gac ttg gtg gct gaa atc      364
Glu Lys Gly Leu Glu His Val Thr Val Asp Asp Leu Val Ala Glu Ile
                 60                  65                  70

act cca aaa ggc aga gcc ctg gta cct gac agt gta aag aag gag ctc      412
Thr Pro Lys Gly Arg Ala Leu Val Pro Asp Ser Val Lys Lys Glu Leu
             75                  80                  85

cta caa aga ata aga aca ttc ctt gct cag cat gcc agc ctt taa gat      460
Leu Gln Arg Ile Arg Thr Phe Leu Ala Gln His Ala Ser Leu  *
         90                  95                 100

tgaattagat tgtgttgttg tggttttatt tctgaaagta aaacttgcca taaattagaa    520

aacaatttcc caaaataaaa tccttttttg tatgatggta aaaaaaaaaa aaa           573



     <210> 113
     <211> 1687
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (477)..(1634)

     <400> 113
tttcaggttc caaagcttat ggttagggag ccaaaacccc caccccctta tttttagaat     60

ggcaatatta ttgtaccaca tctgtcatgc tacggaaaac aaatggaatc tggctttcat    120

gtgaatacaa aggttacaaa gtctatattt accatcatta atactgaata ttatattcca    180

ataagaatct ttagaatttt aagagaaatt tgagtattaa aaaaattatc taatataccc    240

aattagaatc ttttcacatg agactacaga gaaagatttg tatttgtaac aaaaaattag    300

ctgggcatgg tggcaggtgc ctgtaatccc agctacttgg gaggctgagg caggagaatc    360

gcttgaaccc gggaggcgga ggttgagcaa ctacactgcg ctgcatcgga ctcgacgccc    420

gctggtgacg cacacgctgc gccggaagtg tgaactgtct gcctccgggc tttgtc        476
atg gcg gct gct gct gca cgc tgg aac cat gtg tgg gtc ggc acc gag      524
Met Ala Ala Ala Ala Ala Arg Trp Asn His Val Trp Val Gly Thr Glu
  1               5                  10                  15

act ggg atc ttg aaa ggg gta aat ctt cag cga aaa cag gcg gcg aac      572
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Thr Gly Ile Leu Lys Gly Val Asn Leu Gln Arg Lys Gln Ala Ala Asn
             20                  25                  30

ttc acg gcc gga gga cag ccg cgg cgc gag gag gca gtg agc gcc ctg      620
Phe Thr Ala Gly Gly Gln Pro Arg Arg Glu Glu Ala Val Ser Ala Leu
         35                  40                  45

tgt tgg ggc acc ggc ggc gag acc cag atg ctg gtg ggc tgc gcg gac      668
Cys Trp Gly Thr Gly Gly Glu Thr Gln Met Leu Val Gly Cys Ala Asp
     50                  55                  60

agg acg gtg aag cac ttc agc acc gag gat ggc ata ttc cag ggt cag      716
Arg Thr Val Lys His Phe Ser Thr Glu Asp Gly Ile Phe Gln Gly Gln
 65                  70                  75                  80

aga cac tgc ccg ggc ggg gag ggc atg ttc cgt ggc ctc gcc cag gcc      764
Arg His Cys Pro Gly Gly Glu Gly Met Phe Arg Gly Leu Ala Gln Ala
                 85                  90                  95

gac ggc acc ctc atc aca tgt gtg gat tct ggg att ctc aga gtc tgg      812
Asp Gly Thr Leu Ile Thr Cys Val Asp Ser Gly Ile Leu Arg Val Trp
            100                 105                 110

cat gac aag gac aag gac aca tcc tct gac cca ctc ctg gaa ctg aga      860
His Asp Lys Asp Lys Asp Thr Ser Ser Asp Pro Leu Leu Glu Leu Arg
        115                 120                 125

gtg ggc cct ggg gtg tgt agg atg cgc caa gac cca gca cac ccc cat      908
Val Gly Pro Gly Val Cys Arg Met Arg Gln Asp Pro Ala His Pro His
    130                 135                 140

gtg gtt gcc aca ggt ggg aaa gag aat gct ttg aag ata tgg gac ctg      956
Val Val Ala Thr Gly Gly Lys Glu Asn Ala Leu Lys Ile Trp Asp Leu
145                 150                 155                 160

cag ggc tct gag gaa cct gtg ttc agg gcc aag aac gtg cgg aat gac     1004
Gln Gly Ser Glu Glu Pro Val Phe Arg Ala Lys Asn Val Arg Asn Asp
                165                 170                 175

tgg ctg gac ttg cgg gtt ccc atc tgg gac cag gac ata cag ttt ctc     1052
Trp Leu Asp Leu Arg Val Pro Ile Trp Asp Gln Asp Ile Gln Phe Leu
            180                 185                 190

cca gga tca cag aag ctt gtc acc tgc aca ggg tac cac cag gtc cgt     1100
Pro Gly Ser Gln Lys Leu Val Thr Cys Thr Gly Tyr His Gln Val Arg
        195                 200                 205

gtt tat gat cca gca tcc ccc cag cgc cgg cca gtc cta gag acc acc     1148
Val Tyr Asp Pro Ala Ser Pro Gln Arg Arg Pro Val Leu Glu Thr Thr
    210                 215                 220

tat gga gag tac cca cta aca gcc atg acc ctc act ccg gga ggc aac     1196
Tyr Gly Glu Tyr Pro Leu Thr Ala Met Thr Leu Thr Pro Gly Gly Asn
225                 230                 235                 240

tca gtg att gtg gga aac act cat ggg cag ctg gca gaa att gac ctt     1244
Ser Val Ile Val Gly Asn Thr His Gly Gln Leu Ala Glu Ile Asp Leu
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                245                 250                 255

cgg caa ggg cgt cta ctg ggc tgt ctg aag ggg ctg gca ggc agt gtg      1292
Arg Gln Gly Arg Leu Leu Gly Cys Leu Lys Gly Leu Ala Gly Ser Val
            260                 265                 270

cgt ggg ttg cag tgc cac cct tca aag cct cta cta gcc tcc tgt ggc      1340
Arg Gly Leu Gln Cys His Pro Ser Lys Pro Leu Leu Ala Ser Cys Gly
        275                 280                 285

ttg gac aga gtc ttg agg ata cac agg atc cag aat cca cgg ggt ctg      1388
Leu Asp Arg Val Leu Arg Ile His Arg Ile Gln Asn Pro Arg Gly Leu
    290                 295                 300

gag cat aag gtt tat ctc aag tct caa ttg aac tgc ctc ctc ttg tca      1436
Glu His Lys Val Tyr Leu Lys Ser Gln Leu Asn Cys Leu Leu Leu Ser
305                 310                 315                 320

ggc agg gac aac tgg gag gat gag ccc caa gag cct caa gaa ccc aac      1484
Gly Arg Asp Asn Trp Glu Asp Glu Pro Gln Glu Pro Gln Glu Pro Asn
                325                 330                 335

aag gtg ccc cta gaa gac aca gag aca gat gaa ctt tgg gca tcc ttg      1532
Lys Val Pro Leu Glu Asp Thr Glu Thr Asp Glu Leu Trp Ala Ser Leu
            340                 345                 350

gag gca gct gcc aag cgg aag ctc tcg ggt ttg gag cag ccc caa gga      1580
Glu Ala Ala Ala Lys Arg Lys Leu Ser Gly Leu Glu Gln Pro Gln Gly
        355                 360                 365

gct ctc caa acg aga cgg aga aag aag aag cgg cct ggg tcc acc agc      1628
Ala Leu Gln Thr Arg Arg Arg Lys Lys Lys Arg Pro Gly Ser Thr Ser
    370                 375                 380

ccc tga cgcccctgtg cccactttgt aaataaactg ctgaacaccc aaaaaaaaaa       1684
Pro  *
385

aaa                                                                  1687



      <210> 114
      <211> 1416
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (109)..(756)

      <400> 114
atttggccct cgaggccaag aattcggcac gaggtgctat actgggatgc aggcgcggcg      60

gggactggca gcaatcatgc cctgggagct agcgtagagc tttggata atg ctt ttg      117
                                                     Met Leu Leu
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                                                       1

caa gtt gta cga gaa ggg aag ttc tcg ggg ttt ctg acc tcc tgc agc       165
Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr Ser Cys Ser
      5                  10                  15

ctc ctc ttg cct cgg gct gcc cag atc ttg gcg gct gag gct ggc tta       213
Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu Ala Gly Leu
 20                  25                  30                  35

cct tcg agc cgt tcc ttc atg gga ttt gct gct ccc ttc acc aac aag       261
Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe Thr Asn Lys
                 40                  45                  50

cga aag gct tac tcg gag cgt aga atc atg ggg tac tca atg cag gag       309
Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser Met Gln Glu
             55                  60                  65

atg tat gag gtg gtg tcc aac gtc cag gag tat cgt gag ttt gtg ccc       357
Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu Phe Val Pro
         70                  75                  80

tgg tgt aag aag tct ctg gtg gta tcc agc cgt aag ggt cat ttg aaa       405
Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly His Leu Lys
     85                  90                  95

gcc cag ctg gag gtt ggc ttt cca cct gtc atg gaa cgt tac acc tct       453
Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg Tyr Thr Ser
100                 105                 110                 115

gca gtt tcc atg gtc aaa cct cac atg gtc aag gct gtt tgt act gat       501
Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val Cys Thr Asp
                120                 125                 130

ggc aag ctc ttc aac cac tta gag act att tgg cga ttc agc cct ggt       549
Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe Ser Pro Gly
            135                 140                 145

att cct gcc tat cct cga acc tgc act gtg gac ttt tcg att tcc ttt       597
Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser Ile Ser Phe
        150                 155                 160

gaa ttt cgt tct ctg ctg cac tcc cag ctg gcc acc atg ttt ttt gat       645
Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met Phe Phe Asp
    165                 170                 175

gag gtt gtc aaa cag aat gtt gct gcc ttt gag cgt cgg gca gcc acc       693
Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg Ala Ala Thr
180                 185                 190                 195

aag ttt ggt cca gaa aca gcc atc ccc cgt gaa ctg atg ttc cat gag       741
Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met Phe His Glu
                200                 205                 210

gtg cac cag act tga ggcaagggat tgctccctga cctcccttct accccacttc       796
Val His Gln Thr  *
            215
```

```
cctacacaat tctcttattt atttggtttg gctcctgttc caatttgaaa ggagtctgtg     856

ttcataatac tgtttctcct ctcaatttcc cagaaattgg gttctatgct ggctggaaat     916

gttgggggaa agagaaggca aaggatgtgg aaatgagatg tgcttaggaa agggtcaggc     976

ccatcgtagg agcaccatat gcctgcagcc ttttcactac gaattagaat aaggactatg    1036

tggttgtctc tggaccttat caagacacct tagtgtctga ccaggggacg atagtaactt    1096

ttctaaggat tgaataaatt gagcttttct tctggcacag aggtactgag tggtaagtaa    1156

cttttaccct gcctgagatt cctcaggaga aaaggcaacc tgcctccagc ctgaaataca    1216

taaagcctca ttttaagact gtaagtccat gctgcctggc tactagagag caaggggctt    1276

tcttaccacc agtgctgagg agaaaagtac tgaacggaaa cggagttgtc tttgtactct    1336

tgagttgtac cttattcttc cacttggcct gagtttttat aaaatttcaa taaattgtga    1396

cagtgtgaaa aaaaaaaaaa                                                1416



     <210> 115
     <211> 1008
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (392)..(736)

     <400> 115
cagtgtggtg gaattcagaa atactaggga agggccaggc gtggtggctc acgcctctaa      60

acccagcact ttgagaggcc aaggtgggag gatcacctga gggcaagagt tcaagaccag     120

cctgaccaac atggagaaac cccatctcta cttaaaaaaa aaaaaatacg aatttaccca     180

ggcatggtgg tgggcacctg taatcccagc tactcgggag actgaggcgg gagattctct     240

tgaacctggg aggcagaggt tgcggtgagc cgagatcgtg ccattgcact ccagcctggg     300

caacaagagc aaaactccat ctcaaaaaga aaaaagaaag aaagaaatgc taggggaaaa     360

tgttttaact agtcattctt cccagtagct a   atg aag ctg act ttt aaa aag      412
                                     Met Lys Leu Thr Phe Lys Lys
                                      1               5

aag gct gtg agc ttt gca gat gct gct gcc gcc cag ggc ccc ctg ctt      460
Lys Ala Val Ser Phe Ala Asp Ala Ala Ala Ala Gln Gly Pro Leu Leu
        10                  15                  20

cca gcc atg gtc aac ccc acc atg ttt ttc cac att gct gtc gat ggc      508
```

```
Pro Ala Met Val Asn Pro Thr Met Phe Phe His Ile Ala Val Asp Gly
     25                  30                  35

gag ccc ttg ggc tgt gtc tcc ttc gag ctg ttt gca gac aag gtt cca       556
Glu Pro Leu Gly Cys Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro
 40                  45                  50                  55

aag aca gca gaa aat ttc cat gct ctg agc act gga gaa aaa gga ttt       604
Lys Thr Ala Glu Asn Phe His Ala Leu Ser Thr Gly Glu Lys Gly Phe
                 60                  65                  70

ggt tat aag ggt tcc tgc ttt cac aga att att cca ggg ttt acg tgt       652
Gly Tyr Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Thr Cys
             75                  80                  85

cag agt ggt gac ttc aca cgc cat aca gca ttg gtg gca agt cca tct       700
Gln Ser Gly Asp Phe Thr Arg His Thr Ala Leu Val Ala Ser Pro Ser
         90                  95                  100

gca ggg aga aat ttg atg aca aga act tca tcc tga agca tacgggtcct       750
Ala Gly Arg Asn Leu Met Thr Arg Thr Ser Ser  *
    105                 110                 115

ggcatcttgt ccatggcaaa tgctggaccc agcgtgaacg tttcccagtt ttttatctgc     810

cctgccaaga tgccaagaca gagtggttgg attgcaagca tgtggtcttt ggcaaggtga     870

aagatggcat gaatattgtg gaggtcatgg agcacttggg gtccaagaat ggcaagatca     930

gcaatcagca agaagatcac cattgctgac tggacaactg caataaattt gacgggtgtt     990

tctcttaaaa aaaaaaaa                                                  1008



     <210> 116
     <211> 1379
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (160)..(444)

     <400> 116
agtagaaata ccctttgat caccctgcgg taccggtccg gaattcccgg gtcgacccac      60

gcgtccgggc ggggaggtgg acgcgggtac cggcggtcgt cgggtcggca gcctttggtc     120

agttggcagc ggcaagcgcg ctgcggttcc ggtggcgcc   atg tcg ttc tgc agc     174
                                             Met Ser Phe Cys Ser
                                              1               5

ttc ttc ggg ggc gag gtt ttc cag aat cac ttt gaa cct ggc gtt tac       222
Phe Phe Gly Gly Glu Val Phe Gln Asn His Phe Glu Pro Gly Val Tyr
                 10                  15                  20
```

```
gtg tgt gcc aag tgt ggc tat gag ctg ttc tcc agc cgc tcg aag tat        270
Val Cys Ala Lys Cys Gly Tyr Glu Leu Phe Ser Ser Arg Ser Lys Tyr
             25                  30                  35

gca cac tcg tct cca tgg ccg gcg ttc acc gag acc att cac gcc gac        318
Ala His Ser Ser Pro Trp Pro Ala Phe Thr Glu Thr Ile His Ala Asp
         40                  45                  50

agc gtg gcc aag cgt ccg gag cac aat aga tct gaa gcc ttg aag gtg        366
Ser Val Ala Lys Arg Pro Glu His Asn Arg Ser Glu Ala Leu Lys Val
     55                  60                  65

tcc tgt ggc aag tgt ggc aat ggg ttg ggc cac gag ttc ctg aac gac        414
Ser Cys Gly Lys Cys Gly Asn Gly Leu Gly His Glu Phe Leu Asn Asp
 70                  75                  80                  85

ggc ccc aag ccg ggg cag tcc cga ttc tga a tattcagcag ctcgctgaag        465
Gly Pro Lys Pro Gly Gln Ser Arg Phe  *
                 90                  95

tttgtcccta aaggcaaaga aacttctgcc tcccagggtc actaggcggg cagcccacac      525

ccaccccaga cggccaccac actgaggcca cacgttggcc attccacctt ggagttggaa      585

ccctgggcgt cgagacagga aggcagggcg cagtggttga aacatcagga cactcccaag      645

gccccggctc tgaacaagac cttttcgttt cttggaaaag agactcattt gctgatggtt      705

catgccttct gctgggacag gcctgggctg tgcagccaca ctgtcggctg acttagcccc      765

ctgctcactc taggtgcctc caggaggtga gccctgggtg cagctggtct ctgaatgacg      825

ttacaccctc accttctttt cctggccctg tctctgggac tctcccctgt gaggcccaat      885

tccaagacag actctcgtcc tcaccgaagc ttaggcccac atctcccagg ctgcttagga      945

gacagaatgg aaacggaggc cgcccctgcc agccgccctg gccctggtca ctgcatgatc     1005

cgctctggtc aaacccttcc aggccagcca gagtggggat ggtctgtgac ctgctgggaa     1065

ggcaggctga tggggcacac ccttggcctc tcgtccacga ggggagaaac ctaaaccctg     1125

tttcacaatc tgtgcggaag tagcttgcct cacttctgct taggaaagcg gctgttgctc     1185

cataactcta accagcacag ggctgaggcc tgcagtgcac acctgcaggg aggcccttcc     1245

caaggtgtgg tgactgtgcc ttactgtaca tgctcggagg cctggccata taggagggtg     1305

ggtgatgctg aaatcacccc ccatcttaag taattacttt ctggagtaat caggtggaaa     1365

tccatagaca aatg                                                       1379
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<210> 117

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     <211> 2179
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (70)..(1827)

     <400> 117
caaatatcaa gagaccatgg ctggattaag ctagataata attttgaggt caattttgat      60

aaagatcca    atg gaa atg cgc ctc cct att cgt agc cct att aaa cga      108
             Met Glu Met Arg Leu Pro Ile Arg Ser Pro Ile Lys Arg
               1               5                  10

gac ttt tta tca gga att cag att gaa ttt aag cag tct tct cac cag       156
Asp Phe Leu Ser Gly Ile Gln Ile Glu Phe Lys Gln Ser Ser His Gln
     15                  20                  25

aga agt tta agg gcc agg ttg tac tgg ctt cag gtt gat aat cag tta       204
Arg Ser Leu Arg Ala Arg Leu Tyr Trp Leu Gln Val Asp Asn Gln Leu
 30                  35                  40                  45

cca ggt gca atg ttc cct gtt gta ttt cat cct gtt gcc cct cca aaa       252
Pro Gly Ala Met Phe Pro Val Val Phe His Pro Val Ala Pro Pro Lys
                 50                  55                  60

tct att gct tta gat tca gag ccc aag cct ttc att gat gtg agt gtc       300
Ser Ile Ala Leu Asp Ser Glu Pro Lys Pro Phe Ile Asp Val Ser Val
             65                  70                  75

atc aca aga ttt aat gag tac agt aaa gtc tta cag ttc aag tat ttt       348
Ile Thr Arg Phe Asn Glu Tyr Ser Lys Val Leu Gln Phe Lys Tyr Phe
         80                  85                  90

atg gtc ctc att cag gaa atg gcc tta aaa att gat caa ggg ttt cta       396
Met Val Leu Ile Gln Glu Met Ala Leu Lys Ile Asp Gln Gly Phe Leu
     95                 100                 105

gga gct att att gca ctg ttt acc cca aca aca gac cct gaa gct gaa       444
Gly Ala Ile Ile Ala Leu Phe Thr Pro Thr Thr Asp Pro Glu Ala Glu
110                 115                 120                 125

aga aga cgg aca aag tta atc caa caa gat att gat gct cta aat gca       492
Arg Arg Arg Thr Lys Leu Ile Gln Gln Asp Ile Asp Ala Leu Asn Ala
                130                 135                 140

gaa tta atg gag act tca atg act gat atg tca att ctt agt ttc ttt       540
Glu Leu Met Glu Thr Ser Met Thr Asp Met Ser Ile Leu Ser Phe Phe
            145                 150                 155

gaa cat ttc cat att tct cct gtg aag ttg cat ttg agt ttg tct ttg       588
Glu His Phe His Ile Ser Pro Val Lys Leu His Leu Ser Leu Ser Leu
        160                 165                 170

ggt tcc gga ggt gaa gaa tca gac aaa gaa aaa cag gaa atg ttt gca       636
Gly Ser Gly Gly Glu Glu Ser Asp Lys Glu Lys Gln Glu Met Phe Ala
```

```
    175                 180                 185

gtt cat tct gtc aac ttg ctg ttg aaa agc ata ggt gct act ctg act       684
Val His Ser Val Asn Leu Leu Leu Lys Ser Ile Gly Ala Thr Leu Thr
190                 195                 200                 205

gat gtg gat gac ctt ata ttc aaa ctt gct tat tat gaa att cga tat       732
Asp Val Asp Asp Leu Ile Phe Lys Leu Ala Tyr Tyr Glu Ile Arg Tyr
                210                 215                 220

cag ttc tac aag aga gat cag ctt ata tgg agt gtt gtt agg cat tac       780
Gln Phe Tyr Lys Arg Asp Gln Leu Ile Trp Ser Val Val Arg His Tyr
            225                 230                 235

agt gaa cag ttc ttg aaa cag atg tat gtc ctt gta ttg ggg tta gat       828
Ser Glu Gln Phe Leu Lys Gln Met Tyr Val Leu Val Leu Gly Leu Asp
        240                 245                 250

gta ctt gga aac cca ttt gga tta att aga ggt ctg tct gaa gga gtt       876
Val Leu Gly Asn Pro Phe Gly Leu Ile Arg Gly Leu Ser Glu Gly Val
    255                 260                 265

gaa gct tta ttc tat gaa ccc ttc cag ggt gct gtt caa ggc cct gaa       924
Glu Ala Leu Phe Tyr Glu Pro Phe Gln Gly Ala Val Gln Gly Pro Glu
270                 275                 280                 285

gaa ttt gca gag ggg tta gtg att gga gtg aga agc ctc ttt gga cac       972
Glu Phe Ala Glu Gly Leu Val Ile Gly Val Arg Ser Leu Phe Gly His
                290                 295                 300

aca gta ggt ggt gca gca gga gtt gta tct cga atc acc ggt tct gtt      1020
Thr Val Gly Gly Ala Ala Gly Val Val Ser Arg Ile Thr Gly Ser Val
            305                 310                 315

ggg aaa ggt ttg gca gca att aca atg gac aag gaa tat cag caa aaa      1068
Gly Lys Gly Leu Ala Ala Ile Thr Met Asp Lys Glu Tyr Gln Gln Lys
        320                 325                 330

aga aga gaa gag ttg agt cga cag ccc aga gat ttt gga gac agc ctg      1116
Arg Arg Glu Glu Leu Ser Arg Gln Pro Arg Asp Phe Gly Asp Ser Leu
    335                 340                 345

gcc aga gga gga aag ggc ttt ctg cga gga gtt gtt ggt gga gtg act      1164
Ala Arg Gly Gly Lys Gly Phe Leu Arg Gly Val Val Gly Gly Val Thr
350                 355                 360                 365

gga ata ata aca aaa cct gtg gaa ggt gcc aaa aag gaa gga gct gct      1212
Gly Ile Ile Thr Lys Pro Val Glu Gly Ala Lys Lys Glu Gly Ala Ala
                370                 375                 380

gga ttc ttt aaa gga att gga aaa ggg ctt gtg ggt gct gtg gcc cgt      1260
Gly Phe Phe Lys Gly Ile Gly Lys Gly Leu Val Gly Ala Val Ala Arg
            385                 390                 395

cca act ggt gga atc gta gat atg gcc agt agt acc ttc caa ggc att      1308
Pro Thr Gly Gly Ile Val Asp Met Ala Ser Ser Thr Phe Gln Gly Ile
        400                 405                 410
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cag agg gca gca gaa tca act gag gaa gta tct agc ctc cgt ccc cct     1356
Gln Arg Ala Ala Glu Ser Thr Glu Glu Val Ser Ser Leu Arg Pro Pro
    415                 420                 425

cgc ctg atc cat gaa gat ggc atc att cgt cct tat gac aga cag gaa     1404
Arg Leu Ile His Glu Asp Gly Ile Ile Arg Pro Tyr Asp Arg Gln Glu
430                 435                 440                 445

tct gag ggc tct gac tta ctt gag aat cat atc aaa aag ttg gaa gga     1452
Ser Glu Gly Ser Asp Leu Leu Glu Asn His Ile Lys Lys Leu Glu Gly
                450                 455                 460

gag act tac cga tac cac tgt gct att cct gga agc aag aag aca atc     1500
Glu Thr Tyr Arg Tyr His Cys Ala Ile Pro Gly Ser Lys Lys Thr Ile
            465                 470                 475

ctt atg gtt aca aat agg cga gtg ttg tgt ata aag gaa gtt gaa atc     1548
Leu Met Val Thr Asn Arg Arg Val Leu Cys Ile Lys Glu Val Glu Ile
        480                 485                 490

ctg ggc ctt atg tgt gta gac tgg caa tgt cca ttt gaa gat ttt gta     1596
Leu Gly Leu Met Cys Val Asp Trp Gln Cys Pro Phe Glu Asp Phe Val
    495                 500                 505

ttt cct cct agt gtc agt gaa aat gtg cta aaa att tca gtt aag gaa     1644
Phe Pro Pro Ser Val Ser Glu Asn Val Leu Lys Ile Ser Val Lys Glu
510                 515                 520                 525

cag ggt ctg ttc cac aaa aaa gac agt gcc aat caa ggc tgt gtt cga     1692
Gln Gly Leu Phe His Lys Lys Asp Ser Ala Asn Gln Gly Cys Val Arg
                530                 535                 540

aaa gtt tac ctg aag gac acc gcc aca gca gag aga gca tgt aat gcc     1740
Lys Val Tyr Leu Lys Asp Thr Ala Thr Ala Glu Arg Ala Cys Asn Ala
            545                 550                 555

att gag gat gca cag tca acg aga cag cag caa aaa ttg atg aag cag     1788
Ile Glu Asp Ala Gln Ser Thr Arg Gln Gln Gln Lys Leu Met Lys Gln
        560                 565                 570

tca tca gtg aga ctt ctc aga ccc caa ttg cca tct taa tcacagacct      1837
Ser Ser Val Arg Leu Leu Arg Pro Gln Leu Pro Ser  *
    575                 580                 585

caggggctcc aacagggaga aaaaacaatc actggtcttg tctataagtc actctgcttt   1897

atcttgctaa agacaatttt tcaagcaatc ctttagtttt agttttctgg aatagctagt   1957

attgggtttt ctagtttttt caccttttag tttttactct aattttgtaa ccatgtatat   2017

gctagcagtc cacttctacg ccaccaccca aatgggtcag acccttgaag aaacgtcact   2077

tcaaactcag aatgaaattt tcattaatat taaaattgtg aagcaaaggt caataggctt   2137

atatttaatt aaagccttac tgaaaataag aaatgagctt ag                      2179
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tgatgtagcc agaatggctg gttacagtcc cgggaggggc ccaagctggc ttgaacctgg     120

cccaggtcat gcacacagcc agcagtgaca catccaatgg gacactccag gatgaaacct     180

gagaaaggag gtctgggata tgggatattg taatgggaga gcaggaaatt taaggtcgga     240

ggtatttgtt taggatacct cagtattcta gagctatggg atttattttg ctttgaagtc     300

cagaggtatt tagctttatt ctaaaagcg  atg aag ttc ctc tta att aaa gac     353
                                 Met Lys Phe Leu Leu Ile Lys Asp
                                   1               5

gct cct gga aaa aaa aaa agg aaa aat tta atg ctg tct ttt aaa agg       401
Ala Pro Gly Lys Lys Lys Arg Lys Asn Leu Met Leu Ser Phe Lys Arg
     10                  15                  20

aaa cat gcc aaa ggc cag gat ttg ttt gat cag att gtg tac cac ttg       449
Lys His Ala Lys Gly Gln Asp Leu Phe Asp Gln Ile Val Tyr His Leu
 25                  30                  35                  40

gac ctt gtg gaa aca gat tac ttt ggc ctc cag ttc ctc gac tct gcc       497
Asp Leu Val Glu Thr Asp Tyr Phe Gly Leu Gln Phe Leu Asp Ser Ala
                 45                  50                  55

cag gtt gcg cac tgg ctg gat cat gcc aaa ccc ata aaa aag cag atg       545
Gln Val Ala His Trp Leu Asp His Ala Lys Pro Ile Lys Lys Gln Met
             60                  65                  70

aaa att gga cct gct tat gct tta cac ttt cga gtt aaa tac tat tct       593
Lys Ile Gly Pro Ala Tyr Ala Leu His Phe Arg Val Lys Tyr Tyr Ser
         75                  80                  85

tca gaa cca aac aac ctt cgt gag gag ttt aca agg tac ctg ttt gtt       641
Ser Glu Pro Asn Asn Leu Arg Glu Glu Phe Thr Arg Tyr Leu Phe Val
     90                  95                 100

tta caa ctc agg cat gac att ctt tct gga aaa ttg aaa tgc cct tat       689
Leu Gln Leu Arg His Asp Ile Leu Ser Gly Lys Leu Lys Cys Pro Tyr
105                 110                 115                 120

gaa aca gct gtg gaa tta gct gct ctc tgt cta caa gcg gag ctt ggg       737
Glu Thr Ala Val Glu Leu Ala Ala Leu Cys Leu Gln Ala Glu Leu Gly
```

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                125                 130                 135

gag tgc gag ctt cca gaa cac aca cca gag ctt gtg tct gag ttt cgg        785
Glu Cys Glu Leu Pro Glu His Thr Pro Glu Leu Val Ser Glu Phe Arg
            140                 145                 150

ttc att cca aat cag aca gaa gca atg gaa ttt gat atc ttc cag aga        833
Phe Ile Pro Asn Gln Thr Glu Ala Met Glu Phe Asp Ile Phe Gln Arg
        155                 160                 165

tgg aaa gag tgc agg gga aag agc cct gcc cag gcg gaa ctc tcc tat        881
Trp Lys Glu Cys Arg Gly Lys Ser Pro Ala Gln Ala Glu Leu Ser Tyr
    170                 175                 180

ctg aat aaa gcg aag tgg ctg gaa atg tat ggg gta gac atg cac gtt        929
Leu Asn Lys Ala Lys Trp Leu Glu Met Tyr Gly Val Asp Met His Val
185                 190                 195                 200

gtc agg gga aga gat ggc tgt gaa tat tct ctt gga ctg acc ccg aca        977
Val Arg Gly Arg Asp Gly Cys Glu Tyr Ser Leu Gly Leu Thr Pro Thr
                205                 210                 215

ggc ata tta atc ttt gaa gga gct aac aaa ata ggc tta ttc ttt tgg       1025
Gly Ile Leu Ile Phe Glu Gly Ala Asn Lys Ile Gly Leu Phe Phe Trp
            220                 225                 230

cct aaa att acc aaa atg gat ttt aaa aag agc aaa ttg aca ctc gtg       1073
Pro Lys Ile Thr Lys Met Asp Phe Lys Lys Ser Lys Leu Thr Leu Val
        235                 240                 245

gtg gtc gag gat gat gat cag gga cgt gag caa gag cac acg ttt gtg       1121
Val Val Glu Asp Asp Asp Gln Gly Arg Glu Gln Glu His Thr Phe Val
    250                 255                 260

ttc cgg tta gac agt gcc agg acc tgc aaa cac ctt tgg aag tgt gca       1169
Phe Arg Leu Asp Ser Ala Arg Thr Cys Lys His Leu Trp Lys Cys Ala
265                 270                 275                 280

gtt gag cac cac gca ttc ttc cga ctg cgg acg cca gga aac agc aaa       1217
Val Glu His His Ala Phe Phe Arg Leu Arg Thr Pro Gly Asn Ser Lys
                285                 290                 295

tcc aat aga tcc gac ttt atc agg ctg ggc tct cgc ttc aga ttc agt       1265
Ser Asn Arg Ser Asp Phe Ile Arg Leu Gly Ser Arg Phe Arg Phe Ser
            300                 305                 310

ggg cgg aca gaa tat caa gct aca cat ggc tcc agg tta cga aga acc       1313
Gly Arg Thr Glu Tyr Gln Ala Thr His Gly Ser Arg Leu Arg Arg Thr
        315                 320                 325

agc acc ttt gag agg aag cct agt aaa cgt tat cca tcc cgg aga cat       1361
Ser Thr Phe Glu Arg Lys Pro Ser Lys Arg Tyr Pro Ser Arg Arg His
    330                 335                 340

tca acg ttc aaa gca agc aac cca gtg ata gca gcc cag ctc tgc tct       1409
Ser Thr Phe Lys Ala Ser Asn Pro Val Ile Ala Ala Gln Leu Cys Ser
345                 350                 355                 360
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aaa aca aat cca gaa gtc cat aat tac cag cct caa tat cat cct aat      1457
Lys Thr Asn Pro Glu Val His Asn Tyr Gln Pro Gln Tyr His Pro Asn
                365                 370                 375

atc cat ccc agc cag ccc cgg tgg cat cct cac tct cca aat gtc agg      1505
Ile His Pro Ser Gln Pro Arg Trp His Pro His Ser Pro Asn Val Arg
            380                 385                 390

cca tcc ttt cag gat gac agg tcg cat tgg aaa gca tcg gcc agt gga      1553
Pro Ser Phe Gln Asp Asp Arg Ser His Trp Lys Ala Ser Ala Ser Gly
        395                 400                 405

gat gac agc cat ttt gat tat gtc cac gac cag aac cag aag aac tta      1601
Asp Asp Ser His Phe Asp Tyr Val His Asp Gln Asn Gln Lys Asn Leu
    410                 415                 420

gga ggg atg caa agt atg atg tat cga gat aaa ctc atg act gca ctt      1649
Gly Gly Met Gln Ser Met Met Tyr Arg Asp Lys Leu Met Thr Ala Leu
425                 430                 435                 440

tga gaga ctgaagcatc tctcttccat tcaccttcat agtttcattg cattccatga      1706
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aaagtgtctt ggcctcagat ggatggatgt gtttggacga gtgtctttaa ggagtagtcc    1766

tgaaaggtgt ttttggtgtc catgtaaata tttgaagata aaaccactat agcttgtcat    1826

aatttactgt tgactgcatt ctcattaaaa tgaaggtaaa ggctcaggaa tcatattgat    1886

gttctgattt taaaattgga gtcaaagtct atgtttatca ttttactatg ttcctgatgt    1946

tctttgttat ttaattaatg ggagcaaata aaaccagaag agcttgggaa gattgctcag    2006

catatattcc tgtcgtagaa gttgagattg ctagggtcca gtttccctag tgtggcctgg    2066

acgagtcatt tccccttcat tgacctcatt ttccccatct gaaaagagag ggttggacta    2126

agtgatctcc aaggtccttt ccaactctaa aattctgcaa tttgttaaca tttcattttg    2186

tttaggttga ggacatacat tcaaactaat tttatcacaa ggaaaactgc aatacccact    2246

tccttgacag agttactcct ttcagaagct aaataaagta tataacttat tagatgttat    2306

atagatacag gggactttg aatttcacat cttaaagcag ttgagctact ttgaatttaa     2366

gcagtcgtac taatcttaaa ttgcatagca tttgttttga tcgaatttgc tgctcaagta    2426

tgggaataat ttttaatgtc ttaatgattg gtgctgctaa cttgcgtgat ttcagaagac    2486

ataattgtga atacacactg tcagaattgg gggattggtt tttaccctag acttcactct    2546

taaaaagcaa cgtgcaatca agatcattta tggctcaaat gaaagcatat aaggttttct    2606

tgaagttgtg ccaaagcatt ctgtagagta ggatgagatg gttgttgccc tagtctgttg    2666
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gtagaaccag aaatcaatat gttgtctttt aggttaaagc ttgtaccaaa atatttattt   2726

cccccatttc aagccctgag tcaaacattt ttttctctta ataatagacc tgaaatgttt   2786

tattagtatt tctgtgaaat cagttgattc ttgtgccatt tttgtatatg taattgtaat   2846

tttgcccatg ttaggccctc taaaaaatgt ttgacatcct ttgagatatt ttattactaa   2906

aatctgatct tttttggcta ctgcaaaaat ctattcagca agaaggtatc agctgcatac   2966

cttgcacagt ggagctgact acctataaac tctccctaag gcatttgttt acaggtgtat   3026

tccattttag cagacgttct gatgctcagt gtatgtgctg catacaaata aatgtgttct   3086

gaatcttttc atcttattga tagcattttt acaaatgtgt ttccaaggaa taaagattat   3146

tcttgcttta aaaaaaaaaa aa                                             3168



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     <213> Homo sapiens

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     <222> (247)..(1677)

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tagaggagaa gtcgaggtta gagggaactg ggaggcactt tgctgtctgc aatcgaagtt    120

gagaggccca gtatttaggc gacagtgaat ttattactct gaagagggtt ctgcacatat    180

ttccaaatta tattggtggt catcagaagt aggtgatagg aagaaatact tctcaagggt    240

gcaaaa   atg cag agt aat aaa act ttt aac ttg gag aag caa aac cat      288
         Met Gln Ser Asn Lys Thr Phe Asn Leu Glu Lys Gln Asn His
           1               5                  10

act cca aga aag cat cat caa cat cac cac cag cag cag cac cac cag      336
Thr Pro Arg Lys His His Gln His His His Gln Gln Gln His His Gln
 15                  20                  25                  30

cag caa cag cag cag ccg cca cca ccg cca ata cct gca aat ggg caa      384
Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Ile Pro Ala Asn Gly Gln
                 35                  40                  45

cag gcc agc agc caa agt gtg tat atg cta gat gaa ggc ttg act att      432
Gln Ala Ser Ser Gln Ser Val Tyr Met Leu Asp Glu Gly Leu Thr Ile
             50                  55                  60

gac ctg aag aat ttt aga aaa cca gga gag aag acc ttc acc caa cga      480
Asp Leu Lys Asn Phe Arg Lys Pro Gly Glu Lys Thr Phe Thr Gln Arg
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        65                  70                  75

agc cgt ctt ttt gtg gga aat ctt cct ccc gac atc act gag gaa gaa      528
Ser Arg Leu Phe Val Gly Asn Leu Pro Pro Asp Ile Thr Glu Glu Glu
    80                  85                  90

atg agg aaa cta ttt gag aaa tat gga aag gca ggc gaa gtc ttc att      576
Met Arg Lys Leu Phe Glu Lys Tyr Gly Lys Ala Gly Glu Val Phe Ile
 95                 100                 105                 110

cat aag gat aaa gga ttt ggc ttt atc cgc ttg gaa acc cga acc cta      624
His Lys Asp Lys Gly Phe Gly Phe Ile Arg Leu Glu Thr Arg Thr Leu
                115                 120                 125

gcg gag att gcc aaa gtg gag ctg gac aat atg cca ctc cgt gga aag      672
Ala Glu Ile Ala Lys Val Glu Leu Asp Asn Met Pro Leu Arg Gly Lys
            130                 135                 140

cag ctg cgt gtg cgc ttt gcc tgc cat agt gca tcc ctt aca gtt cga      720
Gln Leu Arg Val Arg Phe Ala Cys His Ser Ala Ser Leu Thr Val Arg
        145                 150                 155

aac ctt cct cag tat gtg tcc aac gaa ctg ctg gaa gaa gcc ttt tct      768
Asn Leu Pro Gln Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser
    160                 165                 170

gtg ttt ggc cag gta gag agg gct gta gtc att gtg gat gat cga gga      816
Val Phe Gly Gln Val Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly
175                 180                 185                 190

agg ccc tca gga aaa ggc att gtt gag ttc tca ggg aag cca gct gct      864
Arg Pro Ser Gly Lys Gly Ile Val Glu Phe Ser Gly Lys Pro Ala Ala
                195                 200                 205

cgg aaa gct ctg gac aga tgc agt gaa ggc tcc ttc ctg cta acc aca      912
Arg Lys Ala Leu Asp Arg Cys Ser Glu Gly Ser Phe Leu Leu Thr Thr
            210                 215                 220

ttt cct cgt cct gtg act gtg gag ccc atg gac cag tta gat gat gaa      960
Phe Pro Arg Pro Val Thr Val Glu Pro Met Asp Gln Leu Asp Asp Glu
        225                 230                 235

gag gga ctt cca gag aag ctg gtt ata aaa aac cag caa ttt cac aag     1008
Glu Gly Leu Pro Glu Lys Leu Val Ile Lys Asn Gln Gln Phe His Lys
    240                 245                 250

gaa cga gag cag cca ccc aga ttt gca cag cct ggc tcc ttt gag tat     1056
Glu Arg Glu Gln Pro Pro Arg Phe Ala Gln Pro Gly Ser Phe Glu Tyr
255                 260                 265                 270

gaa tat gcc atg cgc tgg aag gca ctc att gag atg gag aag cag cag     1104
Glu Tyr Ala Met Arg Trp Lys Ala Leu Ile Glu Met Glu Lys Gln Gln
                275                 280                 285

cag gac caa gtg gac cgc aac atc aag gag gct cgt gag aag ctg gag     1152
Gln Asp Gln Val Asp Arg Asn Ile Lys Glu Ala Arg Glu Lys Leu Glu
            290                 295                 300
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atg gag atg gaa gct gca cgc cat gag cac cag gtc atg cta atg aga       1200
Met Glu Met Glu Ala Ala Arg His Glu His Gln Val Met Leu Met Arg
        305                 310                 315

cag gat ttg atg agg cgc caa gaa gaa ctt cgg agg atg gaa gag ctg       1248
Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu
    320                 325                 330

cac aac caa gag gtg caa aaa cga aag caa ctg gag ctc agg cag gag       1296
His Asn Gln Glu Val Gln Lys Arg Lys Gln Leu Glu Leu Arg Gln Glu
335                 340                 345                 350

gaa gag cgc agg cgc cgt gaa gaa gag atg cgg cgg cag caa gaa gaa       1344
Glu Glu Arg Arg Arg Arg Glu Glu Glu Met Arg Arg Gln Gln Glu Glu
                355                 360                 365

atg atg cgg cga cag cag gaa gga ttc aag gga acc ttc cct gat gcg       1392
Met Met Arg Arg Gln Gln Glu Gly Phe Lys Gly Thr Phe Pro Asp Ala
            370                 375                 380

aga gag cag gag att cgg atg ggt cag atg gct atg gga ggt gct atg       1440
Arg Glu Gln Glu Ile Arg Met Gly Gln Met Ala Met Gly Gly Ala Met
        385                 390                 395

ggc ata aac aac aga ggt gcc atg ccc cct gct cct gtg cca gct ggt       1488
Gly Ile Asn Asn Arg Gly Ala Met Pro Pro Ala Pro Val Pro Ala Gly
    400                 405                 410

acc cca gct cct cca gga cct gcc act atg atg ccg gat gga act ttg       1536
Thr Pro Ala Pro Pro Gly Pro Ala Thr Met Met Pro Asp Gly Thr Leu
415                 420                 425                 430

gga ttg acc cca cca aca act gaa cgc ttt ggt cag gct gct aca atg       1584
Gly Leu Thr Pro Pro Thr Thr Glu Arg Phe Gly Gln Ala Ala Thr Met
                435                 440                 445

gaa gga att ggg gca att ggt gga act cct cct gca ttc aac cgt gca       1632
Glu Gly Ile Gly Ala Ile Gly Gly Thr Pro Pro Ala Phe Asn Arg Ala
            450                 455                 460

gct cct gga gct gaa ttt gcc cca aac aaa cgt cgc cga tac taa taa       1680
Ala Pro Gly Ala Glu Phe Ala Pro Asn Lys Arg Arg Arg Tyr  *
        465                 470                 475

gttgcagtgt ctagtttctc aaaaccctta aaagaaggac cctttttgga ctagccagaa     1740

ttctaccctg gaaaagtgtt agggattcct tccaatagtt agatctaccc tgcctgtact     1800

actctaggga gtatgctgga ggcagagggc aagggagggg tggtattaaa caagtcaatt     1860

ctgaaaaaaa aaaaa                                                      1875


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<213> Homo sapiens

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<222> (54)..(686)

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                                                             Met
                                                              1

gga ggt ctg ccc agc aga aga aaa tct ctg cca agc cca agc ttg agt      104
Gly Gly Leu Pro Ser Arg Arg Lys Ser Leu Pro Ser Pro Ser Leu Ser
            5                   10                  15

tcc tct gtc caa ggc cag gga cct gtg acc atg gaa gca gag aga agc      152
Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg Ser
        20                  25                  30

aag gcc aca gcc gtg gcc ctg ggc agt ttc ccg gca ggt ggc ccg gcc      200
Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro Ala
    35                  40                  45

gag ctg tcg ctg aga ctc ggg gag cca ttg acc atc gtc tct gag gat      248
Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu Asp
 50                  55                  60                  65

gga gac tgg tgg acg gtg ctg tct gaa gtc tca ggc aga gag tat aac      296
Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr Asn
                70                  75                  80

atc ccc agc gtc cac gtg gcc aaa gtc tcc cat ggg tgg ctg tat gag      344
Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr Glu
            85                  90                  95

ggc ctg agc agg gag aaa gca gag gaa ctg ctg ttg tta cct ggg aac      392
Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Leu Pro Gly Asn
        100                 105                 110

cct gga ggg gcc ttc ctc atc cgg gag agc cag acc agg aga ggc tct      440
Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly Ser
    115                 120                 125

tac tct ctg tca gtc cgc ctc agc cgc cct gca tcc tgg gac cgg atc      488
Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg Ile
130                 135                 140                 145

aga cac tac agg atc cac tgc ctt gac aat ggc tgg ctg tac atc tca      536
Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile Ser
                150                 155                 160

ccg cgc ctc acc ttc ccc tca ctc cag gcc ctg ggg gac cat tac tct      584
Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Gly Asp His Tyr Ser
            165                 170                 175
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gag ggc tgg ccc gct ccc tgg caa gga tat acc cct acc tgt gac tgt      632
Glu Gly Trp Pro Ala Pro Trp Gln Gly Tyr Thr Pro Thr Cys Asp Cys
        180                 185                 190

gca gag gac acc act caa ctg gaa aga gct gga cag ctc cct cct gtt      680
Ala Glu Asp Thr Thr Gln Leu Glu Arg Ala Gly Gln Leu Pro Pro Val
    195                 200                 205

ttc tga agctgccaca ggggaggagt ctcttctcag tgagggtctc cgggagtccc       736
Phe  *
210

tcagcttcta catcagcctg aatgacgagg ctgtctcttt ggatgatgcc taggcccaaa    796

ggagaggcca aaagggaaac caaggctgca cacctagaac cccaattcag cctcctgggc    856

accccagagg caaggctgtg cactcaggga gggagggtgg gacacagagg tgcatctagg    916

gtcccacctg tacccttgct ctttcctctc ttagccctta gaagtcacct acttccttcc    976

agtgccatga tcccacctgc gacctctagt gcgagtgcag agaaggtggg accagggcca   1036

gggttccaaa aagagaataa gcctcctggg gggtctgacc tagttagttc ttgagtttgg   1096

ggtttccagt accatctgga tgccctgcct gttgagcccc attctacatc cccaccatta   1156

accaggcccc acccacaagg tagaaacaac ccctagagtc aacgagaaag tcattttcag   1216

aaaatctaca agtctcgttg agaccaccac catacctcag aaggtaggac tgtggcctag   1276

aagggaaagg aaagctgaga tgatgtctta ccgtagcagc agatcttgga tggtccaggc   1336

tctatgtgac ctccagagca aagagaaaga cttcggacag tctaggtcct caaatgtccc   1396

ccattgagga caacagc                                                   1413


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      <211> 2554
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (164)..(2323)

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tgcgcacagc tccgcccacc cctccctgcc tccttttctt cctcagcggg tccgcggccc     120

gctactctcc gggaggggcg cttcccgacg ccaagacaaa agg  atg cca cgg aga      175
                                                 Met Pro Arg Arg
                                                  1
```

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aag aaa aaa gtt aaa gaa gtc tcc gaa tct cgg aac ctg gag aag aag       223
Lys Lys Lys Val Lys Glu Val Ser Glu Ser Arg Asn Leu Glu Lys Lys
 5                   10                  15                  20

gat gtg gaa act acc agt tct gtc agt gtg aag agg aag cgt aga ctt       271
Asp Val Glu Thr Thr Ser Ser Val Ser Val Lys Arg Lys Arg Arg Leu
                 25                  30                  35

gag gat gca ttc att gtg ata tcc gat agt gat gga gag gaa cca aag       319
Glu Asp Ala Phe Ile Val Ile Ser Asp Ser Asp Gly Glu Glu Pro Lys
             40                  45                  50

gag gaa aat ggg ttg cag aaa acg aag aca aaa cag tcg aat aga gca       367
Glu Glu Asn Gly Leu Gln Lys Thr Lys Thr Lys Gln Ser Asn Arg Ala
         55                  60                  65

aag tgt ttg gcc aaa aga aaa att gca cag atg aca gaa gaa gaa cag       415
Lys Cys Leu Ala Lys Arg Lys Ile Ala Gln Met Thr Glu Glu Glu Gln
     70                  75                  80

ttt gct ctg gct ctc aaa atg agt gag cag gaa gct agg gag gtg aac       463
Phe Ala Leu Ala Leu Lys Met Ser Glu Gln Glu Ala Arg Glu Val Asn
 85                  90                  95                 100

agc cag gag gag gaa gaa gag gag ctc ttg agg aaa gcc att gct gaa       511
Ser Gln Glu Glu Glu Glu Glu Glu Leu Leu Arg Lys Ala Ile Ala Glu
                105                 110                 115

agc ctg aat agt tgc cgg cct tct gat gct tcc gct acc aga tct cga       559
Ser Leu Asn Ser Cys Arg Pro Ser Asp Ala Ser Ala Thr Arg Ser Arg
            120                 125                 130

cct ctg gcc act gga ccg tct tcc cag tcc cat caa gag aaa acc aca       607
Pro Leu Ala Thr Gly Pro Ser Ser Gln Ser His Gln Glu Lys Thr Thr
        135                 140                 145

gac tct ggg ctc act gaa ggc ata tgg cag ctg gta cct cca tca ctg       655
Asp Ser Gly Leu Thr Glu Gly Ile Trp Gln Leu Val Pro Pro Ser Leu
    150                 155                 160

ttt aaa ggc tca cat atc agt cag gga aac gag gct gag gaa aga gag       703
Phe Lys Gly Ser His Ile Ser Gln Gly Asn Glu Ala Glu Glu Arg Glu
165                 170                 175                 180

gag cct tgg gac cac act gaa aaa act gaa gag gag ccg gtc tct ggc       751
Glu Pro Trp Asp His Thr Glu Lys Thr Glu Glu Glu Pro Val Ser Gly
                185                 190                 195

agc tca gga agc tgg gac cag tca agc cag cca gtg ttt gag aat gtg       799
Ser Ser Gly Ser Trp Asp Gln Ser Ser Gln Pro Val Phe Glu Asn Val
            200                 205                 210

aac gtt aaa tct ttt gac aga tgt act ggc cac tcg gct gag cac aca       847
Asn Val Lys Ser Phe Asp Arg Cys Thr Gly His Ser Ala Glu His Thr
        215                 220                 225

cag tgt ggg aag cca cag gaa agt act ggg agg ggt tct gct ttt ctc       895
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Gln Cys Gly Lys Pro Gln Glu Ser Thr Gly Arg Gly Ser Ala Phe Leu
    230                 235                 240

aaa gct gtc cag ggt agc ggg gac aca tct agg cac tgt cta cct acc        943
Lys Ala Val Gln Gly Ser Gly Asp Thr Ser Arg His Cys Leu Pro Thr
245                 250                 255                 260

cta gca gat gcc aaa ggt ctc cag gac act ggg ggc act gtg aac tat        991
Leu Ala Asp Ala Lys Gly Leu Gln Asp Thr Gly Gly Thr Val Asn Tyr
                265                 270                 275

ttc tgg ggt att cca ttc tgc cct gat gga gta gac cct aac cag tat       1039
Phe Trp Gly Ile Pro Phe Cys Pro Asp Gly Val Asp Pro Asn Gln Tyr
            280                 285                 290

acc aag gtc att ctc tgc cag ttg gag gtt tat caa aag agc ctg aaa       1087
Thr Lys Val Ile Leu Cys Gln Leu Glu Val Tyr Gln Lys Ser Leu Lys
        295                 300                 305

atg gct cag agg cag ctc ctt aat aaa aaa ggt ttt ggg gaa cca gtg       1135
Met Ala Gln Arg Gln Leu Leu Asn Lys Lys Gly Phe Gly Glu Pro Val
    310                 315                 320

tta cct aga cct ccc tct ctg atc cag aat gaa tgt ggc caa gga gag       1183
Leu Pro Arg Pro Pro Ser Leu Ile Gln Asn Glu Cys Gly Gln Gly Glu
325                 330                 335                 340

cag gct agt gag aaa aat gaa tgc atc tca gaa gat atg gga gat gaa       1231
Gln Ala Ser Glu Lys Asn Glu Cys Ile Ser Glu Asp Met Gly Asp Glu
                345                 350                 355

gac aaa gag gag agg cag gag tct agg gca tct gac tgg cac tca aaa       1279
Asp Lys Glu Glu Arg Gln Glu Ser Arg Ala Ser Asp Trp His Ser Lys
            360                 365                 370

acc aag gat ttc cag gaa agc tca att aaa agc ttg aaa gag aaa ctt       1327
Thr Lys Asp Phe Gln Glu Ser Ser Ile Lys Ser Leu Lys Glu Lys Leu
        375                 380                 385

ttg ttg gag gaa gaa cca aca acc agt cat ggt cag tct tcc caa ggg       1375
Leu Leu Glu Glu Glu Pro Thr Thr Ser His Gly Gln Ser Ser Gln Gly
    390                 395                 400

att gtt gaa gaa act tct gaa gag gga aac tct gta cct gct tca caa       1423
Ile Val Glu Glu Thr Ser Glu Glu Gly Asn Ser Val Pro Ala Ser Gln
405                 410                 415                 420

agt gtt gct gct ttg acc agt aag aga agc tta gtc ctt atg cca gag       1471
Ser Val Ala Ala Leu Thr Ser Lys Arg Ser Leu Val Leu Met Pro Glu
                425                 430                 435

agt tct gca gaa gaa atc act gtt tgt cct gag aca cag cta agt tcc       1519
Ser Ser Ala Glu Glu Ile Thr Val Cys Pro Glu Thr Gln Leu Ser Ser
            440                 445                 450

tct gaa act ttt gac ctt gaa aga gaa gtc tct cca ggt agc aga gat       1567
Ser Glu Thr Phe Asp Leu Glu Arg Glu Val Ser Pro Gly Ser Arg Asp
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            455                 460                 465

atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt ggt aac      1615
Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val Gly Asn
    470                 475                 480

aag gaa gat gct gag aag gaa gta gct att tct acc ttc tca tcc agt      1663
Lys Glu Asp Ala Glu Lys Glu Val Ala Ile Ser Thr Phe Ser Ser Ser
485                 490                 495                 500

aac cag gta tcc tgc ccg cta tgt gac caa tgc ttt cca ccc aca aag      1711
Asn Gln Val Ser Cys Pro Leu Cys Asp Gln Cys Phe Pro Pro Thr Lys
                505                 510                 515

att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa gat aca      1759
Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu Asp Thr
            520                 525                 530

gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac agt ggg      1807
Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp Ser Gly
        535                 540                 545

aca gct gcc cag act tct cta gac att gac aag aat gag aag tgt tac      1855
Thr Ala Ala Gln Thr Ser Leu Asp Ile Asp Lys Asn Glu Lys Cys Tyr
    550                 555                 560

ctc tgt aaa tcc ctg gtc cca ttt aga gag tat cag tgt cat gtg gac      1903
Leu Cys Lys Ser Leu Val Pro Phe Arg Glu Tyr Gln Cys His Val Asp
565                 570                 575                 580

tcc tgt ctc cag ctt gca aag gct gac caa gga gat gga cct gaa ggg      1951
Ser Cys Leu Gln Leu Ala Lys Ala Asp Gln Gly Asp Gly Pro Glu Gly
                585                 590                 595

agt gga aga gca tgt tca act gtg gag ggg aag tgg cag cag agg ctg      1999
Ser Gly Arg Ala Cys Ser Thr Val Glu Gly Lys Trp Gln Gln Arg Leu
            600                 605                 610

aag aac cca aag gaa aaa ggc cac agt gaa ggc cga ctc ctt agt ttc      2047
Lys Asn Pro Lys Glu Lys Gly His Ser Glu Gly Arg Leu Leu Ser Phe
        615                 620                 625

ttg gaa cag tct gag cac aag act tca gat gca gac atc aag tct tca      2095
Leu Glu Gln Ser Glu His Lys Thr Ser Asp Ala Asp Ile Lys Ser Ser
    630                 635                 640

gaa aca gga gcc ttc agg gtg cct tca cca ggg atg gaa gag gca ggc      2143
Glu Thr Gly Ala Phe Arg Val Pro Ser Pro Gly Met Glu Glu Ala Gly
645                 650                 655                 660

tgc agc aga gag atg cag agt tct ttc aca cgt cgt gac tta aat gaa      2191
Cys Ser Arg Glu Met Gln Ser Ser Phe Thr Arg Arg Asp Leu Asn Glu
                665                 670                 675

tct ccc gtc aag tct ttt gtt tcc att tca gaa gcc aca gat tgc tta      2239
Ser Pro Val Lys Ser Phe Val Ser Ile Ser Glu Ala Thr Asp Cys Leu
            680                 685                 690
```

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gtg gac ttt aaa aag caa gtt act gtc cag cca ggt agt cgg aca cgg      2287
Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg Thr Arg
        695                 700                 705

acc aaa gct ggc aga gga aga agg aga aaa ttc tga attt ctagggtcca     2337
Thr Lys Ala Gly Arg Gly Arg Arg Arg Lys Phe  *
    710                 715                 720

aaagttgaca aaaccattag taggaggggt gggccatgtt cattaagcca tagtggtccc   2397

tagttcattg ttgagcaagt tttagccctg cagttttcac caccagcacc tacccagcat   2457

tctggttttt atgtttttta tgatctatgc agacaactgt gtattctgtt ttataacagt   2517

ttgtttgaat ttacttacag ttaaaaaatt taaatat                            2554
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<212> DNA
<213> Homo sapiens

<220>
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accggaccgg aattcccggg tcgacgattc gtcgcgctcc caacgtgtgg cggctcgcga     60

cccccggcaa cccggagaag gtctacagag cggcctgcgc cagcgagtga gtacccgccg    120

cctgcgcaca gctccgccca cccctccctg cctccttttc ttcctcagcg ggtccgcggc    180

ccgctactct ccgggagggg cgcttcccga cgccaagaca aaaggatgcc acggagaaag    240

aaaaaagtta aagaagtctc cgaatctcgg aacctggaga agaaggatgt ggaaactacc    300

agttctgtca gtgtgaagag gaagcgtaga cttgaggatg cattcattgt gatatccgat    360

agtgatggag aggaaccaaa ggaggaaaat gggttgcaga aaacgaagac aaaacagtcg    420

aatagagcaa agtgtttggc caaaagaaaa atcgcacaga tgacagaaga agaacagttt    480

gctctggctc tcaaaatgag tgagcaggaa gctagggagg tgaacagcca ggaggaggaa    540

gaagaggagc tcttgaggaa agccattgct gaaagcctga atagttgccg gccttctg      598
atg ctt ccg cta cca gat ctc gac ctc tgg cca ctg gac cgt ctt ccc      646
Met Leu Pro Leu Pro Asp Leu Asp Leu Trp Pro Leu Asp Arg Leu Pro
  1               5                  10                  15

agt ccc atc aag aga aaa cca cag act ctg ggc tca ctg aag tct tcc      694
Ser Pro Ile Lys Arg Lys Pro Gln Thr Leu Gly Ser Leu Lys Ser Ser
             20                  25                  30
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caa ggg att gtt gaa gaa act tct gaa gag gga aac tct gta cct gct        742
Gln Gly Ile Val Glu Glu Thr Ser Glu Glu Gly Asn Ser Val Pro Ala
         35                  40                  45

tca caa agt gtt gct gct ttg acc agt aag aga agc tta gtc ctt atg        790
Ser Gln Ser Val Ala Ala Leu Thr Ser Lys Arg Ser Leu Val Leu Met
     50                  55                  60

cca gag agt tct gca gaa gaa atc act gtt tgt cct gag acc cag cta        838
Pro Glu Ser Ser Ala Glu Glu Ile Thr Val Cys Pro Glu Thr Gln Leu
 65                  70                  75                  80

agt tcc tct gaa act ttt gac ctt gaa aga gaa gtc tct cca ggt agc        886
Ser Ser Ser Glu Thr Phe Asp Leu Glu Arg Glu Val Ser Pro Gly Ser
                 85                  90                  95

aga gat atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt        934
Arg Asp Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val
            100                 105                 110

ggt aac aag gaa gat gct gag aag gaa gta gct att tct acc ttc tca        982
Gly Asn Lys Glu Asp Ala Glu Lys Glu Val Ala Ile Ser Thr Phe Ser
        115                 120                 125

tcc agt aac cag gta tcc tgc ccg cta tgt gac caa tgc ttt cca ccc       1030
Ser Ser Asn Gln Val Ser Cys Pro Leu Cys Asp Gln Cys Phe Pro Pro
    130                 135                 140

aca aag att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa       1078
Thr Lys Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu
145                 150                 155                 160

gat aca gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac       1126
Asp Thr Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp
                165                 170                 175

agt ggg aca gct gcc cag act tct cta gac att gac aag aat gag aag       1174
Ser Gly Thr Ala Ala Gln Thr Ser Leu Asp Ile Asp Lys Asn Glu Lys
            180                 185                 190

tgt tac ctc tgt aaa tcc ctg gtc cca ttt aga gag tat cag tgt cat       1222
Cys Tyr Leu Cys Lys Ser Leu Val Pro Phe Arg Glu Tyr Gln Cys His
        195                 200                 205

gtg gac tcc tgt ctc cag ctt gca aag gct gac caa gga gat gga cct       1270
Val Asp Ser Cys Leu Gln Leu Ala Lys Ala Asp Gln Gly Asp Gly Pro
    210                 215                 220

gaa ggg agt gga aga gca tgt tca act gtg gag ggg aag tgg cag cag       1318
Glu Gly Ser Gly Arg Ala Cys Ser Thr Val Glu Gly Lys Trp Gln Gln
225                 230                 235                 240

agg ctg aag aac cca aag gaa aaa ggc cac agt gaa ggc cga ctc ctt       1366
Arg Leu Lys Asn Pro Lys Glu Lys Gly His Ser Glu Gly Arg Leu Leu
                245                 250                 255

agt ttc ttg gaa cag tct gag cac aag act tca gat gca gac atc aag       1414
```

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Ser Phe Leu Glu Gln Ser Glu His Lys Thr Ser Asp Ala Asp Ile Lys
            260                 265                 270

tct tca gaa aca gga gcc ttc agg gtg cct tca cca ggg atg gaa gag      1462
Ser Ser Glu Thr Gly Ala Phe Arg Val Pro Ser Pro Gly Met Glu Glu
        275                 280                 285

gca ggc tgc agc aga gag atg cag agt tct ttc aca cgt cgt gac tta      1510
Ala Gly Cys Ser Arg Glu Met Gln Ser Ser Phe Thr Arg Arg Asp Leu
    290                 295                 300

aat gaa tct ccc gtc aag tct ttt gtt tcc att tca gaa gcc aca gat      1558
Asn Glu Ser Pro Val Lys Ser Phe Val Ser Ile Ser Glu Ala Thr Asp
305                 310                 315                 320

tgc tta gtg gac ttt aaa aag caa gtt act gtc cag cca ggt agt cgg      1606
Cys Leu Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg
                325                 330                 335

aca cgg acc aaa gct ggc aga gga aga agg aga aaa ttc tga atttcta      1655
Thr Arg Thr Lys Ala Gly Arg Gly Arg Arg Arg Lys Phe  *
            340                 345                 350

gggtccaaaa gttgacaaaa ccattagtag gaggggtggg ccatgttcat taagccatag    1715

tggtccctag ttcattgttg agcaagtttt agccctgcag ttttcaccac cagcacctac    1775

ccagcattct ggtttttatg ttttttatga tctatgcaga caactgtgta ttctgtttta    1835

taacagtttg tttgaattta cttacagtta aaaaatttaa atat                     1879




    <210> 123
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    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (208)..(663)

    <220>
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    <222> (1)...(2288)
    <223> n = a,t,c or g

    <400> 123
aatagaattc gatcgccgat ngccacgagc aacgatggca agccttatgt cttgggagcc      60

tgttttgcta ggcaaagtta caagtgacct aatgggagct caaatgtgtg tgtgtctctc     120

tgtgtgtttg tgtgtgtgtg tgcactcaag acctctaaca gcctcgaagc ctggggtggc     180

atcccggcct tgccattagc atgcctc    atg cat cat cag atg aca agg aca      231
                                 Met His His Gln Met Thr Arg Thr
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                                    1               5

acc ctc atg acg aag caa cat gaa tta ggg ggc ctc ttg gcc ttg gtc      279
Thr Leu Met Thr Lys Gln His Glu Leu Gly Gly Leu Leu Ala Leu Val
     10                  15                  20

caa aat tgt caa tca gaa atg aac ata aag gac tcc aga gca gtg gga      327
Gln Asn Cys Gln Ser Glu Met Asn Ile Lys Asp Ser Arg Ala Val Gly
 25                  30                  35                  40

ctg tct gtc aaa aga ctc tgt ata tct ttt gtg gat gag ttt tgt gag      375
Leu Ser Val Lys Arg Leu Cys Ile Ser Phe Val Asp Glu Phe Cys Glu
                 45                  50                  55

aga aca gag aga cca ttg tac ctg gca caa ggg ctc ttc atg aaa agg      423
Arg Thr Glu Arg Pro Leu Tyr Leu Ala Gln Gly Leu Phe Met Lys Arg
             60                  65                  70

gag act tac tgg gag gtg caa gac agt ggc att tct cct ctc ctc ttg      471
Glu Thr Tyr Trp Glu Val Gln Asp Ser Gly Ile Ser Pro Leu Leu Leu
         75                  80                  85

ctg ctc agc aca gcc ctg gat tgc agc ccc gag gct gag acc aga caa      519
Leu Leu Ser Thr Ala Leu Asp Cys Ser Pro Glu Ala Glu Thr Arg Gln
     90                  95                 100

agc ccg gga ggc aga aag atg ctc caa gaa cca aca cta tca atg tct      567
Ser Pro Gly Gly Arg Lys Met Leu Gln Glu Pro Thr Leu Ser Met Ser
105                 110                 115                 120

ttg caa atc ctc aca gga ttc ctg tgg gtc cag ctt tgg aac tgg gaa      615
Leu Gln Ile Leu Thr Gly Phe Leu Trp Val Gln Leu Trp Asn Trp Glu
                125                 130                 135

acc ttt ctt cgg atc cgc act cat tcc act gat gcc agc tgc ccc tga      663
Thr Phe Leu Arg Ile Arg Thr His Ser Thr Asp Ala Ser Cys Pro  *
            140                 145                 150

aggatgccag tactgtggtg tgtgagtctc agcagccgcc cacacgctcc taactctgct    723

gcatggcaga tgcctaggtg gaaatagcaa aaacaaggcc caggctgggg ccagggccag    783

aggggaaggc cctggattct cactcatgtg agatcttgaa tctctttctt tgttctgttt    843

gtttagttag tatcatctgg taaaatagtt aaaaaacaac aaaaaactct gtatctgttt    903

ctagcatgtg ctgcattgac tctattaatc acatttcaaa ttcaccctac attcctctcc    963

tcttcactag cctctctgaa ggtgtcctgg ccagccctgg agaagcactg gtgtctgcag   1023

cacccctcag ttcctgtgcc tcagcccaca ggccactgtg ataatggtct gtttagcact   1083

tctgtattta ttgtaagaat gattataatg aagatacaca ctgtaactac aagaaattat   1143

aaatgttttt cacatcaggc tgttcttttt ttttttttgg aggcgaggtt aaagcattac   1203

tatttgcaaa gcactctgta gctccctgtt atggggatag gtaactaatc agaataataa   1263
```

```
tgtcactcgc atccacttct tagaacctgg ctccaaagga aaataagctg atagactcaa   1323

tcactttcct gaggatggag gcctatggca tgtgtggctg caggtcgcga agctgcttaa   1383

tggtgctggg aagcctagag gaattaaata aagaccctgg aggaggtggg atcggagctg   1443

caccttgaac aaatagctca gatttgaaca gatggatgga aaagagggag gtgttcccaa   1503

ccaaggggac atgatacagg gaacaggtcc tatgtctctt tactcctgag agtattaaac   1563

ctagtaggtg ggcagcccct cttggttgcc tgttacctta ttttgaattc tttttgcaaa   1623

acatactatc acccgtccaa ataatctttt gtctaaatcc agacttcaca ttctgactgg   1683

ggcaaaaaga ggcagtccag taaaggttat aaaataggta ccatcattgt ttgccttatt   1743

tagaaaagct tccaattttc actataatca ccctaagcct gagagaggtg aactgttcaa   1803

gggtactttg gctccagtgg gtgacagtac ctggcccagc tttggaattg aaacatttct   1863

gatggtctgt actctgctag aacacaggat gcttctgctc tccctgctct ggcatcctgc   1923

caggtgtcct ggccacgcac aggcatgaag acagccggga agccagagtt cccacgaagc   1983

actcactcct tggacttgct cccaccccac tggggagagc actcctggag caggaaatga   2043

gcatctctca tctccctgaa ttccacatcc actggctgaa tgatcaggga ggcatagcag   2103

tgagagccat aggtcggcag agggaactca ggccctcctt taggatggcc atcacctcat   2163

ctcaatccag ccaaatcaac catctagagc acacaggccg agagaaatgt aataaaatat   2223

aacatgagac acgtatgaaa tttaaacttt ccggtagcca cactagaaaa aggtaaaaaa   2283

aaaaa                                                               2288


      <210> 124
      <211> 1047
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (95)..(934)

      <400> 124
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tttccattta gatcaacaac ttcaagttct tacc    atg gaa aat tcc gag aag     112
                                         Met Glu Asn Ser Glu Lys
                                          1               5

act gaa gtg gtt ctc ctt gct tgt ggt tca ttc aat ccc atc acc aac      160
```

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Thr Glu Val Val Leu Leu Ala Cys Gly Ser Phe Asn Pro Ile Thr Asn
            10                  15                  20

atg cac ctc agg ttg ttt gag ctg gcc aag gac tac atg aat gga aca        208
Met His Leu Arg Leu Phe Glu Leu Ala Lys Asp Tyr Met Asn Gly Thr
        25                  30                  35

gga agg tac aca gtt gtc aaa ggc atc atc tct cct gtt ggt gat gcc        256
Gly Arg Tyr Thr Val Val Lys Gly Ile Ile Ser Pro Val Gly Asp Ala
    40                  45                  50

tac aag aag aaa gga ctc att cct gcc tat cac cgg gtc atc atg gca        304
Tyr Lys Lys Lys Gly Leu Ile Pro Ala Tyr His Arg Val Ile Met Ala
55                  60                  65                  70

gaa ctt gct acc aag aat tct aaa tgg gtg gaa gtt gat aca tgg gaa        352
Glu Leu Ala Thr Lys Asn Ser Lys Trp Val Glu Val Asp Thr Trp Glu
                75                  80                  85

agt ctt cag aag gag tgg aaa gag act ctg aag gtg cta aga cac cat        400
Ser Leu Gln Lys Glu Trp Lys Glu Thr Leu Lys Val Leu Arg His His
            90                  95                  100

caa gag aaa ttg gag gct agt gac tgt gat cac cag cag aac tca cct        448
Gln Glu Lys Leu Glu Ala Ser Asp Cys Asp His Gln Gln Asn Ser Pro
        105                 110                 115

act cta gaa agg cct gga agg aag agg aag tgg act gaa aca caa gat        496
Thr Leu Glu Arg Pro Gly Arg Lys Arg Lys Trp Thr Glu Thr Gln Asp
    120                 125                 130

tct agt caa aag aaa tcc cta gag cca aaa aca aaa gct gtg cca aag        544
Ser Ser Gln Lys Lys Ser Leu Glu Pro Lys Thr Lys Ala Val Pro Lys
135                 140                 145                 150

gtc aag ctg ctg tgt ggg gca gat tta ttg gag tcc ttt gct gtt ccc        592
Val Lys Leu Leu Cys Gly Ala Asp Leu Leu Glu Ser Phe Ala Val Pro
                155                 160                 165

aat ttg tgg aag agt gaa gac atc acc caa atc gtg gcc aac tat ggg        640
Asn Leu Trp Lys Ser Glu Asp Ile Thr Gln Ile Val Ala Asn Tyr Gly
            170                 175                 180

ctc ata tgt gtt act cgg gct gga aat gat gct cag aag ttt atc tat        688
Leu Ile Cys Val Thr Arg Ala Gly Asn Asp Ala Gln Lys Phe Ile Tyr
        185                 190                 195

gaa tcg gat gtg ctg tgg aaa cac cgg agc aac att cac gtg gtg aat        736
Glu Ser Asp Val Leu Trp Lys His Arg Ser Asn Ile His Val Val Asn
    200                 205                 210

gaa tgg atc gct aat gac atc tca tcc aca aaa atc cgg aga gcc ctc        784
Glu Trp Ile Ala Asn Asp Ile Ser Ser Thr Lys Ile Arg Arg Ala Leu
215                 220                 225                 230

aga agg ggc cag agc att cgc tac ttg gta cca gat ctt gtc caa gaa        832
Arg Arg Gly Gln Ser Ile Arg Tyr Leu Val Pro Asp Leu Val Gln Glu
```

```
                235                 240                 245

tac att gaa aag cat aat ttg tac agc tct gag agt gaa gac agg aat       880
Tyr Ile Glu Lys His Asn Leu Tyr Ser Ser Glu Ser Glu Asp Arg Asn
            250                 255                 260

gct ggg gtc atc ctg gcc cct ttg cag aga aac act gca gaa gct aag       928
Ala Gly Val Ile Leu Ala Pro Leu Gln Arg Asn Thr Ala Glu Ala Lys
        265                 270                 275

aca tag gaattctaca gcatgatatt tcagacttcc catttgggga tctgaaacaa        984
Thr  *
    280

tctgggagtt aataactggg gaaagaagtt gtgatctgtt gcctaaacta aagcttaaaa    1044

gtt                                                                   1047




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                                 Met Ala Lys Ile Lys Ala Arg Asp
                                   1               5

ctt cgc ggg aag aag aag gag gag ctg ctg aaa cag ctg gac gac ctg       99
Leu Arg Gly Lys Lys Lys Glu Glu Leu Leu Lys Gln Leu Asp Asp Leu
     10                  15                  20

aag gtg gag ctg tcc cag ctg cgc gtc gcc aaa gtg aca ggc ggt gcg      147
Lys Val Glu Leu Ser Gln Leu Arg Val Ala Lys Val Thr Gly Gly Ala
 25                  30                  35                  40

gcc tcc aag ctc tct aag atc cga gtc gtc cgg aaa tcc att gcc cgt      195
Ala Ser Lys Leu Ser Lys Ile Arg Val Val Arg Lys Ser Ile Ala Arg
                 45                  50                  55

gtt ctc aca gtt att aac cag act cag aaa gaa aac ctc agg aaa ttc      243
Val Leu Thr Val Ile Asn Gln Thr Gln Lys Glu Asn Leu Arg Lys Phe
             60                  65                  70

tac aag ggc aag aag tac aag ccc ctg gac ctg cgg cct aag aag aca      291
Tyr Lys Gly Lys Lys Tyr Lys Pro Leu Asp Leu Arg Pro Lys Lys Thr
         75                  80                  85

cgt gcc atg cgc cgc cgg ctc aac aag cac gag gag aac ctg aag acc      339
Arg Ala Met Arg Arg Arg Leu Asn Lys His Glu Glu Asn Leu Lys Thr
```

```
     90                  95                  100

aag aag cag cag cgg aag gag cgg ctg tac ccg ctg cag aag tac aca       387
Lys Lys Gln Gln Arg Lys Glu Arg Leu Tyr Pro Leu Gln Lys Tyr Thr
105                 110                 115                 120

gtg aac gcc tga acg tcacatgggt tcataaaaga gagctggccg aagagaacaa       442
Val Asn Ala  *


aagaaaagtg tgtatttaat atgcaattct gt                                   474




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tattgatcat tccgcagccc tgcggaccgg acacgtgagg aggtagtgac gccgacactg     120

ccagaacaca ctgctacaag gtcccag    atg gcc acg tct ctg gat ttt aaa      171
                                 Met Ala Thr Ser Leu Asp Phe Lys
                                   1               5

act tat gta gat cag gca tgt aga gct gct gag gag ttt gtc aat att       219
Thr Tyr Val Asp Gln Ala Cys Arg Ala Ala Glu Glu Phe Val Asn Ile
    10                  15                  20

tac tat gag aca atg gat aaa aga aga cgg gca cta acc agg ctg tat       267
Tyr Tyr Glu Thr Met Asp Lys Arg Arg Arg Ala Leu Thr Arg Leu Tyr
 25                 30                  35                  40

ctg gac aag gcc acc tta ata tgg aat gga aat gct gtt tca ggg ctg       315
Leu Asp Lys Ala Thr Leu Ile Trp Asn Gly Asn Ala Val Ser Gly Leu
                45                  50                  55

gat gcc cta aat aat ttt ttt gac aca ttg cct tct agt gag ttc cag       363
Asp Ala Leu Asn Asn Phe Phe Asp Thr Leu Pro Ser Ser Glu Phe Gln
            60                  65                  70

gtc aat atg tta gat tgc caa cca gtt cat gag caa gca act cag tcc       411
Val Asn Met Leu Asp Cys Gln Pro Val His Glu Gln Ala Thr Gln Ser
        75                  80                  85

caa act aca gtt ctt gtt gtg acc agt gga act gtg aag ttt gat gga       459
Gln Thr Thr Val Leu Val Val Thr Ser Gly Thr Val Lys Phe Asp Gly
    90                  95                  100
```

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aac aaa caa cat ttc ttc aac cag aac ttc ctg ctg act gct cag tcc      507
Asn Lys Gln His Phe Phe Asn Gln Asn Phe Leu Leu Thr Ala Gln Ser
105                 110                 115                 120

act ccc aac aat act gtg tgg aag att gca agt gat tgc ttc cgt ttt      555
Thr Pro Asn Asn Thr Val Trp Lys Ile Ala Ser Asp Cys Phe Arg Phe
                125                 130                 135

caa gat tgg tct agt agt taa ag gggcaaaagt ccattctcat ttggtccatt      608
Gln Asp Trp Ser Ser Ser  *
            140

agttccagca attgaaattt atgtgaatta ttttgattgt agaagcacta taatatgtgc    668

tgaaactaaa tttctttaat attttctatt cctgtcagca ccttttctag cagctgccag    728

tttggagcat tgccctctaa gagctttaaa actatttttt tacatgcctt atatacattc    788

cactaatgac attcttataa taatattaaa cacatgatct tggtactaac atactcactg    848

tgaacccagc ctattgcaaa aataaaatct ttttataata ttatctatgg gatgtcagca    908

caatataaca ctctgggaag aagtggagtt ttttggttat taggttaatt ttctagtaaa    968

acacattgcc tgttttcagt taacactggt aatgccattt taatatatgg ctttttcaaa   1028

tcagttcagt gaaaatagta cagatttagg tttacataac tactctgaca tactggaatt   1088

gcatatagag atgttcagtg gtcgtttttc attttaagta atttttgttt tggcattttt   1148

ttgtgtgaag taaattaatc aactagagag gtgcaaaacg ttctcagttg atatctgagt   1208

attgggtgca tttggtggct taaaagcaaa gcttcctaaa aagatttttc ttggcagctc   1268

caggtctata catttaggta atgaatggta gtagaactaa tagctttaac aggagaatag   1328

ggaatgagaa atagaaatcc aaggctgaag ccaaaagtaa ggagggtggc caaatggtaa   1388

actattggta cttgttttct acctcctaaa aatgtagctt atttttagga tttaaatcac   1448

taagtaaata agtatccttg ccaagtgatc atgagtgtca tttttgttct aagactaata   1508

tttttagatc tttttacttc acctcatact tatcaccaat gtatatctcc atttattcaa   1568

taacttactg gggtaaaata acagcaataa acctaacctt ttaacagggt ctaacatgag   1628

agttggagtc aaagccattg ttatcttttg gtgacaccct taaattttaa gtcttccagt   1688

cttccatgtg aactttaggc ccaaagtttc ttatgtatca cacatccccc aaataagtga   1748

ttttttccca gtgctttgta ctgtcaactg cattatcttt aattatttaa aggtagaatt   1808

atttaatttt gtgatttgtt cttccatatg acattgagca aatagatctg tttcaaaata   1868

tgttcccgct atgtggataa ctcttctttt taaaaagaaa atagagaata gcaaatcttc   1928

atgataatcc tcaaaagaac aaaatgctta actttatctc ttaatttcta aaggtaaata   1988
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acctaggttc agcttttgct taaacattaa atatcttttc catttttttaa tgtttgtaag 2048

ctagatatgc cagctttgtt tctacattgc aaccaaaaac tgtttctttt cacttaatta 2108

taaaaccagt aattcattta ctcttgccca aaactataca ctgtatttct gttatagtaa 2168

caaaatagag ttatgtagaa ttgtatggaa ctcaaattta aaccatgctt tcttgtagta 2228

ctgattgaaa cttacacgtt ttattctact catagtgagc ttattcttat tttggattga 2288

ttttccaaaa ccacagcttc agcagcaaca atcagaatgt ccaaatgctg tcctttccct 2348

tacagagaag aacaatggta actaaaagct gcatataact agcaataact acattgaacg 2408

gtgtgcattg ttcatgattg ttgtgtttta agacttgtat ataaactgct ttttccaaac 2468

tctgtataac ttttaaatgg ctggaactac tcgtataagg actagactgt atttttgaca 2528

tgctcctatt tttgtaactt gaaaaaataa aattttgcct tgtgacagat tttaaaaaaa 2588

aaaaaa 2594

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ttgggcaaag gagaaattca gttttcagta gcatcattgg aagtattatg acttgtgctt 180

aaacttttac cagtgcattc ttttgataaa tagaaatagt aacaaaat atg aat ttt 237
Met Asn Phe
1

aaa tat gtg ggg aga tac ata aag aac att gct tat ttg ttc ttg aaa 285
Lys Tyr Val Gly Arg Tyr Ile Lys Asn Ile Ala Tyr Leu Phe Leu Lys
5 10 15

ata aca gtg att caa ata ttt cat tca gat tta cct atg cct aat gaa 333
Ile Thr Val Ile Gln Ile Phe His Ser Asp Leu Pro Met Pro Asn Glu
20 25 30 35

aaa aat gat gca gaa ctt gat tct cca cct tca aag aaa aaa aga tta 381
Lys Asn Asp Ala Glu Leu Asp Ser Pro Pro Ser Lys Lys Lys Arg Leu
40 45 50

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ggt ttt ttc cag act tat gat aca gaa tat tta aaa gtt ggt ttt att       429
Gly Phe Phe Gln Thr Tyr Asp Thr Glu Tyr Leu Lys Val Gly Phe Ile
             55                  60                  65

atc tgt cct gga tca aaa gaa agt tca cca agg cca cag tgt gtc att       477
Ile Cys Pro Gly Ser Lys Glu Ser Ser Pro Arg Pro Gln Cys Val Ile
         70                  75                  80

tgt gga gag atc tta tcc agt gaa aac atg aag cca gca aat ctt tct       525
Cys Gly Glu Ile Leu Ser Ser Glu Asn Met Lys Pro Ala Asn Leu Ser
     85                  90                  95

cat cat ttg aag aca aaa cat tca gaa tta gaa aac aaa cca gta gat       573
His His Leu Lys Thr Lys His Ser Glu Leu Glu Asn Lys Pro Val Asp
100                 105                 110                 115

ttt ttt gaa caa aaa tct tta gaa atg gaa tgt caa aat agt tct tta       621
Phe Phe Glu Gln Lys Ser Leu Glu Met Glu Cys Gln Asn Ser Ser Leu
                120                 125                 130

aaa aag tgt tta cta gtt gaa aag tca ctt gtg aaa gct tct tat tta       669
Lys Lys Cys Leu Leu Val Glu Lys Ser Leu Val Lys Ala Ser Tyr Leu
            135                 140                 145

att gct ttc caa act gct gca agc aag aag cca ttc tcc att gct gaa       717
Ile Ala Phe Gln Thr Ala Ala Ser Lys Lys Pro Phe Ser Ile Ala Glu
        150                 155                 160

gaa tta att aaa cca tat tta gta gaa atg tgt tca gaa gtt ttg ggt       765
Glu Leu Ile Lys Pro Tyr Leu Val Glu Met Cys Ser Glu Val Leu Gly
    165                 170                 175

tca agt gct gga gac aaa atg aaa act att cca ctt tct aat gtt aca       813
Ser Ser Ala Gly Asp Lys Met Lys Thr Ile Pro Leu Ser Asn Val Thr
180                 185                 190                 195

att caa cac agg att gat gaa cta tct gca gac att gaa gac cag ctg       861
Ile Gln His Arg Ile Asp Glu Leu Ser Ala Asp Ile Glu Asp Gln Leu
                200                 205                 210

att caa aag gtc aga gag tca aag tgg ttt gcc ctt cag ata gat gag       909
Ile Gln Lys Val Arg Glu Ser Lys Trp Phe Ala Leu Gln Ile Asp Glu
            215                 220                 225

tca tca gaa atc tca aat atc aca ctt ctt ttg tgc tat att cgt ttc       957
Ser Ser Glu Ile Ser Asn Ile Thr Leu Leu Leu Cys Tyr Ile Arg Phe
        230                 235                 240

att gat tat gat tgt cgt gat gta aaa gaa gaa tta tta ttt tgc att      1005
Ile Asp Tyr Asp Cys Arg Asp Val Lys Glu Glu Leu Leu Phe Cys Ile
    245                 250                 255

gaa atg cct act caa ata act ggc ttt gaa ata ttt gaa cta ata aat      1053
Glu Met Pro Thr Gln Ile Thr Gly Phe Glu Ile Phe Glu Leu Ile Asn
260                 265                 270                 275
```

```
aaa tat att gat agt aaa tct ctg aat tgg aaa cat tgt gtt ggt ctc      1101
Lys Tyr Ile Asp Ser Lys Ser Leu Asn Trp Lys His Cys Val Gly Leu
                280                 285                 290

tgt acc gat ggg gct gca agc atg act ggc agg tat tct ggt tta aaa      1149
Cys Thr Asp Gly Ala Ala Ser Met Thr Gly Arg Tyr Ser Gly Leu Lys
            295                 300                 305

gca aaa att caa gaa gtt gcc atg aat aca gcg gca ttt aca cat tgt      1197
Ala Lys Ile Gln Glu Val Ala Met Asn Thr Ala Ala Phe Thr His Cys
        310                 315                 320

ttt att cac cgt gaa cgt tta gtg gca gaa aag ttg tct cca tgt tta      1245
Phe Ile His Arg Glu Arg Leu Val Ala Glu Lys Leu Ser Pro Cys Leu
    325                 330                 335

cat aaa att ctt ttg cag tca gca caa att tta agt ttt ata aag agc      1293
His Lys Ile Leu Leu Gln Ser Ala Gln Ile Leu Ser Phe Ile Lys Ser
340                 345                 350                 355

aat gca tta aat tca cgt atg tta aca att ttg tgt gaa gag atg gga      1341
Asn Ala Leu Asn Ser Arg Met Leu Thr Ile Leu Cys Glu Glu Met Gly
                360                 365                 370

tct gag cat gtg agt tta ccg ctt cat gct gaa gta cgt tgg ata tca      1389
Ser Glu His Val Ser Leu Pro Leu His Ala Glu Val Arg Trp Ile Ser
            375                 380                 385

aga ggg aga atg tta aaa aga tta ttt gaa tta cga cat gag att gaa      1437
Arg Gly Arg Met Leu Lys Arg Leu Phe Glu Leu Arg His Glu Ile Glu
        390                 395                 400

ata ttt tta agt caa aag cat tca gat ttg gcc aag tat ttt cat gat      1485
Ile Phe Leu Ser Gln Lys His Ser Asp Leu Ala Lys Tyr Phe His Asp
    405                 410                 415

gag gaa tgg gtt gga aag ctg gcc tac tta tca gat ata ttt tca ctt      1533
Glu Glu Trp Val Gly Lys Leu Ala Tyr Leu Ser Asp Ile Phe Ser Leu
420                 425                 430                 435

ata aat gaa tta aat tta agt ctc caa gga act ttg act act ttc ttc      1581
Ile Asn Glu Leu Asn Leu Ser Leu Gln Gly Thr Leu Thr Thr Phe Phe
                440                 445                 450

aat ttg tgt aat aaa att gat gta ttt aag aga aag tta aaa atg tgg      1629
Asn Leu Cys Asn Lys Ile Asp Val Phe Lys Arg Lys Leu Lys Met Trp
            455                 460                 465

ttg aag cgc aca caa gag aat gat tat gac atg ttc cct tca ttt tct      1677
Leu Lys Arg Thr Gln Glu Asn Asp Tyr Asp Met Phe Pro Ser Phe Ser
        470                 475                 480

gaa ttc tca aat tca tca ggc tta aat atg aca gac atc aca agg att      1725
Glu Phe Ser Asn Ser Ser Gly Leu Asn Met Thr Asp Ile Thr Arg Ile
    485                 490                 495

att ttt gag cac ctg gaa gga ctt tct caa gtg ttc agt gac tgt ttt      1773
```

```
Ile Phe Glu His Leu Glu Gly Leu Ser Gln Val Phe Ser Asp Cys Phe
500                 505                 510                 515

cca cca gaa caa gac ttg cgt tca gga aat ttg tgg ata att cac cct      1821
Pro Pro Glu Gln Asp Leu Arg Ser Gly Asn Leu Trp Ile Ile His Pro
                520                 525                 530

ttt atg aat cac caa aat aat aat ctc acc gac ttc gaa gaa gaa aag      1869
Phe Met Asn His Gln Asn Asn Asn Leu Thr Asp Phe Glu Glu Glu Lys
            535                 540                 545

cta aca gag cta tct tca gat tta gga tta caa gca cta ttt aaa tca      1917
Leu Thr Glu Leu Ser Ser Asp Leu Gly Leu Gln Ala Leu Phe Lys Ser
        550                 555                 560

gtg tct gta act cag ttt tgg ata aat gca aag aca agt tac cca gaa      1965
Val Ser Val Thr Gln Phe Trp Ile Asn Ala Lys Thr Ser Tyr Pro Glu
    565                 570                 575

ctc cat gaa agg gca atg aaa ttt tta tta ccc ttt tca act gtt tat      2013
Leu His Glu Arg Ala Met Lys Phe Leu Leu Pro Phe Ser Thr Val Tyr
580                 585                 590                 595

tta tgt gat gct gcc ttt tca gct ttg act gag tca aaa caa aaa aat      2061
Leu Cys Asp Ala Ala Phe Ser Ala Leu Thr Glu Ser Lys Gln Lys Asn
                600                 605                 610

ctg ttg ggt tct ggc cct gcc cta aga ctt gca gtc aca tct tta att      2109
Leu Leu Gly Ser Gly Pro Ala Leu Arg Leu Ala Val Thr Ser Leu Ile
            615                 620                 625

cca agg ata gaa aaa tta gtg aag gag aaa gag tag caat atgcacattg      2159
Pro Arg Ile Glu Lys Leu Val Lys Glu Lys Glu  *
        630                 635

cttaacagtg aagtcaataa tcctgtgtta agttttgtat aagtatccta aaagataatt    2219

tcctaatgtg gatttgtgtt ttcagtgatt aaatgtttta ataatttttc ccttttttgtt   2279

gaggaattta ataattatga ttgttataaa taattatgta taattataat ctagggtaga    2339

aaatttagtt atttcattaa atttggacta gtgacaaaga ctgcaggtaa tgagaagccc    2399

agtttataat gtaacagcac aacctggatg ttgaaacagc ttggccttta gaagcaagtg    2459

gaacatttca gtcttctagc caaccagcta cttaccccctg caaggttgtg agtaggtgga   2519


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aagcccgcac agctccgggt gccaggacgg ggggcc atg ccg tgc cgg agg gag       114
                                        Met Pro Cys Arg Arg Glu
                                        1               5

gag gaa gag gaa gcc ggc gag gag gcg gag ggg gag gaa gag gag gac       162
Glu Glu Glu Glu Ala Gly Glu Glu Ala Glu Gly Glu Glu Glu Glu Asp
            10                  15                  20

gac agc ttc ctc ctg ctg cag cag tcg gtg acg ctg ggc agc tcg ggc       210
Asp Ser Phe Leu Leu Leu Gln Gln Ser Val Thr Leu Gly Ser Ser Gly
        25                  30                  35

gag gtg gac cgg ctg gtg gcc cag atc ggc gag acg ctg cag ctg gac       258
Glu Val Asp Arg Leu Val Ala Gln Ile Gly Glu Thr Leu Gln Leu Asp
    40                  45                  50

gcg gcg cag gac agc ccg gcc tcg ccg tgc gcg ccc ccg ggg gtg ccg       306
Ala Ala Gln Asp Ser Pro Ala Ser Pro Cys Ala Pro Pro Gly Val Pro
55                  60                  65                  70

ctg cgg gcc ccg ggg ccc ctg gct gcg gcg gtg ccg acg gac aag gcc       354
Leu Arg Ala Pro Gly Pro Leu Ala Ala Ala Val Pro Thr Asp Lys Ala
                75                  80                  85

cgg ccc ccg gcg gtg ccg ctg ctg ctg ccg ccc gct tcg gct gag acg       402
Arg Pro Pro Ala Val Pro Leu Leu Leu Pro Pro Ala Ser Ala Glu Thr
            90                  95                  100

gtg ggc ccg gcg ccc tct ggg gcc ctg cgc tgc gcc cta ggg gac cgc       450
Val Gly Pro Ala Pro Ser Gly Ala Leu Arg Cys Ala Leu Gly Asp Arg
        105                 110                 115

ggc cgc gtg cgc gga cgc gct gcg ccc tac tgc gtg gcg gag gtc gcc       498
Gly Arg Val Arg Gly Arg Ala Ala Pro Tyr Cys Val Ala Glu Val Ala
    120                 125                 130

gca ggc ccc agc gcg ctg ccg ggg ccg tgc cgg cga gga tgg ctc agg       546
Ala Gly Pro Ser Ala Leu Pro Gly Pro Cys Arg Arg Gly Trp Leu Arg
135                 140                 145                 150

gac gcg gtc acc tcc cgc cgc ttg cag cag cgc cga tgg acc caa gcc       594
Asp Ala Val Thr Ser Arg Arg Leu Gln Gln Arg Arg Trp Thr Gln Ala
                155                 160                 165

ggg gca cgc gcc ggc gac gac gac ccg cat cgg ctc ctc cag cag ctc       642
Gly Ala Arg Ala Gly Asp Asp Asp Pro His Arg Leu Leu Gln Gln Leu
            170                 175                 180

gtg ctc tcg gga aac ctc atc aag gaa gcc gtg cgg aga ctc caa cga       690
Val Leu Ser Gly Asn Leu Ile Lys Glu Ala Val Arg Arg Leu Gln Arg
        185                 190                 195
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gcc gtc gcc gcg gtt gca gcc acg ggc ccc gca agc gcc cct ggg ccc      738
Ala Val Ala Ala Val Ala Ala Thr Gly Pro Ala Ser Ala Pro Gly Pro
    200                 205                 210

ggg gga ggc cgc agc gga cct gac cgc att gcc ctg cag ccc tca ggc      786
Gly Gly Gly Arg Ser Gly Pro Asp Arg Ile Ala Leu Gln Pro Ser Gly
215                 220                 225                 230

tcc ttg ctc tga cgc aggcctcctg gaggaggaag tggaggccgc tgcgtagacc      841
Ser Leu Leu  *


caacagcgtc cagttcctac taactctgag ctgaagccga cgtcgccagc ctgggagcga    901

ccactttggc tgcggggagg cgcgtgggga gagatctcaa ccagagaagt taccagccgc    961

ggcgaggccg tcggagaaaa cttaagcgtg gagaaatgta tgcgccaggg tgcttccgtg   1021

gggcatgaga atttcccggg ccatccaagc ccaaggacct gggataaact gggagaacta   1081

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tgctgtgcaa agaaattcca gaggggagaa gaatgtaaaa gtttggtggt gggtggcttg   1321

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ttaagggact ggagagaggt gaagaatttt gcaggtggga gatttggatt tgaatgtgga   1441

cttgtaaatg acttgacctt gccatctgtg ttcaaggtca cggtttgctg tggggttcct   1501

gggagagctt actcaccccg gagtcttttc tttctcttgc tccaagaaga gccctgttgg   1561

tgctttacca ccgcttggag tctcccgagg acacaaacag gcagagaggg acgtgtaggg   1621

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ctggacgttt ttctgctctc ttctggccct ccatggagcc atgggcctcg gcctcggcgg   1861

ctcctcaccc tcacaattta tttcctcctc ccgtgccagc ccttcttttg tgtctgaaac   1921

cggttttaaa atgtgactct cccagagaag aagccgctgg ctgtatgaaa cttgacggcg   1981

cttttgtaag gtgccacccc caaactttaa ggtagctaaa ccaattttta aaagattcaa   2041

tggcttgttc atcctccaga tgtagctatt gatgtacact tcgcaacgga gtgtctgaaa   2101

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aaaaa                                                               2166
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                     Met Ala Gly Ser Gly Cys Ala Trp Gly Ala Glu
                      1               5                   10

ccg ccg cgt ttt ctg gag gcc ttc ggg cgg ctg tgg cag gta cag agc          159
Pro Pro Arg Phe Leu Glu Ala Phe Gly Arg Leu Trp Gln Val Gln Ser
             15                  20                  25

cgt ctg ggt agc ggc tcc tcc gcc tcg gtg tat cgg gtt cgc tgc tgc          207
Arg Leu Gly Ser Gly Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys
         30                  35                  40

ggc aac cct ggc tcg ccc ccc ggc gcc ctc aag cag ttc ttg ccg cca          255
Gly Asn Pro Gly Ser Pro Pro Gly Ala Leu Lys Gln Phe Leu Pro Pro
     45                  50                  55

gga acc acc ggg gct gcg gcc tct gcc gcc gag tat ggt ttc cgc aaa          303
Gly Thr Thr Gly Ala Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys
 60                  65                  70                  75

gag agg gcg gcg ctg gaa cag ttg cag ggt cac aga aac atc gtg act          351
Glu Arg Ala Ala Leu Glu Gln Leu Gln Gly His Arg Asn Ile Val Thr
                 80                  85                  90

ttg tat gga gtg ttt aca atc cac ttt tct cca aat gtg cca tca cgc          399
Leu Tyr Gly Val Phe Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg
             95                 100                 105

tgt ctg ttg ctt gaa ctc ctg gat gtc agt gtt tcg gaa ttg ctc tta          447
Cys Leu Leu Leu Glu Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu
        110                 115                 120

tat tcc agt cac cag ggt tgt tcc atg tgg atg ata cag cat tgc gcc          495
Tyr Ser Ser His Gln Gly Cys Ser Met Trp Met Ile Gln His Cys Ala
    125                 130                 135

cga gat gtt ttg gag gcc ctt gct ttt ctt cat cat gag ggc tat gtc          543
Arg Asp Val Leu Glu Ala Leu Ala Phe Leu His His Glu Gly Tyr Val
140                 145                 150                 155

cat gcg gac ctc aaa cca cgt aac ata ttg tgg agt gca gag aat gaa          591
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His Ala Asp Leu Lys Pro Arg Asn Ile Leu Trp Ser Ala Glu Asn Glu
                160                 165                 170

tgt ttt aaa ctc att gac ttt gga ctt agc ttc aaa gaa ggc aat cag        639
Cys Phe Lys Leu Ile Asp Phe Gly Leu Ser Phe Lys Glu Gly Asn Gln
            175                 180                 185

gat gta aag tat att cag aca gac ggg tat cgg gct cca gaa gca gaa        687
Asp Val Lys Tyr Ile Gln Thr Asp Gly Tyr Arg Ala Pro Glu Ala Glu
        190                 195                 200

ttg caa aat tgc ttg gcc cag gct ggc ctg cag agt gat aca gaa tgt        735
Leu Gln Asn Cys Leu Ala Gln Ala Gly Leu Gln Ser Asp Thr Glu Cys
    205                 210                 215

acc tca gct gtt gat ctg tgg agc cta gga atc att tta ctg gaa atg        783
Thr Ser Ala Val Asp Leu Trp Ser Leu Gly Ile Ile Leu Leu Glu Met
220                 225                 230                 235

ttc tca gga atg aaa ctg aaa cat aca gtc aga tct cag gaa tgg aag        831
Phe Ser Gly Met Lys Leu Lys His Thr Val Arg Ser Gln Glu Trp Lys
                240                 245                 250

gca aac agt tct gct att att gat cac ata ttt gcc agt aaa gca gtg        879
Ala Asn Ser Ser Ala Ile Ile Asp His Ile Phe Ala Ser Lys Ala Val
            255                 260                 265

gtg aat gcc gca att cca gcc tat cac cta aga gac ctt atc aaa agc        927
Val Asn Ala Ala Ile Pro Ala Tyr His Leu Arg Asp Leu Ile Lys Ser
        270                 275                 280

atg ctt cat gat gat cca agc aga aga att cct gct gaa atg gca ttg        975
Met Leu His Asp Asp Pro Ser Arg Arg Ile Pro Ala Glu Met Ala Leu
    285                 290                 295

tgc agc cca ttc ttt agc att cct ttt gcc cct cat att gaa gat ctg       1023
Cys Ser Pro Phe Phe Ser Ile Pro Phe Ala Pro His Ile Glu Asp Leu
300                 305                 310                 315

gtc atg ctt ccc act cca gtg cta aga ctg ctg aat gtg ctg gat gat       1071
Val Met Leu Pro Thr Pro Val Leu Arg Leu Leu Asn Val Leu Asp Asp
                320                 325                 330

gat tat ctt gag aat gaa gag gaa tat gaa gat gtt gta gaa gat gta       1119
Asp Tyr Leu Glu Asn Glu Glu Glu Tyr Glu Asp Val Val Glu Asp Val
            335                 340                 345

aaa gag gag tgt caa aaa tat gga cca gtg gta tct cta ctt gtt cca       1167
Lys Glu Glu Cys Gln Lys Tyr Gly Pro Val Val Ser Leu Leu Val Pro
        350                 355                 360

aag gaa aat cct ggc aga gga caa gtc ttt gtt gag tat gca aat gct       1215
Lys Glu Asn Pro Gly Arg Gly Gln Val Phe Val Glu Tyr Ala Asn Ala
    365                 370                 375

ggt gat tcc aaa gct gcg cag aaa tta ctg act gga agg atg ttt gat       1263
Gly Asp Ser Lys Ala Ala Gln Lys Leu Leu Thr Gly Arg Met Phe Asp
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380                 385                 390                 395

ggg aag ttt gtt gtg gct aca ttc tac ccg ctg agt gcc tac aag agg     1311
Gly Lys Phe Val Val Ala Thr Phe Tyr Pro Leu Ser Ala Tyr Lys Arg
                400                 405                 410

gga tat ctg tat caa acc ttg ctt taa tcagt aacctaagga ctgtttcctt     1363
Gly Tyr Leu Tyr Gln Thr Leu Leu  *
            415                 420

tttctcctct tccatttctt gggttattcc acatatgaat gcaggactac ccccttacca   1423

ttttaagaag gtactttata catttattta atcctactaa tgtgcagcca ttgcccaagc   1483

agtgactgcg ttgcatacat ttggcactga gtaggacaag acctctcagc tatacattga   1543

ggggttttag agcatccatg tgggcaaccc ttttttgtgc gggagagcag gtgttgctct   1603

tcagtatgta gcctaaaaaa atcttaatta tttcatggat catgaagcaa ggatgaataa   1663

tatcatgtct tggtaaatac taacaaattt gttaggtttg gtgacatcat ttacagatta   1723

tttctttatg ttgtccagtg gttcttcctt attgttgata tccataagct ggcactggat   1783

gctctcagta atgttaagta attgtcaagc agcagttacc tactgtgttc ttaacactga   1843

gttgtgaatt ttttcttaaa gcagtactgt agtactgaat attcctttac aggaactgca   1903

gtgagcctat ctaagtcttt gcctactaag gcttcctatg ggagaaaagt catgcttgac   1963

cttgcaccct tttcatcact gctctctacg cccgagggaa ggccc                   2008




     <210> 130
     <211> 1313
     <212> DNA
     <213> Homo sapiens

     <220>
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     <222> (316)..(1257)

     <400> 130
cgcctgcgta cgtaagcttg gatcctctag agcggccgct gtcgttgttc tgaggtggct     60

catgcctgta aacgtaacat ttggggaggc caaggctggg ggatcactta aggccaggat    120

ttcaagacca gcctgggcaa cacagcaaga cccccatatc tctaccaaaa aaacaaaaca    180

aaacaaaaca aacaaacaaa aaaaacagcc ggttgcggtg gcacatgctt gcagtcctcg    240

ttactcaaga agcagaagca agaggattgc ttgagcccaa cagtgcttgc aaaagacaaa    300

gaacgcctgc aagcc atg atg acc cac ctg cat gtg aag tct aca gaa ccc    351
                 Met Met Thr His Leu His Val Lys Ser Thr Glu Pro
```

```
                  1               5                  10

aaa gcc gcc cct cag ccc ttg aat ctg gta tca agt gtc act ctc tcc        399
Lys Ala Ala Pro Gln Pro Leu Asn Leu Val Ser Ser Val Thr Leu Ser
         15                  20                  25

aag tcc gca tcg gag gct tct cca cag agc tta cct cat act cca acg        447
Lys Ser Ala Ser Glu Ala Ser Pro Gln Ser Leu Pro His Thr Pro Thr
     30                  35                  40

acc cca acc gcc ccc ctg act ccc gtc acc caa ggc ccc tct gtc atc        495
Thr Pro Thr Ala Pro Leu Thr Pro Val Thr Gln Gly Pro Ser Val Ile
 45                  50                  55                  60

aca acc acc agc atg cac acg gtg gga ccc atc cgc agg cgg tac tca        543
Thr Thr Thr Ser Met His Thr Val Gly Pro Ile Arg Arg Arg Tyr Ser
                 65                  70                  75

gac aaa tac aac gtg ccc att tcg tca gca gat att gcg cag aac caa        591
Asp Lys Tyr Asn Val Pro Ile Ser Ser Ala Asp Ile Ala Gln Asn Gln
             80                  85                  90

gaa ttt tat aag aac gca gaa gtt aga cca cca ttt aca tat gca tct        639
Glu Phe Tyr Lys Asn Ala Glu Val Arg Pro Pro Phe Thr Tyr Ala Ser
         95                 100                 105

tta att agg cag gcc att ctc gaa tct cca gaa aag cag cta aca cta        687
Leu Ile Arg Gln Ala Ile Leu Glu Ser Pro Glu Lys Gln Leu Thr Leu
    110                 115                 120

aat gag atc tat aac tgg ttc aca cga atg ttt gct tac ttc cga cgc        735
Asn Glu Ile Tyr Asn Trp Phe Thr Arg Met Phe Ala Tyr Phe Arg Arg
125                 130                 135                 140

aac gcg gcc acg tgg aag aat gca gtg cgt cat aat ctt agt ctt cac        783
Asn Ala Ala Thr Trp Lys Asn Ala Val Arg His Asn Leu Ser Leu His
                145                 150                 155

aag tgt ttt gtg cga gta gaa aac gtt aaa ggg gca gta tgg aca gtg        831
Lys Cys Phe Val Arg Val Glu Asn Val Lys Gly Ala Val Trp Thr Val
            160                 165                 170

gat gaa gta gaa ttc caa aaa cga agg cca caa aag atc agt ggt aac        879
Asp Glu Val Glu Phe Gln Lys Arg Arg Pro Gln Lys Ile Ser Gly Asn
        175                 180                 185

cct tcc ctt att aaa aac atg cag agc agc cac gcc tac tgc aca cct        927
Pro Ser Leu Ile Lys Asn Met Gln Ser Ser His Ala Tyr Cys Thr Pro
    190                 195                 200

ctc aat gca gct tta cag gct tca atg gct gag aat agt ata cct cta        975
Leu Asn Ala Ala Leu Gln Ala Ser Met Ala Glu Asn Ser Ile Pro Leu
205                 210                 215                 220

tac act acc gct tcc atg gga aat ccc act ctg ggc aac tta gcc agc       1023
Tyr Thr Thr Ala Ser Met Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser
                225                 230                 235
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gca ata cgg gaa gag ctg aac ggg gca atg gag cat acc aac agc aac      1071
Ala Ile Arg Glu Glu Leu Asn Gly Ala Met Glu His Thr Asn Ser Asn
            240                 245                 250

gag agt gac agc agt cca ggc aga tct cct atg caa gcc gtg cat cct      1119
Glu Ser Asp Ser Ser Pro Gly Arg Ser Pro Met Gln Ala Val His Pro
        255                 260                 265

gta cac gtc aaa gaa gag ccc ctc gat cca gag gaa gct gaa ggg ccc      1167
Val His Val Lys Glu Glu Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro
    270                 275                 280

ctg tcc tta gtg aca aca gcc aac cac agt cca gat ttt gac cat gac      1215
Leu Ser Leu Val Thr Thr Ala Asn His Ser Pro Asp Phe Asp His Asp
285                 290                 295                 300

aga gat tac gaa gat gaa cca gta aac gag gac atg gag tga ctatcgg      1264
Arg Asp Tyr Glu Asp Glu Pro Val Asn Glu Asp Met Glu  *
                305                 310

ggcgggccaa ccccgagaat gaagattgga aaaaggaaaa aaaaaaaaa                1313



     <210> 131
     <211> 847
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (91)..(657)

     <400> 131
gcacgagcag ggacggaccc tcattcctcc cagggacccc agacctctgt ctctctcggc      60

aggccttggc tccttgaact tttggccgcc     atg tgc ttc ccg aag gtc ctc      111
                                     Met Cys Phe Pro Lys Val Leu
                                      1               5

tct gat gac atg aag aag ctg aag gcc cga atg cac cag gcc ata gaa      159
Ser Asp Asp Met Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu
         10                  15                  20

aga ttt tat gat aaa atg caa aat gca gaa tca gga cgt gga cag gtg      207
Arg Phe Tyr Asp Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val
     25                  30                  35

atg tcg agc ctg gca gag ctg gag gac gac ttc aaa gag ggc tac ctg      255
Met Ser Ser Leu Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu
 40                  45                  50                  55

gag aca gtg gcg gct tat tat gag gag cag cac cca gag ctc act cct      303
Glu Thr Val Ala Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro
                 60                  65                  70
```

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cta ctt gaa aaa gaa aga gat gga tta cgg tgc cga ggc aac aga tcc      351
Leu Leu Glu Lys Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser
             75                  80                  85

cct gtc ccg gat gtt gag gat ccc gca acc gag gag cct ggg gag agc      399
Pro Val Pro Asp Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser
         90                  95                 100

ttt tgt gac aag gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg      447
Phe Cys Asp Lys Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu
    105                 110                 115

cag acc tgg tgg cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg      495
Gln Thr Trp Trp His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val
120                 125                 130                 135

gcc ctg gtc cat gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc      543
Ala Leu Val His Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe
                140                 145                 150

tgc tgc tct ctg tca gag ctc ttc atg tcc tct ttc cag tcc tac gga      591
Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly
            155                 160                 165

gcc cca cgg ggg gac aag gag gag ctg aca ccc cag aag tgc tct gaa      639
Ala Pro Arg Gly Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu
        170                 175                 180

ccc caa tcc tca aaa tga agatac tgacaccacc tttgccctcc ccgtcaccgc      693
Pro Gln Ser Ser Lys  *
    185

gcacccaccc tgacccctcc ctcagctgtc ctgtgccccg ccctctcccg cacactcagt    753

ccccctgcct ggcgttcctg ccgcagctct gacctggtcg tgtcgccctg gcatcttaat    813

aaaacctgct tatacttccc tgaaaaaaaa aaaa                                847



      <210> 132
      <211> 526
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (33)..(419)

      <400> 132
aaggtgttct actgctagag cctatcgaaa cg  atg cct aaa tca aag gaa ctt       53
                                     Met Pro Lys Ser Lys Glu Leu
                                       1               5

gtt tct tca agc tct tct ggc agt gat tct gac agt gag gtt gac aaa      101
```

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Val Ser Ser Ser Ser Ser Gly Ser Asp Ser Asp Ser Glu Val Asp Lys
        10                  15                  20

aag tta aag agg aaa aag caa gtt gct cca gaa aaa cct gta aag aaa      149
Lys Leu Lys Arg Lys Lys Gln Val Ala Pro Glu Lys Pro Val Lys Lys
    25                  30                  35

caa aag aca ggt gag act tcg aga gcc ctg tca tct tct aaa cag agc      197
Gln Lys Thr Gly Glu Thr Ser Arg Ala Leu Ser Ser Ser Lys Gln Ser
40                  45                  50                  55

agc agc agc aga gat gat aac atg ttt cag att ggg aaa atg agg tac      245
Ser Ser Ser Arg Asp Asp Asn Met Phe Gln Ile Gly Lys Met Arg Tyr
                60                  65                  70

gtt agt gtt cgc gat ttt aaa ggc aaa gtg cta att gat att aga gaa      293
Val Ser Val Arg Asp Phe Lys Gly Lys Val Leu Ile Asp Ile Arg Glu
            75                  80                  85

tat tgg atg gat cct gaa ggt gaa atg aaa cca gga aga aaa ggt att      341
Tyr Trp Met Asp Pro Glu Gly Glu Met Lys Pro Gly Arg Lys Gly Ile
        90                  95                  100

tct tta aat cca gaa caa tgg atc cag tcc agc aga aaa gat atg atg      389
Ser Leu Asn Pro Glu Gln Trp Ile Gln Ser Ser Arg Lys Asp Met Met
    105                 110                 115

aca ttg atg aag cac gtg agc ggt ctg taa t aatgcgagcc agattaattt      440
Thr Leu Met Lys His Val Ser Gly Leu  *
120                 125

atcctgtact gttagatttg gggtaatctg tcttatcaca aaggatgttg acttctagat    500

gttctccaga ttatgtatat tgtgat                                         526



    <210> 133
    <211> 1884
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (157)..(864)

    <400> 133
acagaaagaa acgcagctct tgacttcttt tttgtaaaca ttactgtaag agttgtgata     60

actttttatt ctactatgta tatgtatgga atagtattaa taaatgaact agggaaggat    120

gtaataaatt agacatctct tcattttaga gagaag atg gaa aca aca ttg ctt      174
                                        Met Glu Thr Thr Leu Leu
                                         1               5

ttc ttt tct caa ata aat atg tgt gaa tca aaa gaa aaa act ttt ttc      222
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```
Phe Phe Ser Gln Ile Asn Met Cys Glu Ser Lys Glu Lys Thr Phe Phe
             10                  15                  20

aag tta ata cat ggt tca gga aaa gaa gaa aca agc aaa gaa gcc aaa       270
Lys Leu Ile His Gly Ser Gly Lys Glu Glu Thr Ser Lys Glu Ala Lys
         25                  30                  35

atc aga gct aag gaa aaa aga aat aga cta agt ctt ctt gtg cag aaa       318
Ile Arg Ala Lys Glu Lys Arg Asn Arg Leu Ser Leu Leu Val Gln Lys
     40                  45                  50

cct gag ttt cat gaa gac acc cgc tcc agt aga tct ggg cac ttg gcc       366
Pro Glu Phe His Glu Asp Thr Arg Ser Ser Arg Ser Gly His Leu Ala
 55                  60                  65                  70

aaa gaa aca aga gtc tcc cct gaa gag gca gtg aaa tgg ggt gaa tca       414
Lys Glu Thr Arg Val Ser Pro Glu Glu Ala Val Lys Trp Gly Glu Ser
                 75                  80                  85

ttt gac aaa ctg ctt tcc cat aga gat gga cta gag gct ttt acc aga       462
Phe Asp Lys Leu Leu Ser His Arg Asp Gly Leu Glu Ala Phe Thr Arg
             90                  95                 100

ttt ctt aaa act gaa ttc agt gaa gaa aat att gaa ttt tgg ata gcc       510
Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn Ile Glu Phe Trp Ile Ala
        105                 110                 115

tgt gaa gat ttc aag aaa agc aag gga cct caa caa att cac ctt aaa       558
Cys Glu Asp Phe Lys Lys Ser Lys Gly Pro Gln Gln Ile His Leu Lys
    120                 125                 130

gca aaa gca ata tat gag aaa ttt ata cag act gat gcc cca aaa gag       606
Ala Lys Ala Ile Tyr Glu Lys Phe Ile Gln Thr Asp Ala Pro Lys Glu
135                 140                 145                 150

gtt aac ctt gat ttt cac aca aaa gaa gtc att aca aac agc atc act       654
Val Asn Leu Asp Phe His Thr Lys Glu Val Ile Thr Asn Ser Ile Thr
                155                 160                 165

caa cct acc ctc cac agt ttt gat gct gca caa agc aga gtg tat cag       702
Gln Pro Thr Leu His Ser Phe Asp Ala Ala Gln Ser Arg Val Tyr Gln
            170                 175                 180

ctc atg gaa caa gac agt tat aca cgt ttt ctg aaa tct gac atc tat       750
Leu Met Glu Gln Asp Ser Tyr Thr Arg Phe Leu Lys Ser Asp Ile Tyr
        185                 190                 195

tta gac ttg atg gaa gga aga cct cag aga cca aca aat ctt agg aga       798
Leu Asp Leu Met Glu Gly Arg Pro Gln Arg Pro Thr Asn Leu Arg Arg
    200                 205                 210

cga tca cgc tca ttt acc tgc aat gaa ttc caa gat gta caa tca gat       846
Arg Ser Arg Ser Phe Thr Cys Asn Glu Phe Gln Asp Val Gln Ser Asp
215                 220                 225                 230

gtt gcc att tgg tta taa agaaaa ttgattttgc tcatttttat gacaaactta       900
Val Ala Ile Trp Leu  *
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235

tacatctgct tctaacatat cgcatgttta tgttaagatt tggtcccatc ctttaaactg 960

aaatatgtca tgtgaaatta ttttaaaaat gtaaaaacaa aactttctgc taacaaaata 1020

catacagtat ctgccagtat attctgtaaa accttctatt tgatgtcatt ccatttataa 1080

tcagaaaaaa aacttatttc ttaatcaaaa ggcagtacaa aaaaagtaat aatgttttat 1140

aagattgtag agttaagtaa aagttaagct tttgcaaagt tgtcaaaagt tcaaacaaaa 1200

gtctagttgg gattttttac caaagcagca taatatgtgt tatataaaca taataatact 1260

cagatatcca aatgttcaga tagcattttt cataatgaat gttctctttt ttttggtaat 1320

agtgtagaag tgatctggtt cttacaatgg gagatgaaga acatttatta ttgggttact 1380

actaaccctg tcccaagaat agtaatatca cctctagtta taagccagca acaggaactt 1440

ttgtgaagac acattcatct ctacagaact tcagattaaa tataatctag attaatgact 1500

gagaataaga tccacatttg aactcattcc taagtgaaca tggacgtacc cagttataca 1560

aagtacttct gttggtcaca gaaacatgac cagattttgc atatctccag gtagggaact 1620

aagtagacta ccttatcacc ggctaagaaa acttgctact aaactattag gccatcaatg 1680

gcttgaataa aaaccagaga aggtttttcc caggacgtct catgtttggc cctttagaat 1740

tggggtagaa atcagaaatg agatgagggg aagaagcaag gagtctaagg ccctagcgat 1800

ttgggcatct gccacattgg ttcatattca gaaagtgtta tctcattgat tatattcttg 1860

ttaagcaatc tccttaagta atta 1884

<210> 134
<211> 1601
<212> DNA
<213> Homo sapiens

<220>
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<222> (868)..(1098)

<400> 134
tctggtttcg ggttttattt tagaatttat aaaattccag tgtcatccat attcatgagc 60

ctttacacat gtttgcatat aatctccaaa ttccaaagtt aaggccaagg gatggattgt 120

agctatggaa acagatgata tggaagacat ccaacaagga ggaaaagcac acgcacgcct 180

cacccctgcc tcatctctgc ccagggctgt cctgacagca cagacgcttc agggagacag 240

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gcctggggac agtcatgtca tcacccttgc aacaaccacc caaaggaaaa gagagcgctg      300

aacagtttag gaaagggctc gcgtctaaga catcaagcga catacagaga tgtgcaaaac      360

ttggtgagaa ttaaaattga cctttgggag agggtagggg caggatgttt tatgacactg      420

tagaaaagac aggaggaacc cgctgcgatg gagattgggg ggagctggaa gcaagcagcc      480

aacaggacag agttccagaa ctcatgcaga tggggaagag gtgacagccc ttccccactg      540

gcctcccccg tggaggtgga gtagacagat cccgggaaag gcaggaaaag ggccttgctt      600

tctttccctg tttcctaagc cgtggtcacc ctagcctatg aagctggaag ctatattcct      660

tccaatccca atttaccatt cctgtaaaca ggcccattca gggctgcctg agcaaatggg      720

gacttgccga ggcagctgca actagacttg ggctaagccg tctgggtcta ctcaagaatt      780

cgagtctgaa gatgaccaag cttgagttat tcaactgaga gtgaggtgtc aaggcggaag      840

cgactgtccc cagggaaggg ctgtgag    atg gat ggg cgt gag tca gct ttt       891
                                 Met Asp Gly Arg Glu Ser Ala Phe
                                  1               5

cca aaa ctc aag tac ctg gga cag gac aac tcg cta gca gct cag tca        939
Pro Lys Leu Lys Tyr Leu Gly Gln Asp Asn Ser Leu Ala Ala Gln Ser
    10                  15                  20

cct ccg tgg cgg aca cag ata agg atg tta aga cca gaa aac cag aga        987
Pro Pro Trp Arg Thr Gln Ile Arg Met Leu Arg Pro Glu Asn Gln Arg
25                  30                  35                  40

cta ggg ccc cgt cct cag ccc tca cag cat gac aca gat gcc tcc ctc       1035
Leu Gly Pro Arg Pro Gln Pro Ser Gln His Asp Thr Asp Ala Ser Leu
                45                  50                  55

gga gag cag ggt ctc tcg gca tcc agc ggc gtg gtc tgc att ctg ctc       1083
Gly Glu Gln Gly Leu Ser Ala Ser Ser Gly Val Val Cys Ile Leu Leu
            60                  65                  70

tac ctc atg ctc tag gccccatgcc atcgtctcgg ccctagaccg tgaaaactgc       1138
Tyr Leu Met Leu  *
        75

cagtcacccg ggacctgctc ctaggggctg gcctgcacag ccggatggcc tgtgggcggg     1198

gtggaagtgc ccactcccac tccagatggg cctgctggcc actgacccac ctgtgctgag     1258

ggagagcgcc agcctccagc ttaggtacac ggcgcccacc cccagctcca cgggaaaccc     1318

ataaccacca gaaacatctc aatcaagaga cgggtgtgtg gggtggcact aactgcacag     1378

agaccactcc acgccggctg aggtagaaag aaggcaactg aacacacagc agctagggca     1438

ggggcaggga ggggctgcag gtggtgtgaa gaagagccca gctgtcatct aaggcaaact     1498

gcccccactg aggaccagcg ccaggcccta cctcccccaa cctgtgcgca tctcaatcac     1558
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agcagacact gtgacggcca caggcggacg cgtgggtcgt ccc                 1601




     <210> 135
     <211> 941
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (194)..(820)

     <400> 135
ccggaactcc cgggtcgacg atttcgtccc agggattctt gggttccgcg tgtagtttcg      60

gaaggagaca tcgaagcagg gcgaggcgca gagggcgttg cggactcatg ccccagtcgg     120

cagtgcgggg tcccaagccc tgcagtgcta cagctttgag cacacctact ttggcccctt     180

tgacctcagg gcc  atg aag ctg ccc agc atc tcc tgt cct cat gag tgc      229
                Met Lys Leu Pro Ser Ile Ser Cys Pro His Glu Cys
                1               5                   10

ttt gag gct atc ctg tct ctg gac acc ggg tat cgc gcg ccg gtg acc      277
Phe Glu Ala Ile Leu Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr
        15                  20                  25

ctg gtg cgg aag ggc tgc tgg acc ggg cct cct gcg ggc cag acg caa      325
Leu Val Arg Lys Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln
    30                  35                  40

tcg aac ccg gac gcg ctg ccg cca gac tac tcg gtg gtg cgc ggc tgc      373
Ser Asn Pro Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys
45                  50                  55                  60

aca act gac aaa tgc aac gcc cac ctc atg act cat gac gcc ctc ccc      421
Thr Thr Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro
                65                  70                  75

aac ctg agc caa gca ccc gac ccg ccg acg ctc agc ggc gcc gag tgc      469
Asn Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys
            80                  85                  90

tac gcc tgt atc ggg gtc cac cag gat gac tgc gct atc ggc agg tcc      517
Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg Ser
        95                  100                 105

cga cga gtc cag tgt cac cag gac cag acc gcc tgc ttc cag ggc aat      565
Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln Gly Asn
    110                 115                 120

ggc aga atg aca gtt ggc aat ttc tca gtc cct gtg tac atc aga acc      613
Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr Ile Arg Thr
125                 130                 135                 140
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tgc cac cgg ccc tcc tgc acc acc gag ggc acc acc agc ccc tgg aca        661
Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr Ser Pro Trp Thr
                145                 150                 155

gcc atc gac ctc cag ggc tcc tgc tgt gag ggg tac ctc tgc aac agg        709
Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly Tyr Leu Cys Asn Arg
            160                 165                 170

aaa tcc atg acc cag ccc ttc acc agt gct tca gcc acc acc cct ccc        757
Lys Ser Met Thr Gln Pro Phe Thr Ser Ala Ser Ala Thr Thr Pro Pro
        175                 180                 185

cga gca cta cag gtc ctg gcc ctg ctc ctc cca gtc ctc ctg ctg gtg        805
Arg Ala Leu Gln Val Leu Ala Leu Leu Leu Pro Val Leu Leu Leu Val
    190                 195                 200

ggg ctc tca gca tag accgcccctc caggatgctg gggacagggc tcacacacct        860
Gly Leu Ser Ala  *
205

cattcttgct gcttcagccc ctatcacata gctcactgga aatgatgtt aaagtaagaa       920

ttgcaataaa aaaaaaaaaa a                                                941




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     <211> 534
     <212> DNA
     <213> Homo sapiens

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     <222> (120)..(335)

     <400> 136
gcaatagcgt ccctagcgcg atggcgtatc ggcgcaggcg cactctgccg gcaacgccga       60

ggcgcttctg catctgtggg ccgagcattc ttcaggtcat ctgaaccttc tgagaaaac       119
atg gtc aac gtc ttg aaa gga gtg ctt ata gaa tgt gat cct gcc atg        167
Met Val Asn Val Leu Lys Gly Val Leu Ile Glu Cys Asp Pro Ala Met
  1               5                  10                  15

aag cag ttt ctg ctg tac ttg gat gag tcc aat gcc ctg ggg aag aag        215
Lys Gln Phe Leu Leu Tyr Leu Asp Glu Ser Asn Ala Leu Gly Lys Lys
             20                  25                  30

ttc atc att caa gac att gat gac act cac gtc ttt gta ata gca gaa        263
Phe Ile Ile Gln Asp Ile Asp Asp Thr His Val Phe Val Ile Ala Glu
         35                  40                  45

ttg gtt aat gtc ctc cag gag cga gtg ggt gaa tta atg gac caa aat        311
Leu Val Asn Val Leu Gln Glu Arg Val Gly Glu Leu Met Asp Gln Asn
     50                  55                  60
```

gct ttt tcc ctt acc cag aaa tga aaatactcaa tatggaccat ttaggaatta 365
Ala Phe Ser Leu Thr Gln Lys *
65 70

taagcagcaa ctgtgaaaga cttgccactc aatatcttag gtgactgatt agacatagag 425

ggttgtttta ggagcatgcc acgggaaaga ctgagggatc atgatcattt gttcagaaaa 485

aaagcccctg aactgatttt gttaccatag aatttaaaaa aaaaaaaaa 534

<210> 137
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<212> DNA
<213> Homo sapiens

<220>
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<222> (23)..(385)

<400> 137
cggcggaaga ggacaaggca ga atg cag gcc ctt cgg gtg tcc cag gcg ctg 52
Met Gln Ala Leu Arg Val Ser Gln Ala Leu
1 5 10

atc cgc tcc ttc agc tcc acc gcc cgg aac cgc ttt cag aac cga gtg 100
Ile Arg Ser Phe Ser Ser Thr Ala Arg Asn Arg Phe Gln Asn Arg Val
15 20 25

cgc gag aaa cag aag ctc ttc cag gtg ggg ggg gcg ggg ggg gtg ggg 148
Arg Glu Lys Gln Lys Leu Phe Gln Val Gly Gly Ala Gly Gly Val Gly
30 35 40

atc cga cgc gcc agc cgg gag cgc gcc gag ccg ggg cag gcg ggg cgc 196
Ile Arg Arg Ala Ser Arg Glu Arg Ala Glu Pro Gly Gln Ala Gly Arg
45 50 55

gct cta agg agc agc cag cac ccc ttt ctc atc aga cac ccc cac atc 244
Ala Leu Arg Ser Ser Gln His Pro Phe Leu Ile Arg His Pro His Ile
60 65 70

cag gag gac aat gac atc ccg ttg tac ctg aag ggc ggc atc gtt gac 292
Gln Glu Asp Asn Asp Ile Pro Leu Tyr Leu Lys Gly Gly Ile Val Asp
75 80 85 90

aac atc ctg tac cga gtg aca atg acg ctg tgt ctg ggc ggc act gtc 340
Asn Ile Leu Tyr Arg Val Thr Met Thr Leu Cys Leu Gly Gly Thr Val
95 100 105

tac agc ttg tac tcc ctt ggc tgg gcc tcc ttc ccc agg aat taa gac 388
Tyr Ser Leu Tyr Ser Leu Gly Trp Ala Ser Phe Pro Arg Asn *
110 115 120

caagaagcct ggggggcctg agagacttga acaagtgtca ataaacgctg gcctctgaaa 448

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aaaaaaaaaa a                                                          459



     <210> 138
     <211> 691
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (197)..(691)

     <400> 138
ggcacggggc aagccaagaa ggctctggag catcagggag actccaactt aaggcaccaa      60

gcatgggtga ctaagggctt cctgtggact ggcaaatgag agcaaacacc tgtggcttga     120

gcactgcccc ctaaagcagg ccttacagat ctcttacact cgtggtggga agagtctagt     180

gtgaaactgg ggtgga    atg ggg tgt cca cgt atg ttc cct ttt gcc tta      229
                     Met Gly Cys Pro Arg Met Phe Pro Phe Ala Leu
                      1               5                   10

cta tat gtt ctg tca gtt tct ttc agg aaa atc ttc atc tta caa ctt       277
Leu Tyr Val Leu Ser Val Ser Phe Arg Lys Ile Phe Ile Leu Gln Leu
            15                  20                  25

gta ggg ctg gtg tta act tac gac ttc act aac tgt gac ttt gag aag       325
Val Gly Leu Val Leu Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys
        30                  35                  40

att aaa gca gcc tat ctc agt act att tct aaa gac ctg att aca tat       373
Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr
    45                  50                  55

atg agt ggg acc aaa agt acc gag ttc aac aac acc gtc tct tgt agc       421
Met Ser Gly Thr Lys Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser
60                  65                  70                  75

aat cgg cca cat tgc ctt act gaa atc cag agc cta acc ttc aat ccc       469
Asn Arg Pro His Cys Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro
                80                  85                  90

acc gcc ggc tgc gcg tcg ctc gcc aaa gaa atg ttc gcc atg aaa act       517
Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr
            95                  100                 105

aag gct gcc tta gct atc tgg tgc cca ggc tat tcg gaa act cag ata       565
Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile
        110                 115                 120

aat gct act cag gca atg aag aag agg aga aaa agg aaa gtc aca acc       613
Asn Ala Thr Gln Ala Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr
    125                 130                 135
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aat aaa tgt ctg gaa caa gtg tca caa tta caa gga ttg tgg cgt cgc      661
Asn Lys Cys Leu Glu Gln Val Ser Gln Leu Gln Gly Leu Trp Arg Arg
140                 145                 150                 155

ttc aat cga cct tta ctg aaa caa cag taa                              691
Phe Asn Arg Pro Leu Leu Lys Gln Gln  *
                160                 165




     <210> 139
     <211> 924
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (172)..(696)

     <400> 139
gcttttggtt cttacagtag tcggcgtagg ccttaggtgg gttcgtgcgc cttctacctc     60

gctgtttcgg ttttcctggc tcctcggccc ttttctcccc tgttgcagct gggagcggac    120

gaagcgcgaa gctgggattt tttactgtct cctgaagaat ttaacacaaa c atg gat     177
                                                         Met Asp
                                                           1

atc aga cca aat cat aca att tat atc aac aat atg aat gac aaa att      225
Ile Arg Pro Asn His Thr Ile Tyr Ile Asn Asn Met Asn Asp Lys Ile
          5                  10                  15

aaa aag gaa gaa ttg aag aga tcc cta tat gcc ctg ttt tct cag ttt      273
Lys Lys Glu Glu Leu Lys Arg Ser Leu Tyr Ala Leu Phe Ser Gln Phe
     20                  25                  30

ggt cat gtg gtg gac att gtg gct tta aag acc atg aag atg agg ggg      321
Gly His Val Val Asp Ile Val Ala Leu Lys Thr Met Lys Met Arg Gly
 35                  40                  45                  50

cag gcc ttt gtc ata ttt aag gaa ctg ggc tca tcc aca aat gcc ttg      369
Gln Ala Phe Val Ile Phe Lys Glu Leu Gly Ser Ser Thr Asn Ala Leu
                 55                  60                  65

aga cag cta caa gga ttt cca ttt tat ggt aaa cca atg cga ata cag      417
Arg Gln Leu Gln Gly Phe Pro Phe Tyr Gly Lys Pro Met Arg Ile Gln
             70                  75                  80

tat gca aaa aca gat tcg gat ata ata tca aaa atg cgt gga act ttt      465
Tyr Ala Lys Thr Asp Ser Asp Ile Ile Ser Lys Met Arg Gly Thr Phe
         85                  90                  95

gct gac aaa gaa aag aaa aaa gaa aag aaa aaa gcc aaa act gtg gaa      513
Ala Asp Lys Glu Lys Lys Lys Glu Lys Lys Lys Ala Lys Thr Val Glu
    100                 105                 110
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cag act gca aca acc aca aac aaa aag cct ggc ttc aag gaa gta cgt      561
Gln Thr Ala Thr Thr Thr Asn Lys Lys Pro Gly Phe Lys Glu Val Arg
115                 120                 125                 130

ctg gta cca ggg agg cat gac att gct ttt gtt gaa ttt gaa aat gat      609
Leu Val Pro Gly Arg His Asp Ile Ala Phe Val Glu Phe Glu Asn Asp
                135                 140                 145

ggg cag gct gga gct gcc agg gat gct tta cag gga ttt aag atc aca      657
Gly Gln Ala Gly Ala Ala Arg Asp Ala Leu Gln Gly Phe Lys Ile Thr
            150                 155                 160

ccg tcc cat gct atg aag atc acc tat gcc aag aaa taa catttgggat       706
Pro Ser His Ala Met Lys Ile Thr Tyr Ala Lys Lys  *
        165                 170                 175

agtcgtcttt aaaagacttg gtgttattta cagtgtttgt tttgataaca tttggctggg    766

tcattttaat agttagagat gaggaggagt aaaagtgaaa tttttgtgaa ggacttaaat    826

tatccagtgt ttctttagcc ttggtgaact atgaaatacg aaggccttaa ttttgtacaa    886

taaactttta tttgtattct gtgtaaaaaa aaaaaaaa                            924



     <210> 140
     <211> 1773
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (141)..(1667)

     <400> 140
tccggatcct gttagacacc ggcgggcgcg agccgttgca gttctctttg ggtgatcgct     60

ccttccctct tcaacggatc cctccccgcc tccatcctcg ttctgtggga gagaccagcc    120

ttctggtgct gcagtcagga    atg gag ctt gac agc gct ctg gaa gcc cca     170
                         Met Glu Leu Asp Ser Ala Leu Glu Ala Pro
                          1               5                  10

tcg cag gaa gac tct aat ttg tcc gag gag ttg tct cac tcc gcc ttt      218
Ser Gln Glu Asp Ser Asn Leu Ser Glu Glu Leu Ser His Ser Ala Phe
                15                  20                  25

gga cag gcc ttc tcc aag att tta cac tgt ctt gcc cgc ccg gag gca      266
Gly Gln Ala Phe Ser Lys Ile Leu His Cys Leu Ala Arg Pro Glu Ala
            30                  35                  40

cga cga ggc aat gta aaa gat gca gtt ctt aaa gac ctc ggt gat cta      314
Arg Arg Gly Asn Val Lys Asp Ala Val Leu Lys Asp Leu Gly Asp Leu
        45                  50                  55
```

```
ata gaa gcc aca gaa ttt gat agg tta ttt gag ggg act ggt gca cgg       362
Ile Glu Ala Thr Glu Phe Asp Arg Leu Phe Glu Gly Thr Gly Ala Arg
     60                  65                  70

ctc cgc gga atg ccg gag aca ctg ggg cag gta gca aaa gcc ctg gag       410
Leu Arg Gly Met Pro Glu Thr Leu Gly Gln Val Ala Lys Ala Leu Glu
 75                  80                  85                  90

aag tat gca gcc ccc tcc aag gag gag gaa ggt gga ggt gat ggg cac       458
Lys Tyr Ala Ala Pro Ser Lys Glu Glu Glu Gly Gly Gly Asp Gly His
                 95                 100                 105

tcc gaa gcg gcc gag aaa gca gcc caa gtt ggg tta ctg ttt ctt aaa       506
Ser Glu Ala Ala Glu Lys Ala Ala Gln Val Gly Leu Leu Phe Leu Lys
            110                 115                 120

ctg tta ggg aaa gtt gag act gct aag aat tcc ctg gtc ggc cct gca       554
Leu Leu Gly Lys Val Glu Thr Ala Lys Asn Ser Leu Val Gly Pro Ala
        125                 130                 135

tgg cag acg ggc ctg cat cac ttg gca gga ccc gtt tat att ttt gcc       602
Trp Gln Thr Gly Leu His His Leu Ala Gly Pro Val Tyr Ile Phe Ala
    140                 145                 150

atc aca cac agc ttg gag caa cca tgg acc act ccg aga tct cgg gaa       650
Ile Thr His Ser Leu Glu Gln Pro Trp Thr Thr Pro Arg Ser Arg Glu
155                 160                 165                 170

gtt gct agg gag gtg ctc acc tca ctg ctt caa gtt act gaa tgc ggt       698
Val Ala Arg Glu Val Leu Thr Ser Leu Leu Gln Val Thr Glu Cys Gly
                175                 180                 185

tct gtg gca gga ttc cta cat gga gaa aat gaa gat gag aaa ggg aga       746
Ser Val Ala Gly Phe Leu His Gly Glu Asn Glu Asp Glu Lys Gly Arg
            190                 195                 200

ctt tcg gtg ata cta ggg ctt ctc aaa ccc gac ttg tat aag gaa tcc       794
Leu Ser Val Ile Leu Gly Leu Leu Lys Pro Asp Leu Tyr Lys Glu Ser
        205                 210                 215

tgg aag aat aac cct gcc atc aaa cat gtt ttc tca tgg act ctg caa       842
Trp Lys Asn Asn Pro Ala Ile Lys His Val Phe Ser Trp Thr Leu Gln
    220                 225                 230

cag gtc act cgg ccc tgg ctg agc cag cat ctg gaa agg gta ctt ccc       890
Gln Val Thr Arg Pro Trp Leu Ser Gln His Leu Glu Arg Val Leu Pro
235                 240                 245                 250

gca tca ttg gtc att tca gat gac tat cag act gag aac aaa atc ctg       938
Ala Ser Leu Val Ile Ser Asp Asp Tyr Gln Thr Glu Asn Lys Ile Leu
                255                 260                 265

ggt gta cac tgt ctc cat cac att gtg ctt aat gtg cca gct gct gat       986
Gly Val His Cys Leu His His Ile Val Leu Asn Val Pro Ala Ala Asp
            270                 275                 280
```

```
ttg ctc cag tat aac aga gcc cag gtc cta tac cat gcc att tcc aac      1034
Leu Leu Gln Tyr Asn Arg Ala Gln Val Leu Tyr His Ala Ile Ser Asn
        285                 290                 295

cac ctg tac aca cca gag cac cac ctc att cag gct gtg ctc ctg tgt      1082
His Leu Tyr Thr Pro Glu His His Leu Ile Gln Ala Val Leu Leu Cys
    300                 305                 310

ctg ctg gat tta ttc ccc atc ctg gag aaa acc ctg cac tgg aaa gga      1130
Leu Leu Asp Leu Phe Pro Ile Leu Glu Lys Thr Leu His Trp Lys Gly
315                 320                 325                 330

gat gga gct cga ccc acc acc cat tgt gat gag gtc ctg cgg ctg atc      1178
Asp Gly Ala Arg Pro Thr Thr His Cys Asp Glu Val Leu Arg Leu Ile
                335                 340                 345

ctg acc cac atg gag cca gag cac cgc ctt ctt tta cgc agg acc tac      1226
Leu Thr His Met Glu Pro Glu His Arg Leu Leu Leu Arg Arg Thr Tyr
            350                 355                 360

gca aga aac ctg ccg gct ttc gtg aac agg ttg ggg atc cta act gtc      1274
Ala Arg Asn Leu Pro Ala Phe Val Asn Arg Leu Gly Ile Leu Thr Val
        365                 370                 375

cgg cac tta aag agg ctg gag aga gtc atc att ggt tat ctg gag gtt      1322
Arg His Leu Lys Arg Leu Glu Arg Val Ile Ile Gly Tyr Leu Glu Val
    380                 385                 390

tat gat gga cct gag gag gaa gct aga ctg aag ata ttg gaa acc cta      1370
Tyr Asp Gly Pro Glu Glu Glu Ala Arg Leu Lys Ile Leu Glu Thr Leu
395                 400                 405                 410

aaa ctt ctc atg caa cat act tgg ccc aga gtt tcc tgc aga ctt gtg      1418
Lys Leu Leu Met Gln His Thr Trp Pro Arg Val Ser Cys Arg Leu Val
                415                 420                 425

gtc tta ctg aag gcc ctc ttg aaa ctg att tgt gat gta gca agg gat      1466
Val Leu Leu Lys Ala Leu Leu Lys Leu Ile Cys Asp Val Ala Arg Asp
            430                 435                 440

cca aac ctt aca cct gag tct gtt aag agc gcc ctg cta cag gag gcc      1514
Pro Asn Leu Thr Pro Glu Ser Val Lys Ser Ala Leu Leu Gln Glu Ala
        445                 450                 455

aca gac tgc ctg att ctc ctg gac cgc tgt tct caa gga cgg gta aag      1562
Thr Asp Cys Leu Ile Leu Leu Asp Arg Cys Ser Gln Gly Arg Val Lys
    460                 465                 470

ggt ctc ctg gcc aaa att ccc caa agc tgt gaa gac aga aaa gtg gtg      1610
Gly Leu Leu Ala Lys Ile Pro Gln Ser Cys Glu Asp Arg Lys Val Val
475                 480                 485                 490

aac tat atc aga aaa gtg cag cag gtt tct gaa ggc gca ccc tac aat      1658
Asn Tyr Ile Arg Lys Val Gln Gln Val Ser Glu Gly Ala Pro Tyr Asn
                495                 500                 505

gga act taa gacttgt attactttcc caagaggaaa ggattttctt cccatcccaa      1714
```

```
Gly Thr  *


tttgtatgaa tggagttatt taagaaaaaa agatattttt acacgaaaaa aaaaaaaaa    1773




     <210> 141
     <211> 2242
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (100)..(942)

     <220>
     <221> misc_feature
     <222> (1)...(2242)
     <223> n = a,t,c or g

     <400> 141
gaatgccttt tagtgccttg cttcctgaac tagctcacag tagcccggcg gcccagggca      60

atccgaccac atttcactct caccgctgta ggaatccag   atg cag gcc aag tac      114
                                             Met Gln Ala Lys Tyr
                                               1               5

agc agc acg agg gac atg ctg gat gat gat ggg gac acc acc atg agc      162
Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser
                 10                  15                  20

ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc      210
Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg
             25                  30                  35

aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc      258
Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr
         40                  45                  50

ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg      306
Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly
     55                  60                  65

ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc      354
Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr
 70                  75                  80                  85

att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa      402
Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln
                 90                  95                 100

tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg      450
Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val
            105                 110                 115
```

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gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga gca cac agg      498
Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg
        120                 125                 130

tgc agc cct tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc tac      546
Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr
    135                 140                 145

cag ttc tat aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc tgc      594
Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
150                 155                 160                 165

ctt agt gaa aac tct acc atg ctg aag ata aac aaa caa gaa gac ctg      642
Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu
                170                 175                 180

gaa ttt gcc gcg tct cag agc tac tct gag ttt ttc tac tct tat tgg      690
Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp
            185                 190                 195

aca ggg ctt ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg gat      738
Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp
        200                 205                 210

gga acc cct ttc act tct gaa ctg ttc cat att ata ata gat gtc acc      786
Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr
    215                 220                 225

agc cca aga agc aga gac tgt gtg gcc atc ctt aat ggg atg atc ttc      834
Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe
230                 235                 240                 245

tca aag gac tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg gca      882
Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala
                250                 255                 260

gga atg gtg aag cca gag agc ctc cat gtc ccc cct gaa aca tta ggc      930
Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly
            265                 270                 275

gaa ggt gac tga ttc gccctctgca actacaaata gcagagtgag ccaggcggtg      985
Glu Gly Asp  *
        280

ccaaagcaag ggctagttga gacattggga aatggaacat aatcaggaaa gactatctct   1045

ctgactagta caaaatgggt tctcgtgttt cctgttcagg atcaccagca tttctgagct   1105

tgggtttatg cacgtattta acagtcacaa gaagtcttat ttacatgcca ccaaccaacc   1165

tcagaaaccc ataatgtcat ctgccttctt ggcttagaga taacttttag ctctctttct   1225

tctcaatgtc taatatcacc tccctgtttt catgtcttcc ttacacttgg tggaataaga   1285

aactttttga agtagaggaa atacattgag gtaacatcct tttctctgac agtcaagtag   1345

tccatcagaa attggcagtc acttcccaga ttgtaccagc aaatacacaa ggaattcttt   1405
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ttgtttgttt cagttcatac tagtcccttc ccaatccatc agtaaagacc ccatctgcct   1465

tgtccatgcc gtttcccaac agggatgtca cttgatatga gaatctcaaa tctcaatgcc   1525

ttataagcat tccttcctgt gtccattaag actctgataa ttgtctcccc tccataggaa   1585

tttctcccag gaaagaaata tatccccatc tccgtttcat atcagaacta ccgtccccga   1645

tattcccttc agagagatta aagaccagaa aaaagtgagc ctcttcatct gcacctgtaa   1705

tagtttcagt tcctattttc ttccattgac ccatatttat acctttcagg tactgaagat   1765

ttaataataa taaatgtaaa tactgtgaag tgtgtgtgat tttacaatgg acttatggtt   1825

ggtgggaaaa ttcagcatgg aaatgctttt caaaatatga tagcggtcat tattttgatt   1885

gtgccttact gaaagttttt ggggaattta caagagtact gattacatga ttatctggag   1945

aaaataagat gtctttgaaa tacatgttgg cttcaagaaa acagttttaa cgttttccta   2005

aaatgaaatc ttttgaggtg agcttatggc atcaacacat ggttgatgag gaagctgagt   2065

tgcattagtg cacatgattt ccagtcaggt catgggaaat gaacagagac agtgacatct   2125

ttgtagctgc tcctttgtga ggcacttctt tcttgagatg actccatgca caaatataac   2185

agggatcatt gggaatgaca ccatcacagc caccaagntt attgggttac tgataat      2242



      <210> 142
      <211> 2323
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (100)..(1023)

      <220>
      <221> misc_feature
      <222> (1)...(2323)
      <223> n = a,t,c or g

      <400> 142
gaatgccttt tagtgccttg cttcctgaac tagctcacag tagcccggcg gcccagggca     60

atccgaccac atttcactct caccgctgta ggaatccag  atg cag gcc aag tac      114
                                            Met Gln Ala Lys Tyr
                                             1               5

agc agc acg agg gac atg ctg gat gat gat ggg gac acc acc atg agc      162
Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser
                10                  15                  20
```

```
ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc        210
Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg
             25                  30                  35

aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc        258
Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr
         40                  45                  50

ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg        306
Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly
     55                  60                  65

ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc        354
Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr
 70                  75                  80                  85

att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa        402
Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln
                 90                  95                 100

tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg        450
Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val
            105                 110                 115

gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga ggc tat aca        498
Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly Tyr Thr
        120                 125                 130

aga aac atg gtg cca gca tct gct tct tct gag agc ctc agg cag ctt        546
Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg Gln Leu
    135                 140                 145

cca cac atg ggg gaa agt gca gca gca cac agg tgc agc cct tgt aca        594
Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro Cys Thr
150                 155                 160                 165

gaa caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac        642
Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp
                170                 175                 180

agc aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct        690
Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser
            185                 190                 195

acc atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct        738
Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser
        200                 205                 210

cag agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt ttg cgc        786
Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg
    215                 220                 225

cct gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act        834
Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr
230                 235                 240                 245

tct gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga        882
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Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg
                250                 255                 260

gac tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa      930
Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys
            265                 270                 275

gaa ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca      978
Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro
        280                 285                 290

gag agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac tga ttc     1026
Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp  *
    295                 300                 305

gccctctgca actacaaata gcagagtgag ccaggcggtg ccaaagcaag ggctagttga   1086

gacattggga aatggaacat aatcaggaaa gactatctct ctgactagta caaaatgggt   1146

tctcgtgttt cctgttcagg atcaccagca tttctgagct tgggtttatg cacgtattta   1206

acagtcacaa gaagtcttat ttacatgcca ccaaccaacc tcagaaaccc ataatgtcat   1266

ctgccttctt ggcttagaga taacttttag ctctctttct tctcaatgtc taatatcacc   1326

tccctgtttt catgtcttcc ttacacttgg tggaataaga aactttttga agtagaggaa   1386

atacattgag gtaacatcct tttctctgac agtcaagtag tccatcagaa attggcagtc   1446

acttcccaga ttgtaccagc aaatacacaa ggaattcttt ttgtttgttt cagttcatac   1506

tagtcccttc ccaatccatc agtaaagacc ccatctgcct tgtccatgcc gtttcccaac   1566

agggatgtca cttgatatga gaatctcaaa tctcaatgcc ttataagcat tccttcctgt   1626

gtccattaag actctgataa ttgtctcccc tccataggaa tttctcccag gaaagaaata   1686

tatccccatc tccgtttcat atcagaacta ccgtccccga tattcccttc agagagatta   1746

aagaccagaa aaaagtgagc ctcttcatct gcacctgtaa tagtttcagt tcctattttc   1806

ttccattgac ccatatttat acctttcagg tactgaagat ttaataataa taaatgtaaa   1866

tactgtgaag tgtgtgtgat tttacaatgg acttatggtt ggtgggaaaa ttcagcatgg   1926

aaatgctttt caaaatatga tagcggtcat tattttgatt gtgccttact gaaagttttt   1986

ggggaattta caagagtact gattacatga ttatctggag aaaataagat gtctttgaaa   2046

tacatgttgg cttcaagaaa acagttttaa cgttttccta aaatgaaatc ttttgaggtg   2106

agcttatggc atcaacacat ggttgatgag gaagctgagt tgcattagtg cacatgattt   2166

ccagtcaggt catgggaaat gaacagagac agtgacatct ttgtagctgc tcctttgtga   2226

ggcacttctt tcttgagatg actccatgca caaatataac agggatcatt gggaatgaca   2286
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ccatcacagc caccaagntt attgggttac tgataat                           2323



     <210> 143
     <211> 971
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (72)..(767)

     <400> 143
cggccgcgtc gacagacaga cgggagcagt gcttttccta gagtagagta tgctctataa      60

atgtctactg a atg ttg act ggt gtt gga tgt ctt gtc tcc tca gaa tct     110
             Met Leu Thr Gly Val Gly Cys Leu Val Ser Ser Glu Ser
             1               5                   10

ctg agc tgc gtg cag tgt aat tca tgg gaa aaa tcc tgt gtc aac agc      158
Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys Ser Cys Val Asn Ser
     15                  20                  25

att gcc tct gaa tgt ccc tca cat gcc aac acc agc tgt atc agc tcc      206
Ile Ala Ser Glu Cys Pro Ser His Ala Asn Thr Ser Cys Ile Ser Ser
 30                  35                  40                  45

tca gcc agc tcc tct cta gag aca cca gtc aga tta tac cag aat atg      254
Ser Ala Ser Ser Ser Leu Glu Thr Pro Val Arg Leu Tyr Gln Asn Met
                 50                  55                  60

ttc tgc tca gcg gag aac tgc agt gag gag aca cac att aca gcc ttc      302
Phe Cys Ser Ala Glu Asn Cys Ser Glu Glu Thr His Ile Thr Ala Phe
             65                  70                  75

act gtc cac gtg tct gct gaa gaa cac ttt cat ttt gta agc cag tgc      350
Thr Val His Val Ser Ala Glu Glu His Phe His Phe Val Ser Gln Cys
         80                  85                  90

tgc caa gga aag gaa tgc agc aac acc agc gat gcc ctg gac cct ccc      398
Cys Gln Gly Lys Glu Cys Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro
     95                 100                 105

ctg aag aac gtg tcc agc aac gca gag tgc cct gct tgt tat gaa tct      446
Leu Lys Asn Val Ser Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser
110                 115                 120                 125

aat gga act tcc tgt cgt ggg aag ccc tgg aaa tgc tat gaa gaa gaa      494
Asn Gly Thr Ser Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu
                130                 135                 140

cag tgt gtc ttt cta gtt gca gaa ctt aag aat gac att gag tct aag      542
Gln Cys Val Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys
            145                 150                 155
```

```
agt ctc gtg ctg aaa ggc tgt tcc aac gtc agt aac gcc acc tgt cag       590
Ser Leu Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln
        160                 165                 170

ttc ctg tct ggt gaa aac aag act ctt gga gga gtc atc ttt cga aag       638
Phe Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
    175                 180                 185

ttt gag tgt gca aat gta aac agc tta acc ccc acg tct gca cca acc       686
Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro Thr
190                 195                 200                 205

act tcc cac aac gtg ggc tcc aaa gct tcc ctc tac ctc ttg gcc ctt       734
Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu Ala Leu
                210                 215                 220

gcc agc ctc ctt ctt cgg gga ctg ctg ccc tga ggtcctgg ggctgcactt       785
Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro  *
            225                 230

tgcccagcac cccatttctg cttctctgag gtccagagca ccccctgcgg tgctgacacc     845

ctctttccct gctctgcccc gtttaactgc ccagtaagtg ggagtcacag gtctccaggc     905

aatgccgaca gctgccttgt tcttcattat taaagcactg gttcattcac tgcccaaaaa     965

aaaaaa                                                                971



      <210> 144
      <211> 1689
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (354)..(1370)

      <220>
      <221> misc_feature
      <222> (1)...(1689)
      <223> n = a,t,c or g

      <400> 144
cctgaatgct ttacgtaccg gcccggaatt cccgggtcga cccacgcgtc cgctcggcca      60

ccgaagccac cctgccctgg tgaaagggct cccgcaccgc ccggtgctcc ccatctgcct     120

ggcgttgtgc gcagagctgg aaagcatggc tgttataaat gaattctgat tttggggagc     180

agatgccaac ttagagcctc gtaccaatct ctctgtcttt aaaagatgag gtgacttggt     240

gattttcctg gaaaattata ggtgcccagc taagacctga atgccatcac cctccccagg     300

gctctgcagt tttctcgtgg tgaacccttg atggatttgt tgttgcttga gaa   atg     356
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                                                            Met
                                                              1

gcg atg atc gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag        404
Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys
              5                  10                  15

agg aag agt tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg        452
Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val
         20                  25                  30

ctt cta ttt tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt        500
Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys
     35                  40                  45

aat tgg cct gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca        548
Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr
 50                  55                  60                  65

cgt gag cct gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt        596
Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu Leu
                 70                  75                  80

ggg gaa ttc cta ggc cac tgg ctg gac aaa tta cga agg gaa tgg cag        644
Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp Gln
             85                  90                  95

atg gag aga gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc        692
Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val
        100                 105                 110

gtc ttc atc ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct        740
Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro
    115                 120                 125

gag gcc tgg gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac        788
Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His
130                 135                 140                 145

cca agt cat gta cag ctg aag gta gtt gct gga aac cat gac att ggc        836
Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly
                150                 155                 160

ttc cat tat gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg        884
Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val
            165                 170                 175

ttc agc tct gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg        932
Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met
        180                 185                 190

gtc aac agc gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa        980
Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu
    195                 200                 205

aca gaa gca gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga       1028
Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg
```

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210                 215                 220                 225

gag gca cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg      1076
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr
                230                 235                 240

tct gcc cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat      1124
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp
            245                 250                 255

gct aac tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc      1172
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile
        260                 265                 270

cca ttt aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag      1220
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys
    275                 280                 285

ctg ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac      1268
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His
290                 295                 300                 305

agc gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc      1316
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val
                310                 315                 320

cca tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg gta      1364
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Val
            325                 330                 335

ccg tga aagtttattt ttgtctgaaa gctttcataa gtatttaaat caacacagta       1420
Pro  *


atcaactatt taattgctgc aatcggtcaa aatttacaaa agccacacac aaatttctct   1480

ccttctacac gtagctccat acactgcccc ttgccaaaca cccttccggg aaccaatcag   1540

catgacattc ctgggcagtt aatgtgagaa gcgagggcag ggcaccgtcc nagtggactt   1600

tatccttcag ggaggggcgt atcctctctc ttacactctg tgtgtggtta aatttctaaa   1660

gaacaccatt taatccatag ctatatcag                                      1689
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<210> 145
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (104)..(298)

<400> 145

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atttcactgt atgtaatgca tttttgttgt tgttgttgtt gtttttagaa acctagctac      60

tttaagtttt ttttctttat tactgatctt atgcaatttg att  atg ttc ctt ggt      115
                                                 Met Phe Leu Gly
                                                  1

gta gct ttt cag tgt ttc ttc tgc ttt tgg ttt gtt gag ctt ttt gga      163
Val Ala Phe Gln Cys Phe Phe Cys Phe Trp Phe Val Glu Leu Phe Gly
  5                  10                  15                  20

ttt gtg ggt tta cag tta tta tca aat ttg gaa aaa ttt cag ccc tta      211
Phe Val Gly Leu Gln Leu Leu Ser Asn Leu Glu Lys Phe Gln Pro Leu
                 25                  30                  35

tgt ctt caa ata ttt ttt ctg tct ccc tgc ccc atc cgt agt ctt tat      259
Cys Leu Gln Ile Phe Phe Leu Ser Pro Cys Pro Ile Arg Ser Leu Tyr
             40                  45                  50

ata ttt gat cat cta aag ttg tct cac agc tca cag tga cactgcttgt       308
Ile Phe Asp His Leu Lys Leu Ser His Ser Ser Gln  *
         55                  60                  65

ttttccagtc ttttttcccc tctaggtgtt tcattttgaa caattgctat tgctatgtct    368

tcaagatcct taatcttttc ttctgtagtg ccacatctta cccagtgaac ttttcacctc    428

agacatggta ttttttattt ctagaaatta ggactttttt tacatttccc ac            480



    <210> 146
    <211> 557
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (158)..(520)

    <400> 146
agagcagaag tgtgaagagt ggaggagcca gtatgaggct ctgaaggagg actggaggac     60

ccttgggacc cagcacaggg agctggagag ccaactccac gtgcttcagt ccaaactgca    120

ggtaccaggc actgggggtg gggagggaag acagggt atg ggg agg agg gat ggt     175
                                         Met Gly Arg Arg Asp Gly
                                          1               5

gat gaa aga agc tgt tct gga tta ggg act cca aag gca gct gac agc     223
Asp Glu Arg Ser Cys Ser Gly Leu Gly Thr Pro Lys Ala Ala Asp Ser
             10                  15                  20

atc tgg ctt tca gtt cct cag tca cca cta ctt tgt acc aaa ttc act     271
Ile Trp Leu Ser Val Pro Gln Ser Pro Leu Leu Cys Thr Lys Phe Thr
         25                  30                  35
```

```
gtt ttg gct ctg aaa tct aat ttt gag ttt agc aag gat gtc tgc att       319
Val Leu Ala Leu Lys Ser Asn Phe Glu Phe Ser Lys Asp Val Cys Ile
     40                  45                  50

gct cat gca aat gaa cta agc gtt cat tgg aat gac acc atc acc acc       367
Ala His Ala Asn Glu Leu Ser Val His Trp Asn Asp Thr Ile Thr Thr
 55                  60                  65                  70

caa atg aaa aga act ggc tgg aat att cat cag cct act aat gtc atc       415
Gln Met Lys Arg Thr Gly Trp Asn Ile His Gln Pro Thr Asn Val Ile
                 75                  80                  85

tcc caa ccc act ctc caa act cca tcc caa aaa agc atc cag ttc aga       463
Ser Gln Pro Thr Leu Gln Thr Pro Ser Gln Lys Ser Ile Gln Phe Arg
             90                  95                 100

att gcc cac tgt tgg caa aga aag aat gtc act aat tta ttt aca ggg       511
Ile Ala His Cys Trp Gln Arg Lys Asn Val Thr Asn Leu Phe Thr Gly
        105                 110                 115

agc aga tag cagggactta cagatgaacc aggccctgcg atttttg                  557
Ser Arg  *
    120




     <210> 147
     <211> 1190
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (172)..(1071)

     <400> 147
gggagggtct gaaccgataa ccctgcggta ccgctccgga attcccgggt cgacccacgc      60

gtccggggct acacagccag gtgtcagatg tgtctctgct gatctgagtc tgcctgtggc     120

atggacctgc atcttccctg aagcatctcc agggctgaaa aatcactgac c atg gca      177
                                                         Met Ala
                                                           1

cca tgg tct cat cca tct gca cag ctg cag cca gtg gga gga gac gcc       225
Pro Trp Ser His Pro Ser Ala Gln Leu Gln Pro Val Gly Gly Asp Ala
         5                  10                  15

gtg agc cct gcc ctc atg gtt ctg ctc tgc ctc ggg ctg agt ctg ggc       273
Val Ser Pro Ala Leu Met Val Leu Leu Cys Leu Gly Leu Ser Leu Gly
     20                  25                  30

ccc agg acc cac gtg cag gca ggg aac ctc tcc aaa gcc acc ctc tgg       321
Pro Arg Thr His Val Gln Ala Gly Asn Leu Ser Lys Ala Thr Leu Trp
 35                  40                  45                  50
```

```
gct gag cca ggc tct gtg atc agc cgg ggg aac tct gtg acc atc cgg       369
Ala Glu Pro Gly Ser Val Ile Ser Arg Gly Asn Ser Val Thr Ile Arg
             55                  60                  65

tgt cag ggg acc ctg gag gcc cag gaa tac cgt ctg gtt aaa gag gga       417
Cys Gln Gly Thr Leu Glu Ala Gln Glu Tyr Arg Leu Val Lys Glu Gly
         70                  75                  80

agc cca gaa ccc tgg gac aca cag aac cca ctg gag ccc aag aac aag       465
Ser Pro Glu Pro Trp Asp Thr Gln Asn Pro Leu Glu Pro Lys Asn Lys
     85                  90                  95

gcc aga ttc tcc atc cca tcc atg aca gag cac cat gca ggg aga tac       513
Ala Arg Phe Ser Ile Pro Ser Met Thr Glu His His Ala Gly Arg Tyr
    100                 105                 110

cgc tgt tac tac tac agc cct gca ggc tgg tca gag ccc agc gac ccc       561
Arg Cys Tyr Tyr Tyr Ser Pro Ala Gly Trp Ser Glu Pro Ser Asp Pro
115                 120                 125                 130

ctg gag ctg gtg gtg aca gga ttc tac aac aaa ccc acc ctc tca gcc       609
Leu Glu Leu Val Val Thr Gly Phe Tyr Asn Lys Pro Thr Leu Ser Ala
                135                 140                 145

ctg ccc agt cct gtg gtg acc tca gga gag aac gtg acc ctc cag tgt       657
Leu Pro Ser Pro Val Val Thr Ser Gly Glu Asn Val Thr Leu Gln Cys
            150                 155                 160

ggc tca cgg ctg aga ttc gac agg ttc att ctg act gag gaa gga gac       705
Gly Ser Arg Leu Arg Phe Asp Arg Phe Ile Leu Thr Glu Glu Gly Asp
        165                 170                 175

cac aag ctc tcc tgg acc ttg gac tca cag ctg acc ccc agt ggg cag       753
His Lys Leu Ser Trp Thr Leu Asp Ser Gln Leu Thr Pro Ser Gly Gln
    180                 185                 190

ttc cag gcc ctg ttc cct gtg ggc cct gtg acc ccc agc cac agg tgg       801
Phe Gln Ala Leu Phe Pro Val Gly Pro Val Thr Pro Ser His Arg Trp
195                 200                 205                 210

atg ctc aga tgc tat ggc tct cgc agg cat atc ctg cag gta tgg tca       849
Met Leu Arg Cys Tyr Gly Ser Arg Arg His Ile Leu Gln Val Trp Ser
                215                 220                 225

gaa ccc agt gac ctc ctg gag att ccg gtc tca gga gca gct gat aac       897
Glu Pro Ser Asp Leu Leu Glu Ile Pro Val Ser Gly Ala Ala Asp Asn
            230                 235                 240

ctc agt ccg tca caa aac aag tct gac tct ggg act gcc tca cac ctt       945
Leu Ser Pro Ser Gln Asn Lys Ser Asp Ser Gly Thr Ala Ser His Leu
        245                 250                 255

cag gat tac gca gta gag aat ctc atc cgc atg ggc atg gcc ggc ttg       993
Gln Asp Tyr Ala Val Glu Asn Leu Ile Arg Met Gly Met Ala Gly Leu
    260                 265                 270
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atc ctg gtg gtc ctt ggg att ctg ata ttt cag gat tgg cac agc cag      1041
Ile Leu Val Val Leu Gly Ile Leu Ile Phe Gln Asp Trp His Ser Gln
275                 280                 285                 290

aga agc ccc caa gct gca gct gga agg tga a cagaagagag aacaatgcac      1092
Arg Ser Pro Gln Ala Ala Ala Gly Arg  *
                295                 300

cattgaatgc tggagccttg gaagcgaatc tgatggtcct aggaggttcg ggaagaccat   1152

ctgaggccta tgccatctgg actgtctgct ggcaattt                           1190




     <210> 148
     <211> 1260
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (156)..(626)

     <400> 148
ctggctagcg tttaaactta agcttggtac cgagctcgga tccactagtc cagtgtggtg     60

gaattccagc accccggagg tactccagca gcttgtctcc aatccaagct cccaatcacc    120

caccgccgca gccccctacg caggccacgc cactg   atg cac acc aaa ccc aat     173
                                         Met His Thr Lys Pro Asn
                                          1               5

agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga ctt      221
Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu
            10                  15                  20

gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt act      269
Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr
        25                  30                  35

ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc ctg      317
Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu
    40                  45                  50

gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta ccg      365
Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro
55                  60                  65                  70

aga ccg aga cca gta cca aag cca agg aac cgg ccc agc gtg ccc cca      413
Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro
                75                  80                  85

ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc acc      461
Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr
            90                  95                  100
```

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aac aca gca cca aca gct tcc aag ata gta aca gac tcc aat tcc agg      509
Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg
        105                 110                 115

gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac tca      557
Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser
    120                 125                 130

gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat gat      605
Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp
135                 140                 145                 150

acc gag agc act gcc ctg tga ag aaagcccttt cccagccctc caccacttcc      658
Thr Glu Ser Thr Ala Leu  *
                155

accctggcga gtggagcagg ggcaggcgaa cctctttctt tgcagaccga acagtgaaaa    718

gctttcagtg gaggacaaag gagggcctca ctgtgcggga cctggccttc tgcacggccc    778

aaggagaacc tggaggccac cactaaagct gaatgacctg tgtcttgaag aagttggctt    838

tctttacatg ggaaggaaat catgccaaaa aaatccaaaa caaagaagta cctggagtgg    898

agagagtatt cctgctgaaa cgcgcatagg aagcttttgt ccctgctgtt aatgcgggca    958

gcacctacag caacttggaa tgagtaagaa gcagtgcgtt aactatctat ttaataaaat   1018

gcgctcatta tgcaagtcgc ctactctctg ctacctggac gttcattctt atgtattagg   1078

agggaggctg cgctccttca gacttgctgc agaatcattt tgtatcatgt atggtctgtg   1138

tctccccagt cccctcagaa ccatgcccat ggatggtgac tgctggctct gtcacctcat   1198

caaactggat gtgacccatg ccgcctcgtt ggattgtcgg aatgtagaca gaaatgtact   1258

gt                                                                  1260
```

<210> 149
<211> 1929
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (208)..(1395)

<400> 149

```
ccgctccgga attcccgggt cgacccacgc gtccgctaga tcccaggatc acacacgtcc      60

tccttcctct gtctattaca caccatctgc tcatactatc tggtactcac tcaagaaatc     120

caagatgatg catggctgga caaaatctac agacgctatg cctggataaa acgccagctt     180
```

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gtggactatg aggagaaata cggccgc     atg ttt cca cgt gag tgg tgc atg      231
                                  Met Phe Pro Arg Glu Trp Cys Met
                                    1               5

gct gag agg att gcg gtg gaa ttt tgc cat gtg aca agg gca gaa ctt       279
Ala Glu Arg Ile Ala Val Glu Phe Cys His Val Thr Arg Ala Glu Leu
     10                  15                  20

gcc aag att atg cgt acc aga gcg aag gaa att gaa gtg aaa ttg ctt       327
Ala Lys Ile Met Arg Thr Arg Ala Lys Glu Ile Glu Val Lys Leu Leu
 25                  30                  35                  40

ctt ttt gct att caa aga aca act aac ttt gag ggg ttt ctt gca aaa       375
Leu Phe Ala Ile Gln Arg Thr Thr Asn Phe Glu Gly Phe Leu Ala Lys
                 45                  50                  55

cgc ttc tcc ggc tgc acc ctg acc gat ggg acc ctg aaa aag ctt gag       423
Arg Phe Ser Gly Cys Thr Leu Thr Asp Gly Thr Leu Lys Lys Leu Glu
             60                  65                  70

tct cca ccc cca tct acc aat ccc ttc ctg gaa gat gag cca aca cca       471
Ser Pro Pro Pro Ser Thr Asn Pro Phe Leu Glu Asp Glu Pro Thr Pro
         75                  80                  85

gag atg gag gaa ctg gca acg gag aaa gga gat tta gat caa cca aag       519
Glu Met Glu Glu Leu Ala Thr Glu Lys Gly Asp Leu Asp Gln Pro Lys
     90                  95                 100

aag cct aaa gcc cca gac aat cca ttt cat ggc att gtt tcc aag tgt       567
Lys Pro Lys Ala Pro Asp Asn Pro Phe His Gly Ile Val Ser Lys Cys
105                 110                 115                 120

ttt gag cct cat ctc tac gtg tat atc gaa tcc caa gac aag aac ctc       615
Phe Glu Pro His Leu Tyr Val Tyr Ile Glu Ser Gln Asp Lys Asn Leu
                125                 130                 135

gga gag ctg ata gat cgg ttt gtg gct gat ttc aaa gcc cag ggg cca       663
Gly Glu Leu Ile Asp Arg Phe Val Ala Asp Phe Lys Ala Gln Gly Pro
            140                 145                 150

cct aag ccc aac act gat gaa ggg ggt gcc gtg ctc ccc agc tgc gcc       711
Pro Lys Pro Asn Thr Asp Glu Gly Gly Ala Val Leu Pro Ser Cys Ala
        155                 160                 165

gac ctc ttt gtc tac tac aag aag tgc atg gtg caa tgc tct cag ctc       759
Asp Leu Phe Val Tyr Tyr Lys Lys Cys Met Val Gln Cys Ser Gln Leu
    170                 175                 180

agt act ggg gag ccc atg atc gcc ctg acc acc att ttc cag aag tac       807
Ser Thr Gly Glu Pro Met Ile Ala Leu Thr Thr Ile Phe Gln Lys Tyr
185                 190                 195                 200

ctc cga gaa tac gcc tgg aaa atc ctc tct ggc aac ctg ccc aaa acc       855
Leu Arg Glu Tyr Ala Trp Lys Ile Leu Ser Gly Asn Leu Pro Lys Thr
                205                 210                 215

aca acc agc agt gga gga ctg act atc agc agc ctc ctc aag gaa aag       903
```

```
Thr Thr Ser Ser Gly Gly Leu Thr Ile Ser Ser Leu Leu Lys Glu Lys
            220                 225                 230

gag ggc tca gaa gta gcc aag ttc act ctg gag gag ctc tgc ctc atc      951
Glu Gly Ser Glu Val Ala Lys Phe Thr Leu Glu Glu Leu Cys Leu Ile
        235                 240                 245

tgt aac atc ctg agc acg gca gag tac tgt ctg gcc acc acc cag cag      999
Cys Asn Ile Leu Ser Thr Ala Glu Tyr Cys Leu Ala Thr Thr Gln Gln
    250                 255                 260

cta gaa gaa aaa ctc aaa gaa aaa gtg gat gta agt ctg att gaa cga     1047
Leu Glu Glu Lys Leu Lys Glu Lys Val Asp Val Ser Leu Ile Glu Arg
265                 270                 275                 280

atc aat ctg act gga gag atg gac acg ttc agc acc gtc atc tcc agc     1095
Ile Asn Leu Thr Gly Glu Met Asp Thr Phe Ser Thr Val Ile Ser Ser
                285                 290                 295

agt att cag ctg ctg gtt cag gat ctg gat gct gcc tgt gat cct gcc     1143
Ser Ile Gln Leu Leu Val Gln Asp Leu Asp Ala Ala Cys Asp Pro Ala
            300                 305                 310

ctg act gcc atg agc aag atg cag tgg cag aac gtg gag cac gtt ggt     1191
Leu Thr Ala Met Ser Lys Met Gln Trp Gln Asn Val Glu His Val Gly
        315                 320                 325

gac cag agc ccc tac gtc acc tct gtc att ctg cac atc aag cag aac     1239
Asp Gln Ser Pro Tyr Val Thr Ser Val Ile Leu His Ile Lys Gln Asn
    330                 335                 340

gtc ccc atc atc cgt gac aac ctg gct tcc aca cgc aag tac ttc act     1287
Val Pro Ile Ile Arg Asp Asn Leu Ala Ser Thr Arg Lys Tyr Phe Thr
345                 350                 355                 360

cag ttc tgc gtt aaa ttt gca aac tcc ttc att ccc aaa ttc atc acc     1335
Gln Phe Cys Val Lys Phe Ala Asn Ser Phe Ile Pro Lys Phe Ile Thr
                365                 370                 375

cac ctc ttc aag tgc aag cca att agc atg gtg gga gca gaa cag gtg     1383
His Leu Phe Lys Cys Lys Pro Ile Ser Met Val Gly Ala Glu Gln Val
            380                 385                 390

aga tgg acg tag tat caggcatttg cctggcagct tttgttgtag atcaagcaca     1438
Arg Trp Thr  *
        395

tattcttcta gtccagatct acttggcagg aataaaattg atgatgtccc ctgtttgggg   1498

acagtataat gactcacccg gaaggtttct taattcgttc ttccatttat ttttaaaaat   1558

tttgtttgaa cgcctactaa gttctgggtg cagggtataa cacagcaagc accatggaaa   1618

ggtccctgct cctagtgctc acactccaat aagaagaagt ggctgggccg ggcacagcgg   1678

ctcacgctgt aaccccagca tttcgggagg cctgggcagg cagatcacct ggggtaagga   1738
```

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atttgagagc agcctggcca acatggtgaa atcccatctc tactaaaaat acaaaaatta   1798

gctgggcatg gggcaggct accggggagg ctgaggcagg agaatcactt gaacccggga   1858

ggtggaggtt gcagtgagcc gatatcacac cactgcactc cagcctgggt gacaaagtga   1918

gactccatct c                                                        1929



     <210> 150
     <211> 1230
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (70)..(555)

     <400> 150
aaaaaagttg gtgtatcatc ctccatcctc caaggtctct ggatctctta tagcacagaa     60

ggtctttcc    atg gca ctg gcg tct tta cga aat ctc tac act cca aat     108
             Met Ala Leu Ala Ser Leu Arg Asn Leu Tyr Thr Pro Asn
               1               5                  10

ata aag gtc agc cga ctg ctg att ttg gga ggt gcc aat att aat tac      156
Ile Lys Val Ser Arg Leu Leu Ile Leu Gly Gly Ala Asn Ile Asn Tyr
     15                  20                  25

cgg aca gag gtt tta aat aat gct cca att cta tgt gtt cag tcc cat      204
Arg Thr Glu Val Leu Asn Asn Ala Pro Ile Leu Cys Val Gln Ser His
 30                  35                  40                  45

ctt ggt tac aca gaa atg gta gcc ctg ctg ctg gag ttc ggg gcc aac      252
Leu Gly Tyr Thr Glu Met Val Ala Leu Leu Leu Glu Phe Gly Ala Asn
                 50                  55                  60

gtg gat gcc tct tct gaa agt ggc ctg act ccc ctg gga tat gct gca      300
Val Asp Ala Ser Ser Glu Ser Gly Leu Thr Pro Leu Gly Tyr Ala Ala
             65                  70                  75

gca gca ggg tac ctg agc att gtg gtg ctg ctg tgc aag aaa cgg gcc      348
Ala Ala Gly Tyr Leu Ser Ile Val Val Leu Leu Cys Lys Lys Arg Ala
         80                  85                  90

aag gtg gat cat ttg gat aag aac ggg cag tgt gct ttg gtt cat gct      396
Lys Val Asp His Leu Asp Lys Asn Gly Gln Cys Ala Leu Val His Ala
     95                 100                 105

gca ctc cga ggt cat ctg gag gtt gtc aag ttt ttg att cag tgt gac      444
Ala Leu Arg Gly His Leu Glu Val Val Lys Phe Leu Ile Gln Cys Asp
110                 115                 120                 125

tgg acg atg gcc ggc cag cag caa gga gta ttt aag aag agc cat gcc      492
Trp Thr Met Ala Gly Gln Gln Gln Gly Val Phe Lys Lys Ser His Ala
```

```
                130                 135                 140

atc caa cag gcc ctc att gct gca gcc agc atg ggt tat act gag gta       540
Ile Gln Gln Ala Leu Ile Ala Ala Ala Ser Met Gly Tyr Thr Glu Val
            145                 150                 155

aga agt agg caa tag gattgttttt tcaagctctg tattgaagga cccaggaaac       595
Arg Ser Arg Gln  *
        160

caggagaaaa gattgcacga agacaaaatt gccaaccaaa ttaatgtgaa ttcgtgatcg    655

ctgctctgaa taataaggag attaaactcc atgaagcact ttactcaaat gccaaagtcc    715

ctcaaattat aggtatagaa aggtgcgagt tggaaaggac cgtggaaatg atataattat    775

tctccatgtt ttcctccctg tttaacagac agtggcacca aggctcaaag agatgaatta    835

ttgaggtgta gtcacatggt tagataatgt ggcacaggaa cagcataaca tttagaatct    895

cagaaggacc agatttgagt cccagcctcg ctattcatta actctagccc ttgaacaatt    955

tacctatctc ttagaagttt agtttcccat cagcaaagtg aagctaataa actcctttat   1015

acaaggctgt tgtaagggat gcttggtaaa ctgttaaaca ttatacagtt tatttattaa   1075

tgataataac aataatagtg gcaaatgtag ggaattggta gtgtgctagg aaatgtttaa   1135

caaccaactg tgaagagggg tgtggggtgg aacaggggtg tgtgtttgtg tgtgcatacg   1195

tttattataa attttactga tagaatgtgt tgccg                               1230



     <210> 151
     <211> 1335
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (91)..(1257)

     <400> 151
gcgactgcgg acaggttaga gttgtggttg gggcggacgc ggaagcagcc caagggcaga     60

gagggagccc gagccaggcc atctccaacc     atg ttc gac gag gcc tcg gcc     111
                                     Met Phe Asp Glu Ala Ser Ala
                                      1               5

atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttt cca ctc      159
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu
        10                  15                  20

ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc      207
Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly
```

```
    25                  30                  35

tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc      255
Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg
40                  45                  50                  55

acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct      303
Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser
                60                  65                  70

tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca      351
Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser
            75                  80                  85

tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta gat gat      399
Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu Asp Asp
        90                  95                  100

cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc tgc agt      447
Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val Cys Ser
    105                 110                 115

gat gtc tct tct tct att agc act tac tgg gat tgg tca gat agc gag      495
Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp Ser Glu
120                 125                 130                 135

ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt gat gta      543
Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser Asp Val
                140                 145                 150

ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg ctt cct      591
Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu Leu Pro
            155                 160                 165

aaa aag aaa aac aag cac cgg aat tta gat gaa ctc cct tgg agt gca      639
Lys Lys Lys Asn Lys His Arg Asn Leu Asp Glu Leu Pro Trp Ser Ala
        170                 175                 180

atg aca aat gat gag cag gtg gaa tat att gag tat ctg agt cgg aaa      687
Met Thr Asn Asp Glu Gln Val Glu Tyr Ile Glu Tyr Leu Ser Arg Lys
    185                 190                 195

gtg agt act gag atg ggt ctt cgg gag caa ctt gat att att aag atc      735
Val Ser Thr Glu Met Gly Leu Arg Glu Gln Leu Asp Ile Ile Lys Ile
200                 205                 210                 215

att gat cct tct gct cag atc tcc cct aca gac agg gag ttt att att      783
Ile Asp Pro Ser Ala Gln Ile Ser Pro Thr Asp Arg Glu Phe Ile Ile
                220                 225                 230

gaa ctt aac tgt ctc aca gat gaa aaa ctg aag cag gtc aga aac tat      831
Glu Leu Asn Cys Leu Thr Asp Glu Lys Leu Lys Gln Val Arg Asn Tyr
            235                 240                 245

atc aag gaa cat agc cct cgc caa cgg cct gca aga gag gcc tgg aag      879
Ile Lys Glu His Ser Pro Arg Gln Arg Pro Ala Arg Glu Ala Trp Lys
        250                 255                 260
```

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aga agc aac ttt agt tgt gca agc acc agt gga gtg agc ggt gcc agt      927
Arg Ser Asn Phe Ser Cys Ala Ser Thr Ser Gly Val Ser Gly Ala Ser
    265                 270                 275

gcc agc gcc agc agc agc agt gcc agc atg gtc agt tct gca agc agc      975
Ala Ser Ala Ser Ser Ser Ser Ala Ser Met Val Ser Ser Ala Ser Ser
280                 285                 290                 295

agt ggg tcc agt gtt gga aac tct gct tca aac tcc agt gcc aac atg     1023
Ser Gly Ser Ser Val Gly Asn Ser Ala Ser Asn Ser Ser Ala Asn Met
                300                 305                 310

agt cga gca cac agt gac agc aac ctg tct gca agt gca gca gag cgg     1071
Ser Arg Ala His Ser Asp Ser Asn Leu Ser Ala Ser Ala Ala Glu Arg
            315                 320                 325

att cgg gat tca aaa aag cga tcc aag cag cgg aag tta cag cag aag     1119
Ile Arg Asp Ser Lys Lys Arg Ser Lys Gln Arg Lys Leu Gln Gln Lys
        330                 335                 340

gcc ttc cgc aag agg cag ctg aag gag cag agg cag gcc cgg aag gag     1167
Ala Phe Arg Lys Arg Gln Leu Lys Glu Gln Arg Gln Ala Arg Lys Glu
    345                 350                 355

agg ctc agt ggg ctc ttc ctt aac gaa gag gtg ctg tcc ttg aaa gtg     1215
Arg Leu Ser Gly Leu Phe Leu Asn Glu Glu Val Leu Ser Leu Lys Val
360                 365                 370                 375

act gag gaa gac cat gaa gca gat gtt gat gtt ttg atg taa taagggt     1264
Thr Glu Glu Asp His Glu Ala Asp Val Asp Val Leu Met  *
                380                 385

gaatttatca acgttctttg tgagcattaa aatactccat ccttatgggt ttacatgcaa   1324

aaaaaaaaaa a                                                        1335



     <210> 152
     <211> 2251
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (203)..(1582)

     <400> 152
cgcgtgcggt ggaattcggc gaaacttccc tctacccgcc cggcccgcgg cgcgcaccgt     60

tggcgctgga cgcttcctcc ttggaagcgc ctctccctca ggtctcaaga actgttttga    120

gatgcaggaa ttcatctaat tttcactgcc gggcgaggtg tgagagccct agcatctgaa    180

agtggtcgac ttgcgagttg tt atg gag aaa act tgt ata gat gca ctt cct    232
```

```
                            Met Glu Lys Thr Cys Ile Asp Ala Leu Pro
                             1               5                  10

ctt act atg aat tct tca gaa aag caa gag act gta tgt att ttt gga      280
Leu Thr Met Asn Ser Ser Glu Lys Gln Glu Thr Val Cys Ile Phe Gly
                 15                  20                  25

act ggt gat ttt gga aga tca ctg gga ttg aaa atg ctc cag tgt ggt      328
Thr Gly Asp Phe Gly Arg Ser Leu Gly Leu Lys Met Leu Gln Cys Gly
             30                  35                  40

tat tct gtt gtt ttt gga agt cga aac ccc cag aag acc acc cta ctg      376
Tyr Ser Val Val Phe Gly Ser Arg Asn Pro Gln Lys Thr Thr Leu Leu
         45                  50                  55

ccc agt ggt gca gaa gtc ttg agc tat tca gaa gca gcc aag aag tct      424
Pro Ser Gly Ala Glu Val Leu Ser Tyr Ser Glu Ala Ala Lys Lys Ser
     60                  65                  70

ggc atc ata atc ata gca atc cac aga gag cat tat gat ttt ctc aca      472
Gly Ile Ile Ile Ile Ala Ile His Arg Glu His Tyr Asp Phe Leu Thr
 75                  80                  85                  90

gaa tta act gag gtt ctc aat gga aaa ata ttg gta gac atc agc aac      520
Glu Leu Thr Glu Val Leu Asn Gly Lys Ile Leu Val Asp Ile Ser Asn
                 95                 100                 105

aac ctc aaa atc aat caa tat cca gaa tct aat gca gag tac ctt gct      568
Asn Leu Lys Ile Asn Gln Tyr Pro Glu Ser Asn Ala Glu Tyr Leu Ala
            110                 115                 120

cat ttg gtg cca gga gcc cac gtg gta aaa gca ttt aac acc atc tca      616
His Leu Val Pro Gly Ala His Val Val Lys Ala Phe Asn Thr Ile Ser
        125                 130                 135

gcc tgg gct ctc cag tca gga gca ctg gat gca agt cgg cag gtg ttt      664
Ala Trp Ala Leu Gln Ser Gly Ala Leu Asp Ala Ser Arg Gln Val Phe
    140                 145                 150

gtg tgt gga aat gac agc aaa gcc aag caa aga gtg atg gat att gtt      712
Val Cys Gly Asn Asp Ser Lys Ala Lys Gln Arg Val Met Asp Ile Val
155                 160                 165                 170

cgt aat ctt gga ctt act cca atg gat caa gga tca ctc atg gca gcc      760
Arg Asn Leu Gly Leu Thr Pro Met Asp Gln Gly Ser Leu Met Ala Ala
                175                 180                 185

aaa gaa att gaa aag tac ccc ctg cag cta ttt cca atg tgg agg ttc      808
Lys Glu Ile Glu Lys Tyr Pro Leu Gln Leu Phe Pro Met Trp Arg Phe
            190                 195                 200

ccc ttc tat ttg tct gct gtg ctg tgt gtc ttc ttg ttt ttc tat tgt      856
Pro Phe Tyr Leu Ser Ala Val Leu Cys Val Phe Leu Phe Phe Tyr Cys
        205                 210                 215

gtt ata aga gac gta atc tac cct tat gtt tat gaa aag aaa gat aat      904
Val Ile Arg Asp Val Ile Tyr Pro Tyr Val Tyr Glu Lys Lys Asp Asn
```

```
    220                 225                 230

aca ttt cgt atg gct att tcc att cca aat cgt atc ttt cca ata aca      952
Thr Phe Arg Met Ala Ile Ser Ile Pro Asn Arg Ile Phe Pro Ile Thr
235                 240                 245                 250

gca ctt aca ctg ctt gct ttg gtt tac ctc cct ggt gtt att gct gcc     1000
Ala Leu Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Val Ile Ala Ala
                255                 260                 265

att cta caa ctg tac cga ggc aca aaa tac cgt cga ttc cca gac tgg     1048
Ile Leu Gln Leu Tyr Arg Gly Thr Lys Tyr Arg Arg Phe Pro Asp Trp
            270                 275                 280

ctt gac cac tgg atg ctt tgc cga aag cag ctt ggc ttg gta gct ctg     1096
Leu Asp His Trp Met Leu Cys Arg Lys Gln Leu Gly Leu Val Ala Leu
        285                 290                 295

gga ttt gcc ttc ctt cat gtc ctc tac aca ctt gtg att cct att cga     1144
Gly Phe Ala Phe Leu His Val Leu Tyr Thr Leu Val Ile Pro Ile Arg
    300                 305                 310

tat tat gta cga tgg aga ttg gga aac tta acc gtt acc cag gca ata     1192
Tyr Tyr Val Arg Trp Arg Leu Gly Asn Leu Thr Val Thr Gln Ala Ile
315                 320                 325                 330

ctc aag aag gag aat cca ttt agc acc tcc tca gcc tgg ctc agt gat     1240
Leu Lys Lys Glu Asn Pro Phe Ser Thr Ser Ser Ala Trp Leu Ser Asp
                335                 340                 345

tca tat gtg gct ttg gga ata ctt ggg ttt ttt ctg ttt gta ctc ttg     1288
Ser Tyr Val Ala Leu Gly Ile Leu Gly Phe Phe Leu Phe Val Leu Leu
            350                 355                 360

gga atc act tct ttg cca tct gtt agc aat gca gtc aac tgg aga gag     1336
Gly Ile Thr Ser Leu Pro Ser Val Ser Asn Ala Val Asn Trp Arg Glu
        365                 370                 375

ttc cga ttt gtc cag tcc aaa ctg ggt tat ttg acc ctg atc ttg tgt     1384
Phe Arg Phe Val Gln Ser Lys Leu Gly Tyr Leu Thr Leu Ile Leu Cys
    380                 385                 390

aca gcc cac acc ctg gtg tac ggt ggg aag aga ttc ctc agc cct tca     1432
Thr Ala His Thr Leu Val Tyr Gly Gly Lys Arg Phe Leu Ser Pro Ser
395                 400                 405                 410

aat ctc aga tgg tat ctt cct gca gcc tac gtg tta ggg ctt atc att     1480
Asn Leu Arg Trp Tyr Leu Pro Ala Ala Tyr Val Leu Gly Leu Ile Ile
                415                 420                 425

cct tgc act gtg ctg gtg atc aag ttt gtc cta atc atg cca tgt gta     1528
Pro Cys Thr Val Leu Val Ile Lys Phe Val Leu Ile Met Pro Cys Val
            430                 435                 440

gac aac acc ctt aca agg atc cgc cag ggc tgg gaa agg aac tca aaa     1576
Asp Asn Thr Leu Thr Arg Ile Arg Gln Gly Trp Glu Arg Asn Ser Lys
        445                 450                 455
```

```
cac tag aaaaagcatt gaatggaaaa tcaatattta aaacaaagtt caatttagct      1632
His  *
    460

ggatttctga actatggttt tgaatgttta aagaagaatg atgggtacag ttaggaaagt   1692

tttttcttta caccgtgact gagggaaaca ttgcttgtct ttgagaaatt gactgacata   1752

ctggaagaga acaccatttt atctcaggtt agtgaagaat cagtgcaggt ccctgactct   1812

tattttccca gaggccatgg agctgagatt gagactagcc ttgtggtttc acactaaaga   1872

gtttccttgt tatgggcaac atgcatgacc taatgtcttg caaaatccaa tagaagtatt   1932

gcagcttcct tctctggctc aagggctgag ttaagtgaaa ggaaaaacag cacaatggtg   1992

accactgata aaggctttat taggtatatc tgaggaagtg ggtcacatga aatgtaaaaa   2052

gggaatgagg tttttgttgt tttttggaag taaaggcaaa cataaatatt accatgatga   2112

attctagtga aatgacccct tgactttgct tttcttaata cagatattta ctgagaggaa   2172

ctatttttat aacacaagaa aaatttacaa ttgattaaaa gtatccatgt cttggataca   2232

tacgtaaaaa aaaaaaaaa                                                2251



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ggccagagcc caccctcctg ctcatgaggg cagacaggcc tttccaggga cacagtccct    120

cttctcccca ggaccccagg gccaactccc cctgccggcc ctctgccatc aaattggcag    180

tggctccagg ggagtcccct ggggatgggg gaccactgtt ggggacccct ctgcgtgcac    240

ccctgtagtt ggggaagcag gacaggggcc tggggagacg gaagggcgcc aggggttgag    300

agagg    atg gtg gac gtt gtt gga ctt gaa agg gaa aca ggc cct cgg      347
         Met Val Asp Val Val Gly Leu Glu Arg Glu Thr Gly Pro Arg
          1               5                  10

gga agc ccc tgg cca ggc ctg cct ctc ccc tcc ctg gtg ggc cca gcg      395
Gly Ser Pro Trp Pro Gly Leu Pro Leu Pro Ser Leu Val Gly Pro Ala
 15                  20                  25                  30
```

```
ccc ctg ctc act tgt ctc tgc cca cag tgc ctg tct gtg gag gac gcc         443
Pro Leu Leu Thr Cys Leu Cys Pro Gln Cys Leu Ser Val Glu Asp Ala
                35                  40                  45

ctg ggc ctg ggc gag cct gag ggg tca ggg ctg ccc ccg ggc ccg gtc         491
Leu Gly Leu Gly Glu Pro Glu Gly Ser Gly Leu Pro Pro Gly Pro Val
            50                  55                  60

ctg gag gcc agg tac gtc gcc cgc ctc agt gcc gcc gcc gtc ctg tac         539
Leu Glu Ala Arg Tyr Val Ala Arg Leu Ser Ala Ala Ala Val Leu Tyr
        65                  70                  75

ctc agc aac ccc gag ggc acc tgt gag gac gct cgg gct ggc ctc tgg         587
Leu Ser Asn Pro Glu Gly Thr Cys Glu Asp Ala Arg Ala Gly Leu Trp
    80                  85                  90

gcc tct cat gca gac cac ctc ctg gcc ctg ctc gag agc ccc aag gcc         635
Ala Ser His Ala Asp His Leu Leu Ala Leu Leu Glu Ser Pro Lys Ala
95                  100                 105                 110

ctg acc ccg ggc ctg agc tgg ctg ctg cag agg atg cag gcc cgg gct         683
Leu Thr Pro Gly Leu Ser Trp Leu Leu Gln Arg Met Gln Ala Arg Ala
                115                 120                 125

gcc ggc cag acc ccc aag acg gcc tgc gta gat atc cct cag ctg ctg         731
Ala Gly Gln Thr Pro Lys Thr Ala Cys Val Asp Ile Pro Gln Leu Leu
            130                 135                 140

gag gag gcg gtg ggg gcg ggg gct ccg ggc agt gct ggc ggc gtc ctg         779
Glu Glu Ala Val Gly Ala Gly Ala Pro Gly Ser Ala Gly Gly Val Leu
        145                 150                 155

gct gcc ctg ctg gac cat gtc agg agc ggg tct tgc ttc cac gcc ttg         827
Ala Ala Leu Leu Asp His Val Arg Ser Gly Ser Cys Phe His Ala Leu
    160                 165                 170

ccg agc cct cag tac ttc gtg gac ttt gtg ttc cag cag cac agc agc         875
Pro Ser Pro Gln Tyr Phe Val Asp Phe Val Phe Gln Gln His Ser Ser
175                 180                 185                 190

gag gtc cct atg acg ctg gcc gag ctg tca gcc ttg atg cag cgc ctg         923
Glu Val Pro Met Thr Leu Ala Glu Leu Ser Ala Leu Met Gln Arg Leu
                195                 200                 205

ggg gtg ggc agg gag gcc cac agt gac cac agt cat cgg cac agg gga         971
Gly Val Gly Arg Glu Ala His Ser Asp His Ser His Arg His Arg Gly
            210                 215                 220

gcc agc agc cgg gac cct gtg ccc ctc atc agc tcc agc aac agc tcc        1019
Ala Ser Ser Arg Asp Pro Val Pro Leu Ile Ser Ser Ser Asn Ser Ser
        225                 230                 235

agt gtg tgg gac acg gta tgc ctg agt gcc agg gac gtg atg gct gca        1067
Ser Val Trp Asp Thr Val Cys Leu Ser Ala Arg Asp Val Met Ala Ala
    240                 245                 250
```

```
tat gga ctg tcg gaa cag gct ggg gtg acc ccg gag gcc tgg gcc caa      1115
Tyr Gly Leu Ser Glu Gln Ala Gly Val Thr Pro Glu Ala Trp Ala Gln
255                 260                 265                 270

ctg agc cct gcc ctg ctc caa cag cag ctg agt gga gcc tgc acc tcc      1163
Leu Ser Pro Ala Leu Leu Gln Gln Gln Leu Ser Gly Ala Cys Thr Ser
                275                 280                 285

cag tcc agg ccc ccc gtc cag gac cag ctc agc cag tca gag agg tat      1211
Gln Ser Arg Pro Pro Val Gln Asp Gln Leu Ser Gln Ser Glu Arg Tyr
            290                 295                 300

ctg tac ggc tcc ctg gcc acg ctg ctc atc tgc ctc tgc gcg gtc ttt      1259
Leu Tyr Gly Ser Leu Ala Thr Leu Leu Ile Cys Leu Cys Ala Val Phe
        305                 310                 315

ggc ctc ctg ctg ctg acc tgc act ggc tgc agg ggg gtc gcc cac tac      1307
Gly Leu Leu Leu Leu Thr Cys Thr Gly Cys Arg Gly Val Ala His Tyr
    320                 325                 330

atc ctg cag acc ttc ctg agc ctg gca gtg ggt gca ctc act ggg gac      1355
Ile Leu Gln Thr Phe Leu Ser Leu Ala Val Gly Ala Leu Thr Gly Asp
335                 340                 345                 350

gct gtc ctg cat ctg acg ccc aag gtg ctg ggg ctg cat aca cac agc      1403
Ala Val Leu His Leu Thr Pro Lys Val Leu Gly Leu His Thr His Ser
                355                 360                 365

gaa gag ggc ctc agc cca cag ccc acc tgg cgc ctc ctg gct atg ctg      1451
Glu Glu Gly Leu Ser Pro Gln Pro Thr Trp Arg Leu Leu Ala Met Leu
            370                 375                 380

gcc ggg ctc tac gcc ttc ttc ctg ttt gag aac ctc ttc aat ctc ctg      1499
Ala Gly Leu Tyr Ala Phe Phe Leu Phe Glu Asn Leu Phe Asn Leu Leu
        385                 390                 395

ctg ccc agg gac ccg gag gac ctg gag gac ggg ccc tgc ggc cac agc      1547
Leu Pro Arg Asp Pro Glu Asp Leu Glu Asp Gly Pro Cys Gly His Ser
    400                 405                 410

agc cat agc cac ggg ggc cac agc cac ggt gtg tcc ctg cag ctg gca      1595
Ser His Ser His Gly Gly His Ser His Gly Val Ser Leu Gln Leu Ala
415                 420                 425                 430

ccc agc gag ctc cgg cag ccc aag ccc ccc cac gag ggc tcc cgc gca      1643
Pro Ser Glu Leu Arg Gln Pro Lys Pro Pro His Glu Gly Ser Arg Ala
                435                 440                 445

gac ctg gtg gcg gag gag agc ccg gag ctg ctg aac cct gag ccc agg      1691
Asp Leu Val Ala Glu Glu Ser Pro Glu Leu Leu Asn Pro Glu Pro Arg
            450                 455                 460

aga ctg agc cca gag ttg agg cta ctg ccc tat atg atc act ctg ggc      1739
Arg Leu Ser Pro Glu Leu Arg Leu Leu Pro Tyr Met Ile Thr Leu Gly
        465                 470                 475

gac gcc gtg cac aac ttc gcc gac ggg ctg gcc gtg ggc gcc gcc ttc      1787
```

```
Asp Ala Val His Asn Phe Ala Asp Gly Leu Ala Val Gly Ala Ala Phe
    480                 485                 490

gcg tcc tcc tgg aag acc ggg ctg gcc acc tcg ctg gcc gtg ttc tgc      1835
Ala Ser Ser Trp Lys Thr Gly Leu Ala Thr Ser Leu Ala Val Phe Cys
495                 500                 505                 510

cac gag ttg cca cac gag ctg ggg gac ttc gcc gcc ttg ctg cac gcg      1883
His Glu Leu Pro His Glu Leu Gly Asp Phe Ala Ala Leu Leu His Ala
                515                 520                 525

ggg ctg tcc gtg cgc caa gca ctg ctg ctg aac ctg gcc tcc gcg ctc      1931
Gly Leu Ser Val Arg Gln Ala Leu Leu Leu Asn Leu Ala Ser Ala Leu
            530                 535                 540

acg gcc ttc gct ggt ctc tac gtg gca ctc gcg gtt gga gtc agc gag      1979
Thr Ala Phe Ala Gly Leu Tyr Val Ala Leu Ala Val Gly Val Ser Glu
        545                 550                 555

gag agc gag gcc tgg atc ctg gca gtg gcc acc ggc ctg ttc ctc tac      2027
Glu Ser Glu Ala Trp Ile Leu Ala Val Ala Thr Gly Leu Phe Leu Tyr
    560                 565                 570

gta gca ctc tgc gac atg ctc ccg gcg atg ttg aaa gta cgg gac ccg      2075
Val Ala Leu Cys Asp Met Leu Pro Ala Met Leu Lys Val Arg Asp Pro
575                 580                 585                 590

cgg ccc tgg ctc ctc ttc ctg ctg cac aac gtg ggc ctg ctg ggc ggc      2123
Arg Pro Trp Leu Leu Phe Leu Leu His Asn Val Gly Leu Leu Gly Gly
                595                 600                 605

tgg acc gtc ctg ctg ctg ctg tcc ctg tac gag gat gac atc acc ttc      2171
Trp Thr Val Leu Leu Leu Leu Ser Leu Tyr Glu Asp Asp Ile Thr Phe
            610                 615                 620

tga tacc ctgccctagt cccccacctt tgacttaaga tcccacacct cacaaaccta      2228
 *

cagcccagaa accagaagcc cctatagagg ccccagtccc aactccagta aagacactct    2288

tgtccttgga aaaaaaaaaa aa                                             2310



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ttcccagggt tcacgccaca ctctaggaag tgcctgagct agtgagctgg ccaacgagct    120

ccgcgggctg ggacc atg ggc tgc ttc ttc tcc aag aga cgg aag gct gac     171
                 Met Gly Cys Phe Phe Ser Lys Arg Arg Lys Ala Asp
                  1               5                  10

aag gag tcg cgg ccc gag aac gag gag gag cgg cca aag cag tac agc      219
Lys Glu Ser Arg Pro Glu Asn Glu Glu Glu Arg Pro Lys Gln Tyr Ser
        15                  20                  25

tgg gat cag cgc gag aag gtt gat cca aaa gac tac atg ttc agt gga      267
Trp Asp Gln Arg Glu Lys Val Asp Pro Lys Asp Tyr Met Phe Ser Gly
    30                  35                  40

ctg aag gat gaa aca gta ggt cgc tta cct ggg acg gta gca gga caa      315
Leu Lys Asp Glu Thr Val Gly Arg Leu Pro Gly Thr Val Ala Gly Gln
45                  50                  55                  60

cag ttt ctc att caa gac tgt gag aac tgt aac atc tat att ttt gat      363
Gln Phe Leu Ile Gln Asp Cys Glu Asn Cys Asn Ile Tyr Ile Phe Asp
                65                  70                  75

cac tct gct aca gtt acc att gat gac tgt act aac tgc ata att ttt      411
His Ser Ala Thr Val Thr Ile Asp Asp Cys Thr Asn Cys Ile Ile Phe
            80                  85                  90

ctg gga ccc gtg aaa ggc agc gtg ttt ttc cgg aat tgc aga gat tgc      459
Leu Gly Pro Val Lys Gly Ser Val Phe Phe Arg Asn Cys Arg Asp Cys
        95                 100                 105

aag tgc aca tta gcc tgc caa caa ttt cgt gtg cga gat tgt aga aag      507
Lys Cys Thr Leu Ala Cys Gln Gln Phe Arg Val Arg Asp Cys Arg Lys
    110                 115                 120

ctg gaa gtc ttt ttg tgt tgt gcc act caa ccc atc att gag tct tcc      555
Leu Glu Val Phe Leu Cys Cys Ala Thr Gln Pro Ile Ile Glu Ser Ser
125                 130                 135                 140

tca aat atc aaa ttt gga tgt ttt caa tgg tac tat cct gaa tta gct      603
Ser Asn Ile Lys Phe Gly Cys Phe Gln Trp Tyr Tyr Pro Glu Leu Ala
                145                 150                 155

ttc cag ttc aaa gat gca ggg cta agt atc ttc gac aat aca tgg agt      651
Phe Gln Phe Lys Asp Ala Gly Leu Ser Ile Phe Asp Asn Thr Trp Ser
            160                 165                 170

aac att cat gac ttt aca cct gtg tca gga gaa ctc aac tgg agc ctt      699
Asn Ile His Asp Phe Thr Pro Val Ser Gly Glu Leu Asn Trp Ser Leu
        175                 180                 185

ctt cca gaa gat gct gtg gtt cag gac tat gtt cct ata cct act acc      747
Leu Pro Glu Asp Ala Val Val Gln Asp Tyr Val Pro Ile Pro Thr Thr
    190                 195                 200

gaa gag ctc aaa gct gtt cgt gtt tcc aca gaa gcc aat aga agc att      795
Glu Glu Leu Lys Ala Val Arg Val Ser Thr Glu Ala Asn Arg Ser Ile
```

```
205                 210                 215                 220

gtt cca ata tcc cgg ggt cag aga cag aag agc agc gat gaa tca tgc       843
Val Pro Ile Ser Arg Gly Gln Arg Gln Lys Ser Ser Asp Glu Ser Cys
                225                 230                 235

tta gtg gta tta ttt gct ggt gat tac act att gca aat gcc aga aaa       891
Leu Val Val Leu Phe Ala Gly Asp Tyr Thr Ile Ala Asn Ala Arg Lys
            240                 245                 250

cta att gat gag atg gtt ggt aaa ggc ttt ttc cta gtt cag aca aag       939
Leu Ile Asp Glu Met Val Gly Lys Gly Phe Phe Leu Val Gln Thr Lys
        255                 260                 265

gaa gtg tcc atg aaa gct gag gat gct caa agg gtt ttt cgg gaa aaa       987
Glu Val Ser Met Lys Ala Glu Asp Ala Gln Arg Val Phe Arg Glu Lys
    270                 275                 280

gca cct gac ttc ctt cct ctt ctg aac aaa ggt cct gtt att gcc ttg      1035
Ala Pro Asp Phe Leu Pro Leu Leu Asn Lys Gly Pro Val Ile Ala Leu
285                 290                 295                 300

gag ttt aat ggg gat ggt gct gta gaa gta tgt caa ctt att gta aac      1083
Glu Phe Asn Gly Asp Gly Ala Val Glu Val Cys Gln Leu Ile Val Asn
                305                 310                 315

gag ata ttc aat ggg acc aag atg ttt gta tct gaa agc aag gag aca      1131
Glu Ile Phe Asn Gly Thr Lys Met Phe Val Ser Glu Ser Lys Glu Thr
            320                 325                 330

ggt ttc tgg aga tgt aga cac gct cta aca ctt ggc tga tatacagatg       1180
Gly Phe Trp Arg Cys Arg His Ala Leu Thr Leu Gly  *
        335                 340                 345

ggaatatgaa gtgcaatgtg gaacccggac ttggtataag acctttccca ctt          1233


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ctaaggaggt tgtctcagtt tttgtcagca tctccacccc gaggtggttt gaactttgag     120

ccttttgtag tcctgatgaa taatttcatt ttcctcaagt ttatgacact cggaacgtca     180

agaactggag gtttgtgcaa tttgagaccg gtcggcactg tgcagagatc agagtactaa     240
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gagacagaga ttaaa atg gct tcc aga gga aag aca gag aca agc aaa tta     291
                 Met Ala Ser Arg Gly Lys Thr Glu Thr Ser Lys Leu
                   1               5                  10

aag cag aat tta gaa gaa cag ttg gat aga ctc atg caa caa tta caa      339
Lys Gln Asn Leu Glu Glu Gln Leu Asp Arg Leu Met Gln Gln Leu Gln
         15                  20                  25

gat ctg gag gaa tgc aga gag gaa ctt gat aca gat gaa tat gaa gaa      387
Asp Leu Glu Glu Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr Glu Glu
     30                  35                  40

acc aaa aag gaa act ctg gag caa cta agt gaa ttt aat gat tca cta      435
Thr Lys Lys Glu Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp Ser Leu
 45                  50                  55                  60

aag aaa att atg tct gga aat atg act ttg gta gat gaa cta agt gga      483
Lys Lys Ile Met Ser Gly Asn Met Thr Leu Val Asp Glu Leu Ser Gly
                 65                  70                  75

atg cag ctg gct att cag gca gct atc agc cag gcc ttt aaa acc cca      531
Met Gln Leu Ala Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys Thr Pro
             80                  85                  90

gag gtc atc aga ttg ttt gca aag aaa caa cca ggt cag ctt cgg aca      579
Glu Val Ile Arg Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu Arg Thr
         95                  100                 105

agg tta gca gag atg gat aga gat ctg atg gta gga aag ctg gaa aga      627
Arg Leu Ala Glu Met Asp Arg Asp Leu Met Val Gly Lys Leu Glu Arg
     110                 115                 120

gac ctg tac act caa cag aaa gtg gag ata cta aca gct ctt agg aaa      675
Asp Leu Tyr Thr Gln Gln Lys Val Glu Ile Leu Thr Ala Leu Arg Lys
125                 130                 135                 140

ctt gga gag aag ctg act gca gat gat gag gcc ttc ttg tca gca aat      723
Leu Gly Glu Lys Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser Ala Asn
                145                 150                 155

gca ggt gct ata ctc agc cag ttt gag aaa gtc tct aca gac ctt gga      771
Ala Gly Ala Ile Leu Ser Gln Phe Glu Lys Val Ser Thr Asp Leu Gly
            160                 165                 170

cgg ccc cca agt tac atg aac tac ctg cta gac tca cac ccc agc aaa      819
Arg Pro Pro Ser Tyr Met Asn Tyr Leu Leu Asp Ser His Pro Ser Lys
        175                 180                 185

aat att gat gtc ccc agc aag att agc ttc ctg tta aag atc cag gac      867
Asn Ile Asp Val Pro Ser Lys Ile Ser Phe Leu Leu Lys Ile Gln Asp
    190                 195                 200

ctg tga atacatgcgt aactgcaaga atggaagcaa aggatgaacc caagttaaag      923
Leu  *
205

cccagcacaa gaatatgatg taagcgcttt tgggaaatgc agagattttc ttttctcttc    983
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aaataataaa ttacatctaa aaattaaaaa aaaaaaaa 1021

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Met Glu Ala Glu Glu Ser Glu Lys Ala Ala Thr Glu Gln Glu Pro Leu
1 5 10 15

gaa ggg aca gaa cag aca cta gat gcg gag gag gag cag gag gaa tcc 96
Glu Gly Thr Glu Gln Thr Leu Asp Ala Glu Glu Glu Gln Glu Glu Ser
20 25 30

gaa gaa gcg gcc tgt ggc agc aag aag cgg gta gtg cca ggt att gtg 144
Glu Glu Ala Ala Cys Gly Ser Lys Lys Arg Val Val Pro Gly Ile Val
35 40 45

tac ctg ggc cat atc ccg ccg cgc ttc cgg ccc ctg cac gtc cgc aac 192
Tyr Leu Gly His Ile Pro Pro Arg Phe Arg Pro Leu His Val Arg Asn
50 55 60

ctt ctc agc gcc tat ggc gag gtc gga cgc gtc ttc ttt cag gct gag 240
Leu Leu Ser Ala Tyr Gly Glu Val Gly Arg Val Phe Phe Gln Ala Glu
65 70 75 80

gac cgg ttc gtg aga cgc aag aag aag gca gca gca gct gcc gga gga 288
Asp Arg Phe Val Arg Arg Lys Lys Lys Ala Ala Ala Ala Ala Gly Gly
85 90 95

aaa aag cgg tcc tac acc aag gac tac acc gag gga tgg gtg gag ttc 336
Lys Lys Arg Ser Tyr Thr Lys Asp Tyr Thr Glu Gly Trp Val Glu Phe
100 105 110

cgt gac aag cgc ata gcc aag cgc gtg gcg gcc agt cta cac aac acg 384
Arg Asp Lys Arg Ile Ala Lys Arg Val Ala Ala Ser Leu His Asn Thr
115 120 125

cct atg ggt gcc cgc agg cgc agc ccc ttc cgt tat gat ctt tgg aac 432
Pro Met Gly Ala Arg Arg Arg Ser Pro Phe Arg Tyr Asp Leu Trp Asn
130 135 140

ctc aag tac ttg cac cgt ttc acc tgg tcc cac ctc agc gag cac ctc 480
Leu Lys Tyr Leu His Arg Phe Thr Trp Ser His Leu Ser Glu His Leu
145 150 155 160

gcc ttt gag cgc cag gtg cgc agg cag cgc ttg aga gcg gag gtt gct 528

```
Ala Phe Glu Arg Gln Val Arg Arg Gln Arg Leu Arg Ala Glu Val Ala
            165                 170                 175

caa gcc aag cgt gag acc gac ttc tat ctt caa agt gtg gaa cgg gga      576
Gln Ala Lys Arg Glu Thr Asp Phe Tyr Leu Gln Ser Val Glu Arg Gly
        180                 185                 190

caa cgc ttt ctt gcg gcc gat ggg gac cct gct cgc cca gat ggc tcc      624
Gln Arg Phe Leu Ala Ala Asp Gly Asp Pro Ala Arg Pro Asp Gly Ser
    195                 200                 205

tgg aca ttt gcc cag cgt cct act gag cag gaa ctg agg gcc cgt aaa      672
Trp Thr Phe Ala Gln Arg Pro Thr Glu Gln Glu Leu Arg Ala Arg Lys
210                 215                 220

gca gca cgg cca ggg gga cgt gaa cgg gct cgc ctg gca act gcc cag      720
Ala Ala Arg Pro Gly Gly Arg Glu Arg Ala Arg Leu Ala Thr Ala Gln
225                 230                 235                 240

gac aag gcc cgc tcc aac aaa ggg ctc ctg gcc agg atc ttt gga gcc      768
Asp Lys Ala Arg Ser Asn Lys Gly Leu Leu Ala Arg Ile Phe Gly Ala
                245                 250                 255

ccg cca ccc tca gag agc atg gag gga cct tcc ctt gtc agg gac tcc      816
Pro Pro Pro Ser Glu Ser Met Glu Gly Pro Ser Leu Val Arg Asp Ser
            260                 265                 270

tga gggc ctgggtggcc ccttccattt cctggccctg ctctgcttcc tgtctacctc      873
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atactagaat gatcgtgact acccgggcag acattttact gtgtttctca gaccaagtgt     933

ctactgatgg cccaaacatg gagttttgtg ggcttccact gtccccactc cgaactcctg     993

tatgtgcctg gctgagtcac ctaattcata ctgtcatact agcataatta tgactattgc    1053

atatgcttgt tttgtttgac tcttggctgc ctacgtctgt agggtcccct gaaaatccca    1113

cttcctgccc ccagaaaggg cctttatttc caactaggag gataatgcct agtccaggca    1173

atctttctct gtttagcagt cacaggtgag ggtggtatta gcatcttttt tatgtagaaa    1233

aaattgagtt aatggggtgg actgggttgg gaagaaatac atttcctaat gtatttatag    1293

aaaataaaaa tatttttatg tgccttttta tttttgttgg tggggaggtc attggacaag    1353

ttccaacttt catcttgtgt tcccttcacc ttcatatcct gatcttagag ccccccctccc   1413

cctggcaccc accttactgt ttaacctgga tttttttttc tatttaattt ttgtctaata    1473

tattagccca gtttatcaat cagttatctt aagtcagcat tttctaagcc attgtttgag    1533

ggaacagtga caatagggaa taacaccact tagtattaag ggtttttc                 1581
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<210> 157
<211> 1642
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<222> (228)..(911)

<400> 157
aaggatcctt aattaaatta atcccccccc cccccccgag tagcggcagc ggcgacgacg      60

gcggcggcag cgctccaact ggctcctcgc tccgggctcc gccgtcgagc cgggagagag     120

cctccgccag cggccaggca ccagccagac gacgccagcg accccggcct ctcggcggca     180

ccgcgctaac tcaggggctg cataggcacc cagagccgaa ctccaag atg gga ggc       236
                                                    Met Gly Gly
                                                    1

aag ctc agc aag aag aag aag ggc tac aat gtg aac gac gag aaa gcc       284
Lys Leu Ser Lys Lys Lys Lys Gly Tyr Asn Val Asn Asp Glu Lys Ala
    5                   10                  15

aag gag aaa gac aag aag gcc gag ggc gcg gcg acg gaa gag gag ggg       332
Lys Glu Lys Asp Lys Lys Ala Glu Gly Ala Ala Thr Glu Glu Glu Gly
20                  25                  30                  35

acc ccg aag gag agt gag ccc cag gcg gcc gca gag ccc gcc gag gcc       380
Thr Pro Lys Glu Ser Glu Pro Gln Ala Ala Ala Glu Pro Ala Glu Ala
                40                  45                  50

aag gag ggc aag gag aag ccc gac cag gac gcc gag ggc aag gcc gag       428
Lys Glu Gly Lys Glu Lys Pro Asp Gln Asp Ala Glu Gly Lys Ala Glu
            55                  60                  65

gag aag gag ggc gag aag gac gcg gcg gct gcc aag gag gag gcc ccg       476
Glu Lys Glu Gly Glu Lys Asp Ala Ala Ala Ala Lys Glu Glu Ala Pro
        70                  75                  80

aag gcg gag ccc gag aag acg gag ggc gcg gca gag gcc aag gct gag       524
Lys Ala Glu Pro Glu Lys Thr Glu Gly Ala Ala Glu Ala Lys Ala Glu
    85                  90                  95

ccc ccg aag gcg ccc gag cag gag cag gcg gcc ccc ggc ccc gct gcg       572
Pro Pro Lys Ala Pro Glu Gln Glu Gln Ala Ala Pro Gly Pro Ala Ala
100                 105                 110                 115

ggc ggc gag gcc ccc aaa gct gct gag gcc gcc gcg gcc ccg gcc gag       620
Gly Gly Glu Ala Pro Lys Ala Ala Glu Ala Ala Ala Ala Pro Ala Glu
                120                 125                 130

agc gcg gcc cct gcc gcc ggg gag gag ccc agc aag gag gaa ggg gaa       668
Ser Ala Ala Pro Ala Ala Gly Glu Glu Pro Ser Lys Glu Glu Gly Glu
            135                 140                 145
```

```
ccc aaa aag act gag gcg ccc gca gct cct gcc gcc cag gag acc aaa      716
Pro Lys Lys Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Glu Thr Lys
        150                 155                 160

agt gac ggg gcc cca gct tca gac tca aaa ccc ggc agc tcg gag gct      764
Ser Asp Gly Ala Pro Ala Ser Asp Ser Lys Pro Gly Ser Ser Glu Ala
    165                 170                 175

gcc ccc tct tcc aag gag acc ccc gca gcc acg gaa gcg cct agt tcc      812
Ala Pro Ser Ser Lys Glu Thr Pro Ala Ala Thr Glu Ala Pro Ser Ser
180                 185                 190                 195

aca ccc aag gcc cag ggc ccc gca gcc tct gca gaa gag ccc aag ccg      860
Thr Pro Lys Ala Gln Gly Pro Ala Ala Ser Ala Glu Glu Pro Lys Pro
                200                 205                 210

gtg gag gcc ccg gca gct aat tcc gac caa acc gta acc gtg aaa gag      908
Val Glu Ala Pro Ala Ala Asn Ser Asp Gln Thr Val Thr Val Lys Glu
            215                 220                 225

tga caag gacagcctat aggaaaaaca ataccactta aaacaatctc ctctctctct      965
 *


ctctctctct ctctatctct ctctctatct cctctctctc tctcctctcc tatctctcct   1025

ctctctctct cctatactaa cttgtttcaa attggaagta atgatatgta ttgcccaagg   1085

aaaaatacag gatgttgtcc catcaaggga gggagggggt gggagaatcc aaatagtatt   1145

tttgtgggga aatatctaat ataccttcag tcaactttac caagaagtcc tggatttcca   1205

agatccgcgt ctgaaagtgc agtacatcgt ttgtacctga aactgccgcc acatgcactc   1265

ctccaccgct gagagttgaa tagcttttct tctgcaatgg gagttgggag tgatgcgttt   1325

gattctgccc acagggcctg tgccaaggca atcagatctt tatgagagca gtattttctg   1385

tgttttcttt ttaatttaca gcctttctta ttttgatatt tttttaatgt tgtggatgaa   1445

tgccagcttt cagacagagc ccacttagct tgtccacatg gatctcaatg ccaatcctcc   1505

attcttcctc tccagatatt tttgggagtg acaaacattc tctcatccta cttagcctac   1565

ctagatttct catgacgagt taatgcatgt ccgtggttgg gtgcacctgt agttctgttt   1625

attggtcagt ggaaatg                                                  1642
```

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<210> 158
<211> 1521
<212> DNA
<213> Homo sapiens

<220>
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     <221> CDS
     <222> (417)..(1403)

     <400> 158
aaggatcctt aattaaatta atcccccccc cccccccggg cgagggggag gcgggacccg      60

cgaggagtcg cgccgaggac ggaggccacg atacctgcgt ggctggggct gcgggctccg     120

gggtcaccac cctgggcgac ccggaggtgg cgcctccgcc ggccgcagct ggagaggagc     180

gtgtccccaa gccgggggag caggacttga gcaggcacgc ggggtcaccg ccgggcagcg     240

tggaggagcc atctcctgga ggagaaaact cacctggtgg cggaggctcc ccttgtttgt     300

cctcccggag cctggcgtgg ggttcttctg cgggaagaga gagtgcgcgc ggagatagca     360

gtgtggaaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc         416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta       464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
1               5                   10                  15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct       512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
            20                  25                  30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac       560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
        35                  40                  45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa       608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
    50                  55                  60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att       656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
65                  70                  75                  80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat       704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
                85                  90                  95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag       752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
            100                 105                 110

gaa agg tta ttt gtc aat gaa gaa aat gtt aat gag ttt ctt gaa gag       800
Glu Arg Leu Phe Val Asn Glu Glu Asn Val Asn Glu Phe Leu Glu Glu
        115                 120                 125

gtc ctg agc tct cca ttc aaa cag tct atg tcc ttg acc cca cca tta       848
Val Leu Ser Ser Pro Phe Lys Gln Ser Met Ser Leu Thr Pro Pro Leu
    130                 135                 140

att gaa gtt ctt caa gtt act gat aat aag att caa att aat gca aag       896
Ile Glu Val Leu Gln Val Thr Asp Asn Lys Ile Gln Ile Asn Ala Lys
145                 150                 155                 160
```

```
ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga       944
Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg
                165                 170                 175

gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt       992
Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys
            180                 185                 190

aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta      1040
Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu
        195                 200                 205

caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt      1088
Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu
    210                 215                 220

gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa      1136
Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys
225                 230                 235                 240

atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag      1184
Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu
                245                 250                 255

gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca      1232
Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr
            260                 265                 270

gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat      1280
Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn
        275                 280                 285

ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt      1328
Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser
    290                 295                 300

gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag      1376
Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln
305                 310                 315                 320

aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gacttttaaa      1428
Asn Ser Leu Leu Tyr Asp Leu Asp  *
                325

tattaaggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaact    1488

aaaggtatta aagtataaaa ttaaaatttg caa                                 1521



     <210> 159
     <211> 1377
     <212> DNA
     <213> Homo sapiens

     <220>
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<221>  CDS
<222>  (417)..(1259)

<400>  159
aaggatcctt aattaaatta atcccccccc cccccccgg cgagggggag gcgggacccg      60

cgaggagtcg cgccgaggac ggaggccacg atacctgcgt ggctggggct gcgggctccg     120

gggtcaccac cctgggcgac ccggaggtgg cgcctccgcc ggccgcagct ggagaggagc     180

gtgtccccaa gccgggggag caggacttga gcaggcacgc ggggtcaccg ccgggcagcg     240

tggaggagcc atctcctgga ggagaaaact cacctggtgg cggaggctcc ccttgtttgt     300

cctcccggag cctggcgtgg ggttcttctg cgggaagaga gagtgcgcgc ggagatagca     360

gtgtggaaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc         416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta       464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
 1               5                  10                  15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct       512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
            20                  25                  30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac       560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
        35                  40                  45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa       608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
    50                  55                  60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att       656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
65                  70                  75                  80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat       704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
                85                  90                  95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag       752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
            100                 105                 110

ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga       800
Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg
        115                 120                 125

gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt       848
Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys
    130                 135                 140

aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta       896
Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu
145                 150                 155                 160
```

```
caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt       944
Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu
                165                 170                 175

gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa       992
Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys
            180                 185                 190

atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag      1040
Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu
        195                 200                 205

gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca      1088
Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr
    210                 215                 220

gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat      1136
Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn
225                 230                 235                 240

ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt      1184
Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser
                245                 250                 255

gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag      1232
Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln
            260                 265                 270

aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gacttttaaa      1284
Asn Ser Leu Leu Tyr Asp Leu Asp  *
        275                 280

tattaaggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaact   1344

aaaggtatta aagtataaaa ttaaaatttg caa                                 1377


     <210> 160
     <211> 1611
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (510)..(1112)

     <400> 160
cggccgccgg ggtcggcagc ctggggctcc gctgatctag ggcaacgagc gggggacgct      60

tcgagcccgc agcgagagtg accagcatgg tccctgccgg cagctcgggg ccggagggtt     120

ttgactgcaa ggccagccca cgccgagggt ccaagcatcg ggatatgccg ccagcacctg     180

gctgctgcag caccgcgctg gacatgagcg ctccgcccaa cccgacggcg tcagctggcg     240
```

```
cgcgcgcccg cgaccgacgt gcgcaggcgc ccacgggccg cgcagccgcc attgctctcc    300

tgccacggag gggagcgctt ggtggcagtc cgcgggcccg gacggaaggc tgaggcgacg    360

cctcgacgac agcggaccgg agctgcaggg gcaacacatt cagggcgggg tgccccattt    420

aggcctggct gaccggagta agaaactaca acccccgaag tgccttgcgc ctcaaggtta    480

cggaggcagt gaccacccac cctggagcc  atg gtc cac gcc ttc ctc att cac     533
                                 Met Val His Ala Phe Leu Ile His
                                  1               5

acc ttg agg gcc ccg aat act gag gac acg ggc ctt tgc cga gtg ctg      581
Thr Leu Arg Ala Pro Asn Thr Glu Asp Thr Gly Leu Cys Arg Val Leu
     10                  15                  20

tac tcc tgc gtc ttc ggt gct gag aag tca cct gat gac cca cgg ccg      629
Tyr Ser Cys Val Phe Gly Ala Glu Lys Ser Pro Asp Asp Pro Arg Pro
 25                  30                  35                  40

cat ggt gcc gag agg gac agg ctt ctc cgg aag gaa cag att tta gct      677
His Gly Ala Glu Arg Asp Arg Leu Leu Arg Lys Glu Gln Ile Leu Ala
                 45                  50                  55

gtg gcc agg cag gta gag tca atg tgt cgg ctg cag cag cag gca tct      725
Val Ala Arg Gln Val Glu Ser Met Cys Arg Leu Gln Gln Gln Ala Ser
             60                  65                  70

ggc cgg ccc ccc atg gac ctg cag ccg caa tcc tca gat gag caa gtg      773
Gly Arg Pro Pro Met Asp Leu Gln Pro Gln Ser Ser Asp Glu Gln Val
         75                  80                  85

ccg ctg cac gag gcc cca cgt ggg gct ttc cgc ctg gca gca gag aac      821
Pro Leu His Glu Ala Pro Arg Gly Ala Phe Arg Leu Ala Ala Glu Asn
     90                  95                 100

cct ttc cag gag cca cgg acg gtg gtg tgg ctg ggc gtg ctc tcg tta      869
Pro Phe Gln Glu Pro Arg Thr Val Val Trp Leu Gly Val Leu Ser Leu
105                 110                 115                 120

ggc ttt gcc ctg gtg ctg gat gcc cat gag aac ctg cta ctg gct gag      917
Gly Phe Ala Leu Val Leu Asp Ala His Glu Asn Leu Leu Leu Ala Glu
                125                 130                 135

ggc acg ctc cgg ctg ctg aca cgc ctc ctc ctt gac cac ctc cgg ctg      965
Gly Thr Leu Arg Leu Leu Thr Arg Leu Leu Leu Asp His Leu Arg Leu
            140                 145                 150

ctg gcg ccc agc acc agc ctt ctg ctg cgg gct gac cgc att gag ggc     1013
Leu Ala Pro Ser Thr Ser Leu Leu Leu Arg Ala Asp Arg Ile Glu Gly
        155                 160                 165

atc ctc acc cgc ttc ctg cca cat ggt cag ctg ctt ttc ctc aac gac     1061
Ile Leu Thr Arg Phe Leu Pro His Gly Gln Leu Leu Phe Leu Asn Asp
    170                 175                 180

cag ttt gtc caa ggc ctg gag aag gaa ttc agt gcc gct tgg ccc cgc     1109
```

```
Gln Phe Val Gln Gly Leu Glu Lys Glu Phe Ser Ala Ala Trp Pro Arg
185                 190                 195                 200

tga ttcc tcgttgggat ggtgcttctg agggcaggca gagggtagac acacagccag     1166
 *


atgaagcttg gcatctccct cctacccagc agctctgatg tgctgctata ccaggacaag   1226

tgggtgacac aagcctgcag aaagggggct gggcagaggg tggaggaggt cctgcctgtc   1286

ctcaggttag tggaaccaca gaacttcctg agcctagagc tgctgtgtta cttagaccgc   1346

tgccgtgcgg cagccacgct tgtccttgaa cccaccttcc tccatccctg ccagccgata   1406

gtgctagggt gaggagctgc ctggagctca ccccgctctt cttccaaacc cacagccacc   1466

atgcctggcc tcaatctttt cttttaaaca attattccta tattttattg taatgcagtt   1526

aaccgtgttt gtcagattca atactctgtg acccgttaac caagtctctg tatgtttatt   1586

actgcaattc aagtggccct gtatt                                         1611



     <210> 161
     <211> 568
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (193)..(555)

     <400> 161
acggccagtg aattgaattt aggtgacact atagaagagc tatgacgtcg catgcacgcg     60

tacgtaagct tggatcctct agagcggccg cctactacta ctaaattcgc ggccgcgtcg    120

accgccgccg agtcgcgcgg aggcggaggc ttgggtgcgt tcaagattca gcttcacccg    180

taacccaccg cc    atg gcc gag gaa ggc att gct gct gga ggt gta atg     228
                 Met Ala Glu Glu Gly Ile Ala Ala Gly Gly Val Met
                  1               5                  10

gac gtt aat act gct tta caa gag gtt ctg aag act gcc ctc atc cac      276
Asp Val Asn Thr Ala Leu Gln Glu Val Leu Lys Thr Ala Leu Ile His
         15                  20                  25

gat ggc cta gca cgt gga att cgc gaa gct gcc aaa gcc tta gac aag      324
Asp Gly Leu Ala Arg Gly Ile Arg Glu Ala Ala Lys Ala Leu Asp Lys
     30                  35                  40

cgc caa gcc cat ctt tgt gtg ctt gca tcc aac tgt gat gag cct atg      372
Arg Gln Ala His Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro Met
 45                  50                  55                  60
```

```
tat gtc aag ttg gtg gag gcc ctt tgt gct gaa cac caa atc aac cta      420
Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn Leu
                 65                  70                  75

att aag gtt gat gac aac aag aaa cta gga gaa tgg gta ggc ctt tgt      468
Ile Lys Val Asp Asp Asn Lys Lys Leu Gly Glu Trp Val Gly Leu Cys
             80                  85                  90

aaa att gac aga gag ggg tgt att gcg gcc gct cta gag gat cca agc      516
Lys Ile Asp Arg Glu Gly Cys Ile Ala Ala Ala Leu Glu Asp Pro Ser
         95                 100                 105

tta cgt acg cgt gca tgc gac gtc ata gct ctt cta tag tgtcacctaa       565
Leu Arg Thr Arg Ala Cys Asp Val Ile Ala Leu Leu  *
    110                 115                 120

att                                                                  568
```

<210> 162
<211> 1837
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (784)..(1473)

<400> 162

```
attctagaac acattatcac ctttttaaat aagcaaaatg atgatcccag gttaaaaaac      60

cttggtaaaa actggttctt aagaacccca agttcgccaa aagaaggttc aagctaataa     120

aggaaacttc tggttaccaa ttccatctgc ctccttctca gtgactcctg acgagctgct     180

catttacaca cacctgctcc cacccccacc ccacagtctg gattgcgaaa cctaccgcac     240

cccacccccca gtgcaggaag aaggtgaccc tggtctgggg tggggacaga gagtctggga    300

gggggtggtg gctggcagtc tcggtggctg gcgacgcctc ttccgctctt ccttcctggg     360

aggaggcggg caaggcgaag cctctccgct cagtcgatgg tttccttcag gacgtctcat     420

agaggtgtgg gtgagatccc aggtctgggc cgcaatttct agccacgctg cccaaccttc     480

aggcaagcag tcaggttcca cagctacccc accacactct cagagtcgag gggaacaaga     540

agagggagtg gtctgtaaat gcgtcgggac aagagtgccc tcctaactcc acctggagct     600

ggcgtcaggg cgatctctgg atgcccagcc cataagcctg gcctgtctgt gaggaggctg     660

cgtctggctc ccgctctcac agccattgca gtacattgag ctccatagag acagcgccgg     720

ggcaagtgag agccggacgg gcactgggcg actctgtgcc tcgctgagga aaaataacta     780
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```
aac  atg ggc aaa gga gat cct aag aag ccg aga ggc aaa atg tca tca      828
     Met Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser
      1               5                  10                  15

tat gca ttt ttt gtg caa act tgt cgg gag gag cat aag aag aag cac      876
Tyr Ala Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His
                20                  25                  30

cca gat gct tca gtc aac ttc tca gag ttt tct aag aag tgc tca gag      924
Pro Asp Ala Ser Val Asn Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu
            35                  40                  45

agg tgg aag acc atg tct gct aaa gag aaa gga aaa ttt gaa gat atg      972
Arg Trp Lys Thr Met Ser Ala Lys Glu Lys Gly Lys Phe Glu Asp Met
        50                  55                  60

gca aag gcg gac aag gcc cgt tat gaa aga gaa atg aaa acc tat atc     1020
Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile
    65                  70                  75

cct ccc aaa ggg gag aca aaa aag aag ttc aag gat ccc aat gca ccc     1068
Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro
80                  85                  90                  95

aag agg cct cct tcg gcc ttc ttc ctc ttc tgc tct gag tat cgc cca     1116
Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr Arg Pro
                100                 105                 110

aaa atc aaa gga gaa cat cct ggc ctg tcc att ggt gat gtt gcg aag     1164
Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
            115                 120                 125

aaa ctg gga gag atg tgg aat aac act gct gca gat gac aag cag cct     1212
Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro
        130                 135                 140

tat gaa aag aag gct gcg aag ctg aag gaa aaa tac gaa aag gat att     1260
Tyr Glu Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile
    145                 150                 155

gct gca tat cga gct aaa gga aag cct gat gca gca aaa aag gga gtt     1308
Ala Ala Tyr Arg Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val
160                 165                 170                 175

gtc aag gct gaa aaa agc aaa aaa aag aag gaa gag gag gaa gat gag     1356
Val Lys Ala Glu Lys Ser Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu
                180                 185                 190

gaa gat gaa gag gat gag gag gag gag gaa gat gaa gaa gat gaa gat     1404
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Asp
            195                 200                 205

gaa gaa gaa gaa gat gat gat atg atg aat aag ttg gtt cta gcg cag     1452
Glu Glu Glu Glu Asp Asp Asp Met Met Asn Lys Leu Val Leu Ala Gln
        210                 215                 220
```

```
ttt ttt ttt tct tgt cta taa ag catttaaccc ccctgttaca caactcactc     1505
Phe Phe Phe Ser Cys Leu  *
    225                 230

cttttaaaga aaaaaattga aatgtaaggc tgtgtaagat ttgtttttaa actgtacagt   1565

gtcttttttt gtatagttaa cacactaccg aatgtgtctt tagatagccc tgtcctggtg   1625

gtattttcaa tagccactaa ccttgcctgg tacagtatgg gggttgtaaa ttggcatgga   1685

aatttaaagc aggttcttgt tggtgcacag cacaaattag ttatatatgg ggatggtagt   1745

tttttcatct tcagttgtct ctgatgcagc ttatacgaaa taattgttgt tctgttaact   1805

gaataccact ctgtaattgc aaaaaaaaaa aa                                 1837




     <210> 163
     <211> 1454
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (269)..(718)

     <400> 163
ccaccttggt ccggtttatt tcagtttaat ggttatgtaa caacggtccg tctctcctac     60

caaccggtac cccgcccacg ccagcagcca cgggtcgcca gcgccacgca gcggaggcgg    120

gcggcatggc tggcccaagg tgcgcaggcg cactagccct gggggtgctt ccgtgtctgc    180

gccctgagac atttttggcg ccggccccag cctgagcggg gacggcggcc gggagggcgc    240

ggcccgggtt cccgttcccc gcggagcc   atg cgg tac aac gag aag gag ctg     292
                                 Met Arg Tyr Asn Glu Lys Glu Leu
                                  1               5

cag gct ctg tcc cgg cag ccg gcc gag atg gcg gcc gag ctg ggc atg      340
Gln Ala Leu Ser Arg Gln Pro Ala Glu Met Ala Ala Glu Leu Gly Met
     10                  15                  20

agg ggc ccc aag aag ggc agc gtg ctg aag cgg cgg ctg gtg aag ctg      388
Arg Gly Pro Lys Lys Gly Ser Val Leu Lys Arg Arg Leu Val Lys Leu
 25                  30                  35                  40

gtg gtg aat ttc ctc ttc tac ttt cgg aca gac gag gcc gag ccc gtc      436
Val Val Asn Phe Leu Phe Tyr Phe Arg Thr Asp Glu Ala Glu Pro Val
                 45                  50                  55

gga gcc ctg ctg ctg gag cgc tgc aga gtc gtc cgg gaa gag ccc ggc      484
Gly Ala Leu Leu Leu Glu Arg Cys Arg Val Val Arg Glu Glu Pro Gly
                 60                  65                  70
```

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acc ttc tcc atc agc ttc att gag gac cct gag agg aag tat cac ttt      532
Thr Phe Ser Ile Ser Phe Ile Glu Asp Pro Glu Arg Lys Tyr His Phe
         75              80                      85

gag tgc agc agc gag gag cag tgt cag gag tgg atg gag gct ctg cgt      580
Glu Cys Ser Ser Glu Glu Gln Cys Gln Glu Trp Met Glu Ala Leu Arg
     90                  95                 100

cgg gcc agc tac gag ttc atg cgg aga agc ctc atc ttc tac agg aac      628
Arg Ala Ser Tyr Glu Phe Met Arg Arg Ser Leu Ile Phe Tyr Arg Asn
105                 110                 115                 120

gaa atc cgg aag gtg acg ggc aag gac ccc ctg gaa cag ttc ggc ata      676
Glu Ile Arg Lys Val Thr Gly Lys Asp Pro Leu Glu Gln Phe Gly Ile
                125                 130                 135

tcc gag gag gcc agg ttc cag ctg agt ggc ttg cag gcg tga gcgcagg      725
Ser Glu Glu Ala Arg Phe Gln Leu Ser Gly Leu Gln Ala  *
            140                 145                 150

gcacggtggt cagcgtgcag cgggacggga ctggccctgc ccagccatga atcgcttggc    785

catgcctgga tctgttttgt tttggttttt ggtttttggg tcagggtttc actgtgttgc    845

ccaggctaga gtgcagtggt gccacagctc actgtgacct tgaccttctg gactcaagtg    905

atcctcctgc ctcagcttcc caagtagcgg ggatcacagg catgagccgc cacacccggc    965

catcacacct ggattttcag tgggaggttt ttggtttgga gacatccaaa gcctgaagcc   1025

aggtgggtgt gggcaggggc tgcattttat gaaactgccc agcaagctgc gctccctggg   1085

gccccaggat ccacctaact ggcctggcac ctggtgccac gtgctgctgc cgccaggata   1145

tgcgccttcc cacaggtgcc ctgcctgagt tgtgtgcatc caggggcctg gtgagccccc   1205

aggctggtgg catggccccc ctgccccgtg ctgaatgaat gtacagagcc agacaaagct   1265

gtgaatggcc taggggctga gtcccacacc agctgtgaat tctcctgcag acaggagggc   1325

cctggctgtg cacctgggga agtggttgcc ctggggccag ggtgcttgtt ctgttcaaat   1385

aaaggtacct cttttccaaa aaaaaaaata aaaatgtatt tttatttcgg gggccggagg   1445

cttattctt                                                           1454
```

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<210> 164
<211> 1162
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (9)..(917)
```

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     <400> 164
acggcgcg atg gcg gcg gct gcc gcc gag acc ccc gaa gtc ctt cgg gaa       50
         Met Ala Ala Ala Ala Ala Glu Thr Pro Glu Val Leu Arg Glu
           1               5                  10

tgc ggt tgc aag ggc atc cgg acc tgt ctg atc tgc gag cgg cag cgc        98
Cys Gly Cys Lys Gly Ile Arg Thr Cys Leu Ile Cys Glu Arg Gln Arg
 15                  20                  25                  30

ggc agt gac ccg ccc tgg gag ctg ccc cca gcg aaa aca tac cgt ttc       146
Gly Ser Asp Pro Pro Trp Glu Leu Pro Pro Ala Lys Thr Tyr Arg Phe
                 35                  40                  45

att tac tgc tcc gac acc ggc tgg gcc gtg ggc aca gag gag tct gac       194
Ile Tyr Cys Ser Asp Thr Gly Trp Ala Val Gly Thr Glu Glu Ser Asp
             50                  55                  60

ttt gag ggc tgg gcc ttc ccc ttc cca gga gtg atg ctg atc gag gac       242
Phe Glu Gly Trp Ala Phe Pro Phe Pro Gly Val Met Leu Ile Glu Asp
         65                  70                  75

ttt gtg acc cgg gag gaa gaa gcc gag ttg gtg cgg ctc atg gac cgt       290
Phe Val Thr Arg Glu Glu Glu Ala Glu Leu Val Arg Leu Met Asp Arg
     80                  85                  90

gac ccc tgg aag ctc tcc cag tct gga cgg agg aag cag gac tat ggc       338
Asp Pro Trp Lys Leu Ser Gln Ser Gly Arg Arg Lys Gln Asp Tyr Gly
 95                 100                 105                 110

ccc aaa gtc aac ttt cgg aaa cag aag cta aag acc gag ggc ttc tgc       386
Pro Lys Val Asn Phe Arg Lys Gln Lys Leu Lys Thr Glu Gly Phe Cys
                115                 120                 125

ggc ctc ccc agc ttc agc cgg gag gtg gtg cgg agg atg ggc ctc tac       434
Gly Leu Pro Ser Phe Ser Arg Glu Val Val Arg Arg Met Gly Leu Tyr
            130                 135                 140

ccg ggg ctg gag ggc ttc cgg ccc gtc gag cag tgc aac ctg gac tac       482
Pro Gly Leu Glu Gly Phe Arg Pro Val Glu Gln Cys Asn Leu Asp Tyr
        145                 150                 155

tgc ccc gag cgg ggc tct gcc att gac ccc cac ctg gac gac gcc tgg       530
Cys Pro Glu Arg Gly Ser Ala Ile Asp Pro His Leu Asp Asp Ala Trp
    160                 165                 170

ctg tgg ggg gag cgg ctg gtc agc ctc aac ctc ctg tcc ccc acc gtg       578
Leu Trp Gly Glu Arg Leu Val Ser Leu Asn Leu Leu Ser Pro Thr Val
175                 180                 185                 190

ctg tcc atg tgt cgg gag gcg ccc ggg agc ctg ctc ctc tgc tcg gcc       626
Leu Ser Met Cys Arg Glu Ala Pro Gly Ser Leu Leu Leu Cys Ser Ala
                195                 200                 205

ccg tcg gct gcc ccg gag gcc ttg gtg gac agc gtg ata gca ccc agc       674
Pro Ser Ala Ala Pro Glu Ala Leu Val Asp Ser Val Ile Ala Pro Ser
            210                 215                 220
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cgg tcg gtg cta tgc cag gag gtg gag gtg gcc atc ccc tta ccc gcc      722
Arg Ser Val Leu Cys Gln Glu Val Glu Val Ala Ile Pro Leu Pro Ala
        225                 230                 235

cgc tcc ctg ctg gtc ctc acc ggg gcg gca cgg cac cag tgg aag cat      770
Arg Ser Leu Leu Val Leu Thr Gly Ala Ala Arg His Gln Trp Lys His
    240                 245                 250

gcc atc cac cgc aga cac atc gag gcc cgc cgc gtc tgc gtc act ttc      818
Ala Ile His Arg Arg His Ile Glu Ala Arg Arg Val Cys Val Thr Phe
255                 260                 265                 270

cgg gag ctg tcg gct gag ttt ggc cct gga ggg agg cag caa gag ctg      866
Arg Glu Leu Ser Ala Glu Phe Gly Pro Gly Gly Arg Gln Gln Glu Leu
                275                 280                 285

ggc cag gaa ctg ctg cgg atc gcc ctc tcc ttc cag gga aga ccc gtg      914
Gly Gln Glu Leu Leu Arg Ile Ala Leu Ser Phe Gln Gly Arg Pro Val
            290                 295                 300

tga accg cctccttggc tccagacttg actgatcccg ggattgaaat gaggagcaca      971
 *


gaacagggcc tcctgcaact cacggggttt caagagaaga tggctgaccc ctgatgctgt   1031

gagcagtgtg agccctgccc aggagcaggt tttgatggga acgtacctcc aggcagcccc   1091

cttccacctg gaccgtggcc acactttttt ggttatttag tttgtcacag tcttggggac   1151

atgggatcat t                                                        1162



     <210> 165
     <211> 1018
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (40)..(747)

     <400> 165
gctcactctt ggcgccttcg cggaaggtgc gtccgagcc   atg gcc gct gcc aac       54
                                             Met Ala Ala Ala Asn
                                               1               5

ccg tgg gac ccg gcg tcc gcg cct aac ggc gct ggg cta gtg cta ggc      102
Pro Trp Asp Pro Ala Ser Ala Pro Asn Gly Ala Gly Leu Val Leu Gly
                10                  15                  20

cac ttc ata gct tcg ggg atg gtc aat cag gag atg tta aac atg tct      150
His Phe Ile Ala Ser Gly Met Val Asn Gln Glu Met Leu Asn Met Ser
            25                  30                  35
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aag aaa aca gtt tct tgt ttt gtg aac ttc acc aga cta cag cag atc      198
Lys Lys Thr Val Ser Cys Phe Val Asn Phe Thr Arg Leu Gln Gln Ile
         40                  45                  50

aca aat att caa gct gaa atc tac cag aaa aac ctg gaa att gaa ctc      246
Thr Asn Ile Gln Ala Glu Ile Tyr Gln Lys Asn Leu Glu Ile Glu Leu
     55                  60                  65

ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt ttg      294
Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe Leu
 70                  75                  80                  85

gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa gca      342
Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu Ala
                 90                  95                 100

gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc atg      390
Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro Met
            105                 110                 115

tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg gta      438
Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met Val
        120                 125                 130

cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc cac      486
His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr His
    135                 140                 145

ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag aaa      534
Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys Lys
150                 155                 160                 165

atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca gaa      582
Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr Glu
                170                 175                 180

gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa gtt      630
Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu Val
            185                 190                 195

tcg tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat aaa      678
Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr Lys
        200                 205                 210

cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat gtc      726
His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His Val
    215                 220                 225

caa act att aat gcc aag tag tc atcaacttta tttttgctta attatgtgta      779
Gln Thr Ile Asn Ala Lys  *
230                 235

gtcatatgaa gtctatttct agttgactgt aacatgggta ttaatagtct ttgctgctgg   839

taatactgaa agaacctgct ttatattgga gtatcaagat ctcaggttca ttaagaccaa   899
```

```
actgactttt cctttgtttt tcatatattt ttattctacc tttcagtaaa actagagaag     959

ctaaaaaata gccatgacaa tttattaata taagtgaatt aaccattaaa aaaaaaaaa     1018




     <210> 166
     <211> 925
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (40)..(654)

     <400> 166
gctcactctt ggcgccttcg cggaaggtgc gtccgagcc  atg gcc gct gcc aac       54
                                            Met Ala Ala Ala Asn
                                             1               5

ccg tgg gac ccg gcg tcc gcg cct aac ggc gct ggg cta gtg cta ggc      102
Pro Trp Asp Pro Ala Ser Ala Pro Asn Gly Ala Gly Leu Val Leu Gly
                 10                  15                  20

cac ttc ata gct tcg ggg atg gtc aat cag aaa aac ctg gaa att gaa      150
His Phe Ile Ala Ser Gly Met Val Asn Gln Lys Asn Leu Glu Ile Glu
             25                  30                  35

ctc ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt      198
Leu Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe
         40                  45                  50

ttg gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa      246
Leu Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu
     55                  60                  65

gca gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc      294
Ala Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro
 70                  75                  80                  85

atg tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg      342
Met Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met
                 90                  95                  100

gta cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc      390
Val His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr
             105                 110                 115

cac ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag      438
His Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys
         120                 125                 130

aaa atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca      486
Lys Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr
     135                 140                 145
```

```
gaa gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa       534
Glu Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu
150                 155                 160                 165

gtt tcg tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat       582
Val Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr
                170                 175                 180

aaa cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat       630
Lys His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His
            185                 190                 195

gtc caa act att aat gcc aag tag tcatcaactt tatttttgct taattatgtg      684
Val Gln Thr Ile Asn Ala Lys  *
        200                 205

tagtcatatg aagtctattt ctagttgact gtaacatggg tattaatagt ctttgctgct     744

ggtaatactg aaagaacctg ctttatattg gagtatcaag atctcaggtt cattaagacc     804

aaactgactt ttcctttgtt tttcatatat ttttattcta cctttcagta aaactagaga     864

agctaaaaaa tagccatgac aatttattaa tataagtgaa ttaaccatta aaaaaaaaaa     924

a                                                                     925



     <210> 167
     <211> 1058
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (190)..(828)

     <400> 167
gctcagcttt agattctccc tgtactggaa agggatgtcg caaggttggg gacgaaacct      60

ctgagtttgc gaccgtagct gtcgctttcc ggccaacaca gaggtgcctg aaggctggtt     120

ggggtggtga ggcccgaggc agctcttgtt cagcttctgg aatttctgag cagccctcgt     180

cagtacaag    atg gac ccc gta gtc ttg agt tac atg gac agt cta ctg     228
             Met Asp Pro Val Val Leu Ser Tyr Met Asp Ser Leu Leu
               1               5                  10

cgg caa tca gat gtc tca cta ttg gat ccg cca agc tgg ctc aat gac       276
Arg Gln Ser Asp Val Ser Leu Leu Asp Pro Pro Ser Trp Leu Asn Asp
     15                  20                  25

cat att att ggg ttt gcg ttt gag tac ttt gcc aac agt cag ttt cat       324
His Ile Ile Gly Phe Ala Phe Glu Tyr Phe Ala Asn Ser Gln Phe His
 30                  35                  40                  45
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```
gac tgc tct gat cac gtc agt ttc atc agc cct gaa gtc acc cag ttc       372
Asp Cys Ser Asp His Val Ser Phe Ile Ser Pro Glu Val Thr Gln Phe
                50                  55                  60

atc aag tgc act agc aac cca gca gag att gcc atg ttc ctt gaa cca       420
Ile Lys Cys Thr Ser Asn Pro Ala Glu Ile Ala Met Phe Leu Glu Pro
            65                  70                  75

ctg gac ctc ccc aac aag aga gtt gta ttt tta gcc atc aat gat aac       468
Leu Asp Leu Pro Asn Lys Arg Val Val Phe Leu Ala Ile Asn Asp Asn
        80                  85                  90

tcc aac cag gca gct gga gga acc cac tgg agt tta ttg gtc tac ctc       516
Ser Asn Gln Ala Ala Gly Gly Thr His Trp Ser Leu Leu Val Tyr Leu
    95                  100                 105

caa gat aaa aat agc ttt ttt cat tat gat tcc cat agc agg agc aac       564
Gln Asp Lys Asn Ser Phe Phe His Tyr Asp Ser His Ser Arg Ser Asn
110                 115                 120                 125

tca gtt cac gca aag cag gta gca gag aaa ctg gag gct ttc tta ggc       612
Ser Val His Ala Lys Gln Val Ala Glu Lys Leu Glu Ala Phe Leu Gly
                130                 135                 140

aga aaa gga gac aaa ctg gcc ttt gtg gaa gag aaa gcc cct gcc caa       660
Arg Lys Gly Asp Lys Leu Ala Phe Val Glu Glu Lys Ala Pro Ala Gln
            145                 150                 155

caa aac agc tat gac tgt ggg atg tac gtg ata tgt aac act gag gcc       708
Gln Asn Ser Tyr Asp Cys Gly Met Tyr Val Ile Cys Asn Thr Glu Ala
        160                 165                 170

ttg tgt cag aac ttc ttt agg caa cag aca gaa tca ctg ctg cag cta       756
Leu Cys Gln Asn Phe Phe Arg Gln Gln Thr Glu Ser Leu Leu Gln Leu
    175                 180                 185

ctc acc cct gca tac atc aca aag aag agg gga gaa tgg aaa gat ctc       804
Leu Thr Pro Ala Tyr Ile Thr Lys Lys Arg Gly Glu Trp Lys Asp Leu
190                 195                 200                 205

att gcc aca ctt gct aaa aag tag ctattgaagt atatttgcga cttttgaagg      858
Ile Ala Thr Leu Ala Lys Lys  *
                210

ctcctctttc tgcccttccc catttgttgg atggctgcaa tctcagtgcc tgagggaaga     918

tgcctagtag aggaaagctt aatactcttt ttcctgaaag aatatcatcc tctgcattat     978

ccccatggaa cgtttcactt taaccctgac tggggagcaa tatgttctgt gaaaatatct    1038

tgaaattgta caccaaaacc                                                1058
```

<210> 168
<211> 7643

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (99)..(5618)

<400> 168
gccgctcctg cactgcgccg gccctgagcg gacctgtggc tcggactatc tattacatcg      60

cagccgagct ggtccggctg gtggggtctg tggactcc   atg aag ccc gtg ctc       113
                                            Met Lys Pro Val Leu
                                             1               5

cag tcc ctc tac cac cga gtg ctg ctc tac ccc cca ccc cag cac cgg       161
Gln Ser Leu Tyr His Arg Val Leu Leu Tyr Pro Pro Pro Gln His Arg
                10                  15                  20

gtg gaa gcc atc aaa ata atg aaa gag ata ctt ggg agc cca cag cgt       209
Val Glu Ala Ile Lys Ile Met Lys Glu Ile Leu Gly Ser Pro Gln Arg
            25                  30                  35

ctc tgt gac ttg gca gga ccc agc tcc act gaa tca gag tcc aga aaa       257
Leu Cys Asp Leu Ala Gly Pro Ser Ser Thr Glu Ser Glu Ser Arg Lys
        40                  45                  50

aga tca att tca aaa aga aag tct cat ctg gat ctc ctc aaa ctc atc       305
Arg Ser Ile Ser Lys Arg Lys Ser His Leu Asp Leu Leu Lys Leu Ile
    55                  60                  65

atg gat ggc atg acc gaa gca tgc atc aag ggt ggc atc gaa gct tgc       353
Met Asp Gly Met Thr Glu Ala Cys Ile Lys Gly Gly Ile Glu Ala Cys
70                  75                  80                  85

tat gca gcc gtg tcc tgt gtc tgc acc ttg ctg ggt gcc ctg gat gag       401
Tyr Ala Ala Val Ser Cys Val Cys Thr Leu Leu Gly Ala Leu Asp Glu
                90                  95                  100

ctc agc cag ggg aag ggc ttg agc gaa ggt cag gtg caa ctg ctg ctt       449
Leu Ser Gln Gly Lys Gly Leu Ser Glu Gly Gln Val Gln Leu Leu Leu
            105                 110                 115

ctg cgc ctt gag gag ctg aag gat ggg gct gag tgg agc cga gat tcc       497
Leu Arg Leu Glu Glu Leu Lys Asp Gly Ala Glu Trp Ser Arg Asp Ser
        120                 125                 130

atg gag atc aat gag gct gac ttc cgc tgg cag cgg cga gtg ctg tcc       545
Met Glu Ile Asn Glu Ala Asp Phe Arg Trp Gln Arg Arg Val Leu Ser
    135                 140                 145

tca gaa cac acg ccg tgg gag tca ggg aac gag agg agc ctt gac atc       593
Ser Glu His Thr Pro Trp Glu Ser Gly Asn Glu Arg Ser Leu Asp Ile
150                 155                 160                 165

agc atc agt gtc acc aca gac aca ggc cag acc act ctc gag gga gag       641
Ser Ile Ser Val Thr Thr Asp Thr Gly Gln Thr Thr Leu Glu Gly Glu
                170                 175                 180
```

```
ttg ggt cag act aca ccc gag gac cat tcg gga aac cac aag aac agt        689
Leu Gly Gln Thr Thr Pro Glu Asp His Ser Gly Asn His Lys Asn Ser
        185                 190                 195

ctc aag tcg cca gcc atc cca gag ggt aag gag acg ctg agc aaa gta        737
Leu Lys Ser Pro Ala Ile Pro Glu Gly Lys Glu Thr Leu Ser Lys Val
        200                 205                 210

ttg gaa aca gag gcg gta gac cag cca gat gtc gtg cag aga agc cac        785
Leu Glu Thr Glu Ala Val Asp Gln Pro Asp Val Val Gln Arg Ser His
    215                 220                 225

acg gtc cct tac cct gac ata act aac ttc ctg tca gta gac tgc agg        833
Thr Val Pro Tyr Pro Asp Ile Thr Asn Phe Leu Ser Val Asp Cys Arg
230                 235                 240                 245

aca agg tcc tat gga tct agg tat agt gag agc aat ttt agc gtt gat        881
Thr Arg Ser Tyr Gly Ser Arg Tyr Ser Glu Ser Asn Phe Ser Val Asp
                250                 255                 260

gac caa gac ctt tct agg aca gag ttt gat tcc tgt gat cag tac tct        929
Asp Gln Asp Leu Ser Arg Thr Glu Phe Asp Ser Cys Asp Gln Tyr Ser
            265                 270                 275

atg gca gca gaa aag gac tcg ggc agg tcc gac gtg tca gac att ggg        977
Met Ala Ala Glu Lys Asp Ser Gly Arg Ser Asp Val Ser Asp Ile Gly
        280                 285                 290

tcg gac aac tgt tca cta gcc gat gaa gag cag aca ccc cgg gac tgc       1025
Ser Asp Asn Cys Ser Leu Ala Asp Glu Glu Gln Thr Pro Arg Asp Cys
    295                 300                 305

cta ggc cac cgg tcc ctg cga act gcc gcc ctg tct cta aaa ctg ctg       1073
Leu Gly His Arg Ser Leu Arg Thr Ala Ala Leu Ser Leu Lys Leu Leu
310                 315                 320                 325

aag aac cag gag gcg gat cag cac agc gcc agg ctg ttc ata cag tcc       1121
Lys Asn Gln Glu Ala Asp Gln His Ser Ala Arg Leu Phe Ile Gln Ser
                330                 335                 340

ctg gaa ggc ctc ctc cct cgg ctc ctg gct ctc tcc aat gta gag gag       1169
Leu Glu Gly Leu Leu Pro Arg Leu Leu Ala Leu Ser Asn Val Glu Glu
            345                 350                 355

gtg gac acc gct ctg cag aac ttt gcc tct act ttc tgc tca ggc atg       1217
Val Asp Thr Ala Leu Gln Asn Phe Ala Ser Thr Phe Cys Ser Gly Met
        360                 365                 370

atg cac tct cct ggc ttt gac ggg aat agc agc ctc agc ttc cag atg       1265
Met His Ser Pro Gly Phe Asp Gly Asn Ser Ser Leu Ser Phe Gln Met
    375                 380                 385

ctg atg aac gca gac agc ctc tac aca gct gca cac tgc gcc ctg ctc       1313
Leu Met Asn Ala Asp Ser Leu Tyr Thr Ala Ala His Cys Ala Leu Leu
390                 395                 400                 405
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ctc aac ctg aag ctc tcc cac ggt gac tac tac agg aag cgg ccg acc      1361
Leu Asn Leu Lys Leu Ser His Gly Asp Tyr Tyr Arg Lys Arg Pro Thr
                410                 415                 420

ctg gcg cca ggc gtg atg aag gac ttc atg aag cag gtg cag acc agc      1409
Leu Ala Pro Gly Val Met Lys Asp Phe Met Lys Gln Val Gln Thr Ser
            425                 430                 435

ggc gtg ctg atg gtc ttc tct cag gcc tgg att gag gag ctc tac cat      1457
Gly Val Leu Met Val Phe Ser Gln Ala Trp Ile Glu Glu Leu Tyr His
        440                 445                 450

cag gtg ctc gac agg aac atg ctt gga gag gct ggc tat tgg ggc agc      1505
Gln Val Leu Asp Arg Asn Met Leu Gly Glu Ala Gly Tyr Trp Gly Ser
    455                 460                 465

cca gaa gat aac agc ctt ccc ctc atc aca atg ctg acc gat att gac      1553
Pro Glu Asp Asn Ser Leu Pro Leu Ile Thr Met Leu Thr Asp Ile Asp
470                 475                 480                 485

ggc tta gag agc agt gcc att ggt ggc cag ctg atg gcc tcg gct gct      1601
Gly Leu Glu Ser Ser Ala Ile Gly Gly Gln Leu Met Ala Ser Ala Ala
                490                 495                 500

aca gag tct cct ttc gcc cag agc agg aga att gat gac tcc aca gtg      1649
Thr Glu Ser Pro Phe Ala Gln Ser Arg Arg Ile Asp Asp Ser Thr Val
            505                 510                 515

gca ggc gtg gca ttt gct cgc tat att ctg gtg ggc tgc tgg aag aac      1697
Ala Gly Val Ala Phe Ala Arg Tyr Ile Leu Val Gly Cys Trp Lys Asn
        520                 525                 530

ttg atc gat act tta tca acc cca ctg act ggt cga atg gcg ggg agc      1745
Leu Ile Asp Thr Leu Ser Thr Pro Leu Thr Gly Arg Met Ala Gly Ser
    535                 540                 545

tcc aaa ggg ctg gcc ttc att ctg gga gct gaa ggc atc aaa gag cag      1793
Ser Lys Gly Leu Ala Phe Ile Leu Gly Ala Glu Gly Ile Lys Glu Gln
550                 555                 560                 565

aac cag aag gag cgg gac gcc atc tgc atg agc ctc gac ggg ctg cgg      1841
Asn Gln Lys Glu Arg Asp Ala Ile Cys Met Ser Leu Asp Gly Leu Arg
                570                 575                 580

aaa gcc gca cgg ctg agc tgc gct cta ggc gtt gct gct aac tgc gcc      1889
Lys Ala Ala Arg Leu Ser Cys Ala Leu Gly Val Ala Ala Asn Cys Ala
            585                 590                 595

tca gcc ctt gcc cag atg gca gct gcc tcc tgt gtc caa aaa aaa aaa      1937
Ser Ala Leu Ala Gln Met Ala Ala Ala Ser Cys Val Gln Lys Lys Lys
        600                 605                 610

gaa gag agg gag gcc caa gaa ccc agt gat gcc atc aca caa gtg aaa      1985
Glu Glu Arg Glu Ala Gln Glu Pro Ser Asp Ala Ile Thr Gln Val Lys
    615                 620                 625

cta aaa gtg gag cag aaa ctg gag cag att ggg aag gtg cag ggg gtg      2033
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Leu Lys Val Glu Gln Lys Leu Glu Gln Ile Gly Lys Val Gln Gly Val
630                 635                 640                 645

tgg ctg cac act gcc cac gtc ttg tgc atg gag gcc atc ctc agc gta      2081
Trp Leu His Thr Ala His Val Leu Cys Met Glu Ala Ile Leu Ser Val
                650                 655                 660

ggc ctg gag atg gga agc cac aac ccg gac tgc tgg cca cac gtg ttc      2129
Gly Leu Glu Met Gly Ser His Asn Pro Asp Cys Trp Pro His Val Phe
            665                 670                 675

agg gtg tgt gaa tac gtg ggc acc ctg gag cac aac cac ttc agc gat      2177
Arg Val Cys Glu Tyr Val Gly Thr Leu Glu His Asn His Phe Ser Asp
        680                 685                 690

ggt gcc tcg cag ccc cct ctg acc atc agc cag ccc cag aag gcc act      2225
Gly Ala Ser Gln Pro Pro Leu Thr Ile Ser Gln Pro Gln Lys Ala Thr
    695                 700                 705

gga agc gct ggc ctc ctt ggg gac ccc gag tgt gag ggc tcg ccc ccc      2273
Gly Ser Ala Gly Leu Leu Gly Asp Pro Glu Cys Glu Gly Ser Pro Pro
710                 715                 720                 725

gag cac agc ccg gag cag ggg cgc tcc ctg agc acg gcc cct gtc gtc      2321
Glu His Ser Pro Glu Gln Gly Arg Ser Leu Ser Thr Ala Pro Val Val
                730                 735                 740

cag ccc ctg tcc atc cag gac ctc gtc cgg gaa ggc agc cgg ggt cgg      2369
Gln Pro Leu Ser Ile Gln Asp Leu Val Arg Glu Gly Ser Arg Gly Arg
            745                 750                 755

gcc tcc gac ttc cgc ggc ggg agc ctc atg agc ggg agc agc gcg gcc      2417
Ala Ser Asp Phe Arg Gly Gly Ser Leu Met Ser Gly Ser Ser Ala Ala
        760                 765                 770

aag gtg gtg ctc acc ctc tcc acg caa gcc gac agg ctc ttt gaa gat      2465
Lys Val Val Leu Thr Leu Ser Thr Gln Ala Asp Arg Leu Phe Glu Asp
    775                 780                 785

gct acg gat aag ttg aac ctc atg gcc ttg gga ggt ttt ctt tac cag      2513
Ala Thr Asp Lys Leu Asn Leu Met Ala Leu Gly Gly Phe Leu Tyr Gln
790                 795                 800                 805

ctg aag aaa gca tcg cag tct cag ctt ttc cat tct gtt aca gat aca      2561
Leu Lys Lys Ala Ser Gln Ser Gln Leu Phe His Ser Val Thr Asp Thr
                810                 815                 820

gtt gat tac tct ctg gca atg cca gga gaa gtt aaa tcc act caa gac      2609
Val Asp Tyr Ser Leu Ala Met Pro Gly Glu Val Lys Ser Thr Gln Asp
            825                 830                 835

cga aaa agc gcc ctc cac ctg ttc cgc ctg ggg aat gcc atg ctg agg      2657
Arg Lys Ser Ala Leu His Leu Phe Arg Leu Gly Asn Ala Met Leu Arg
        840                 845                 850

att gtg cgg agc aaa gca cgg ccc ctg ctc cac gtg atg cgc tgc tgg      2705
Ile Val Arg Ser Lys Ala Arg Pro Leu Leu His Val Met Arg Cys Trp
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    855                 860                 865

agc ctt gtg gcc cca cac ctg gtg gag gct gct tgc cat aag gaa aga      2753
Ser Leu Val Ala Pro His Leu Val Glu Ala Ala Cys His Lys Glu Arg
870                 875                 880                 885

cat gtg tct cag aag gct gtt tcc ttc atc cat gac ata ctg aca gaa      2801
His Val Ser Gln Lys Ala Val Ser Phe Ile His Asp Ile Leu Thr Glu
                890                 895                 900

gtc ctc act gac tgg aat gag cca cct cat ttt cac ttc aat gaa gca      2849
Val Leu Thr Asp Trp Asn Glu Pro Pro His Phe His Phe Asn Glu Ala
            905                 910                 915

ctc ttc cga cct ttc gag cgc att atg cag ctg gaa ttg tgt gat gag      2897
Leu Phe Arg Pro Phe Glu Arg Ile Met Gln Leu Glu Leu Cys Asp Glu
        920                 925                 930

gac gtc caa gac cag gtt gtc aca tcc att ggt gag ctg gtt gaa gtg      2945
Asp Val Gln Asp Gln Val Val Thr Ser Ile Gly Glu Leu Val Glu Val
    935                 940                 945

tgt tcc acg cag atc cag tcg gga tgg aga ccc ttg ttc agt gcc ctg      2993
Cys Ser Thr Gln Ile Gln Ser Gly Trp Arg Pro Leu Phe Ser Ala Leu
950                 955                 960                 965

gaa aca gtg cat ggc ggg aac aag tca gag atg aag gag tac ctg gtt      3041
Glu Thr Val His Gly Gly Asn Lys Ser Glu Met Lys Glu Tyr Leu Val
                970                 975                 980

ggt gac tac tcc atg gga aaa ggc caa gct cca gtg ttt gat gta ttt      3089
Gly Asp Tyr Ser Met Gly Lys Gly Gln Ala Pro Val Phe Asp Val Phe
            985                 990                 995

gaa gct ttt ctc aat act gac aac atc cag gtc ttt gct aat gca gcc      3137
Glu Ala Phe Leu Asn Thr Asp Asn Ile Gln Val Phe Ala Asn Ala Ala
       1000                1005                1010

act agc tac atc atg tgc ctt atg aag ttt gcc aaa ggg ctg ggg gag      3185
Thr Ser Tyr Ile Met Cys Leu Met Lys Phe Ala Lys Gly Leu Gly Glu
   1015                1020                1025

gtg gac tgt aaa gag att gga gac tgt gcc cca gca ccc gga gcc ccg      3233
Val Asp Cys Lys Glu Ile Gly Asp Cys Ala Pro Ala Pro Gly Ala Pro
1030                1035                1040                1045

tcc aca gac ctg tgc ctc ccg gcc ctg gat tac ctc agg cgc tgc tct      3281
Ser Thr Asp Leu Cys Leu Pro Ala Leu Asp Tyr Leu Arg Arg Cys Ser
               1050                1055                1060

cag tta ttg gcc aaa atc tac aaa atg ccc ttg aag cca ata ttc ctt      3329
Gln Leu Leu Ala Lys Ile Tyr Lys Met Pro Leu Lys Pro Ile Phe Leu
           1065                1070                1075

agt ggg aga ctt gcc ggc ttg cct cga aga ctt cag gaa cag tca gcc      3377
Ser Gly Arg Leu Ala Gly Leu Pro Arg Arg Leu Gln Glu Gln Ser Ala
       1080                1085                1090
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agc agt gag gat gga att gaa tca gtc ctg tct gat ttt gat gat gac      3425
Ser Ser Glu Asp Gly Ile Glu Ser Val Leu Ser Asp Phe Asp Asp Asp
    1095                1100                1105

acc ggt ctg ata gaa gtc tgg ata atc ctg ctg gag cag ctg aca gcg      3473
Thr Gly Leu Ile Glu Val Trp Ile Ile Leu Leu Glu Gln Leu Thr Ala
1110                1115                1120                1125

gct gtg tcc aat tgt cca cgg cag cac caa cca cca act ctg gat tta      3521
Ala Val Ser Asn Cys Pro Arg Gln His Gln Pro Pro Thr Leu Asp Leu
                1130                1135                1140

ctc ttt gag ctg ttg aga gat gtg acg aaa aca cca gga cca ggg ttt      3569
Leu Phe Glu Leu Leu Arg Asp Val Thr Lys Thr Pro Gly Pro Gly Phe
            1145                1150                1155

ggt atc tat gca gtg gtt cac ctc ctc ctt cct gtg atg tcc gtt tgg      3617
Gly Ile Tyr Ala Val Val His Leu Leu Leu Pro Val Met Ser Val Trp
        1160                1165                1170

ctc cgc cgg agc cat aaa gac cat tcc tac tgg gat atg gcc tct gcc      3665
Leu Arg Arg Ser His Lys Asp His Ser Tyr Trp Asp Met Ala Ser Ala
    1175                1180                1185

aat ttc aag cac gct att ggt ctg tcc tgt gag ctg gtg gtg gag cac      3713
Asn Phe Lys His Ala Ile Gly Leu Ser Cys Glu Leu Val Val Glu His
1190                1195                1200                1205

att caa agc ttt cta cat tca gat atc agg tac gag agc atg atc aat      3761
Ile Gln Ser Phe Leu His Ser Asp Ile Arg Tyr Glu Ser Met Ile Asn
                1210                1215                1220

acc atg ctg aag gac ctc ttt gag ttg ctg gtc gcc tgt gtg gcc aag      3809
Thr Met Leu Lys Asp Leu Phe Glu Leu Leu Val Ala Cys Val Ala Lys
            1225                1230                1235

ccc act gaa acc atc tcc aga gtg ggc tgc tcc tgt att aga tac gtc      3857
Pro Thr Glu Thr Ile Ser Arg Val Gly Cys Ser Cys Ile Arg Tyr Val
        1240                1245                1250

ctt gtg aca gcg ggc cct gtg ttc act gag gag atg tgg agg ctt gcc      3905
Leu Val Thr Ala Gly Pro Val Phe Thr Glu Glu Met Trp Arg Leu Ala
    1255                1260                1265

tgc tgt gcc ctg caa gat gcg ttc tct gcc aca ctc aag cca gtg aag      3953
Cys Cys Ala Leu Gln Asp Ala Phe Ser Ala Thr Leu Lys Pro Val Lys
1270                1275                1280                1285

gac ctg ctg ggc tgc ttc cac agc ggc acg gag agc ttc agc ggg gaa      4001
Asp Leu Leu Gly Cys Phe His Ser Gly Thr Glu Ser Phe Ser Gly Glu
                1290                1295                1300

ggc tgc cag gtg cga gtg gcg gcc ccg tcc tcc tcc cca agt gcc gag      4049
Gly Cys Gln Val Arg Val Ala Ala Pro Ser Ser Ser Pro Ser Ala Glu
            1305                1310                1315
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 gcc gag tac tgg cgc atc cga gcc atg gcc cag cag gtg ttt atg ctg     4097
 Ala Glu Tyr Trp Arg Ile Arg Ala Met Ala Gln Gln Val Phe Met Leu
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 gac acc cag tgc tca cca aag aca cca aac aac ttt gac cac gct cag     4145
 Asp Thr Gln Cys Ser Pro Lys Thr Pro Asn Asn Phe Asp His Ala Gln
    1335                1340                1345

 tcc tgc cag ctc att att gag ctg cct cct gat gaa aaa cca aat gga     4193
 Ser Cys Gln Leu Ile Ile Glu Leu Pro Pro Asp Glu Lys Pro Asn Gly
1350                1355                1360                1365

 cac acc aag aaa agc gtg tct ttc agg gaa att gtg gtg agc ctg ctg     4241
 His Thr Lys Lys Ser Val Ser Phe Arg Glu Ile Val Val Ser Leu Leu
                1370                1375                1380

 tct cat cag gtg tta ctc cag aac tta tat gac atc ttg tta gaa gag     4289
 Ser His Gln Val Leu Leu Gln Asn Leu Tyr Asp Ile Leu Leu Glu Glu
            1385                1390                1395

 ttt gtc aaa ggc ccc tct cct gga gag gaa aag acg ata caa gtg cca     4337
 Phe Val Lys Gly Pro Ser Pro Gly Glu Glu Lys Thr Ile Gln Val Pro
        1400                1405                1410

 gaa gcc aag ctg gct ggc ttc ctc aga tac atc tct atg cag aac ttg     4385
 Glu Ala Lys Leu Ala Gly Phe Leu Arg Tyr Ile Ser Met Gln Asn Leu
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 gca gtc ata ttc gac ctg ctg ctg gac tct tat agg act gcc agg gag     4433
 Ala Val Ile Phe Asp Leu Leu Leu Asp Ser Tyr Arg Thr Ala Arg Glu
1430                1435                1440                1445

 ttt gac acc agc ccc ggg ctg aag tgc ctg ctg aag aaa gtg tct ggc     4481
 Phe Asp Thr Ser Pro Gly Leu Lys Cys Leu Leu Lys Lys Val Ser Gly
                1450                1455                1460

 atc ggg ggc gcc gcc aac ctc tac cgc cag tct gcg atg agc ttt aac     4529
 Ile Gly Gly Ala Ala Asn Leu Tyr Arg Gln Ser Ala Met Ser Phe Asn
            1465                1470                1475

 att tat ttc cac gcc ctg gtg tgt gct gtt ctc acc aat caa gaa acc     4577
 Ile Tyr Phe His Ala Leu Val Cys Ala Val Leu Thr Asn Gln Glu Thr
        1480                1485                1490

 atc acg gcc gag caa gtg aag aag gtc ctt ttt gag gac gac gag aga     4625
 Ile Thr Ala Glu Gln Val Lys Lys Val Leu Phe Glu Asp Asp Glu Arg
    1495                1500                1505

 agc acg gat tct tcc cag cag tgt tca tct gag gat gaa gac atc ttt     4673
 Ser Thr Asp Ser Ser Gln Gln Cys Ser Ser Glu Asp Glu Asp Ile Phe
1510                1515                1520                1525

 gag gaa acc gcc cag gtc agc ccc ccg aga ggc aag gag aag aga cag     4721
 Glu Glu Thr Ala Gln Val Ser Pro Pro Arg Gly Lys Glu Lys Arg Gln
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 tgg cgg gca cgg atg ccc ttg ctc agc gtc cag cct gtc agc aac gca     4769
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 Trp Arg Ala Arg Met Pro Leu Leu Ser Val Gln Pro Val Ser Asn Ala
            1545                1550                1555

 gat tgg gtg tgg ctg gtc aag agg ctg cac aag ctg tgc atg gaa ctg     4817
 Asp Trp Val Trp Leu Val Lys Arg Leu His Lys Leu Cys Met Glu Leu
        1560                1565                1570

 tgc aac aac tac atc cag atg cac ttg gac ctg gag aac tgt atg gag     4865
 Cys Asn Asn Tyr Ile Gln Met His Leu Asp Leu Glu Asn Cys Met Glu
    1575                1580                1585

 gag cct ccc atc ttc aag ggc gac ccg ttc ttc atc ctg ccc tcc ttc     4913
 Glu Pro Pro Ile Phe Lys Gly Asp Pro Phe Phe Ile Leu Pro Ser Phe
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 cag tcc gag tca tcc acc cca tcc acc ggg ggc ttc tct ggg aaa gaa     4961
 Gln Ser Glu Ser Ser Thr Pro Ser Thr Gly Gly Phe Ser Gly Lys Glu
                1610                1615                1620

 acc cct tcc gag gat gac aga agc cag tcc cgg gag cac atg ggc gag     5009
 Thr Pro Ser Glu Asp Asp Arg Ser Gln Ser Arg Glu His Met Gly Glu
            1625                1630                1635

 tcc ctg agc ctg aag gcc ggt ggt ggg gac ctg ctg ctg ccc ccc agc     5057
 Ser Leu Ser Leu Lys Ala Gly Gly Gly Asp Leu Leu Leu Pro Pro Ser
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 ccc aaa gtg gag aag aag gat ccc agc cgg aag aag gag tgg tgg gag     5105
 Pro Lys Val Glu Lys Lys Asp Pro Ser Arg Lys Lys Glu Trp Trp Glu
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 aat gcg ggg aac aaa atc tac acc atg gca gcc gac aag acc att tca     5153
 Asn Ala Gly Asn Lys Ile Tyr Thr Met Ala Ala Asp Lys Thr Ile Ser
1670                1675                1680                1685

 aag ttg atg acc gaa tac aaa aag agg aaa cag cag cac aac ctg tcc     5201
 Lys Leu Met Thr Glu Tyr Lys Lys Arg Lys Gln Gln His Asn Leu Ser
                1690                1695                1700

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 Ala Phe Pro Lys Glu Val Lys Val Glu Lys Lys Gly Glu Pro Leu Gly
            1705                1710                1715

 ccc agg ggc cag gac tcc ccg ctg ctt cag cgt ccc cag cac ttg atg     5297
 Pro Arg Gly Gln Asp Ser Pro Leu Leu Gln Arg Pro Gln His Leu Met
        1720                1725                1730

 gac caa ggg caa atg cgg cat tcc ttc agc gca ggc ccc gag ctg ctg     5345
 Asp Gln Gly Gln Met Arg His Ser Phe Ser Ala Gly Pro Glu Leu Leu
    1735                1740                1745

 cga cag gac aag agg ccc cgc tca ggc tcc acc ggg agc tcc ctc agt     5393
 Arg Gln Asp Lys Arg Pro Arg Ser Gly Ser Thr Gly Ser Ser Leu Ser
1750                1755                1760                1765

 gtc tcg gtg aga gac gca gaa gca cag atc cag gca tgg acc aac atg     5441
 Val Ser Val Arg Asp Ala Glu Ala Gln Ile Gln Ala Trp Thr Asn Met
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                 1770                1775                1780

  gtg cta aca gtt ctc aat cag att cag att ctc cca gac cag acc ttc     5489
  Val Leu Thr Val Leu Asn Gln Ile Gln Ile Leu Pro Asp Gln Thr Phe
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  acg gcc ctc cag ccc gca gtg ttc ccg tgc atc agt cag ctg acc tgt     5537
  Thr Ala Leu Gln Pro Ala Val Phe Pro Cys Ile Ser Gln Leu Thr Cys
         1800                1805                1810

  cac gtg acc gac atc aga gtt cgc cag gct gtg agg gag tgg ctg ggc     5585
  His Val Thr Asp Ile Arg Val Arg Gln Ala Val Arg Glu Trp Leu Gly
     1815                1820                1825

  agg gtg ggc cgt gtc tat gac atc att gtg tag ccgactcc tgttctactc     5636
  Arg Val Gly Arg Val Tyr Asp Ile Ile Val  *
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aatagtatta aaagtcagag gctttactaa tctacctata tgtattccat ggctaacaaa    240

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                   Met Ser Ser Gly Gly Ser Pro Gly Cys Leu Arg
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ctt gca gaa ggc tgc ccc aat cac aga gcc tgg gta agg tgg aac agg      338
Leu Ala Glu Gly Cys Pro Asn His Arg Ala Trp Val Arg Trp Asn Arg
            15                  20                  25
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agg cag ccc cac tcg gct ttt ctg att gca tcc cac ctg ttt ctg agt        386
Arg Gln Pro His Ser Ala Phe Leu Ile Ala Ser His Leu Phe Leu Ser
         30                  35                  40

gtg ttg gtt tgg ttt aat tct ttt caa ggg ttg gag ttg gaa agt gaa        434
Val Leu Val Trp Phe Asn Ser Phe Gln Gly Leu Glu Leu Glu Ser Glu
     45                  50                  55

aac cct aga cac ttg ctg tgg aat gtt tgc ctg gtt gta ttg gtg tgt        482
Asn Pro Arg His Leu Leu Trp Asn Val Cys Leu Val Val Leu Val Cys
 60                  65                  70                  75

ccc tct tct tca ctg gca tgt cgc ttt caa gtg tac caa agg aca ttt        530
Pro Ser Ser Ser Leu Ala Cys Arg Phe Gln Val Tyr Gln Arg Thr Phe
                 80                  85                  90

tgt tct gtt gaa agc cac agg acc aaa agg aaa ata ttg caa cta ttt        578
Cys Ser Val Glu Ser His Arg Thr Lys Arg Lys Ile Leu Gln Leu Phe
             95                 100                 105

gca aac ata ctt ccc tac cta tac aag cag cca tat act aaa aag cac        626
Ala Asn Ile Leu Pro Tyr Leu Tyr Lys Gln Pro Tyr Thr Lys Lys His
        110                 115                 120

taa acaa gcacaaatga acactaaata gccttatacc aaaaagcatt cttgtaactg        683
 *

tcagggcatg gtatgaattc cttcctcttt aagcagcaac ttaccacagg cttggtggct      743

ttaagtaata tagcattaag caaatggtca gttatttttt aatgttgaaa acttccaagt      803

gtgaataata cggacatagt ttactacctt ttgcttttaa tatacctggt tatctatttc      863

catttgaaat aaaatgaaag gagacctcaa actgatgctg agaagtagac aaaatcagct      923

ctcagactta actctcccca attaaaatag ttttttttttc ccttcccatt tttttgtttt     983

taagagatag ggtcttgctg tgttgcccag gctagagtgc agcagtgaca tgatcatagc     1043

tcactgcagc ctggaactcc tgggctcagg atccttctgc ttcggcctcc tgagtagcta     1103

agaccacagg tgtgtgccac cacacctggc taattttttt aaaatttttt gtagagatgg     1163

ggacttgcta tgttgcccag actggtctcg aactcctggc ctcaagccac caacctctca     1223

aattgctaga attacaagca tgagccacca cacctggcct gttattcctt ctttatctaa     1283

tgtgtgctaa gcttgtgaaa aatatatgtt gaggtaaata gggcaaaaca ttagttgata     1343

aattatgcta attaatggga aaaatagaca tgttcctctc tgaacattta gaaggactct     1403

gccctacaac tatcttctgt ttttagaatt tgtagtcact gttcttagtg ccactggaaa     1463

tatattcatt ctttgagcat gtacagggtg ggctccctgt tgtatttatt acacttttca     1523
```

aaatgccagc aagtttttgt ttgtatagag ttggaatgta ttgttcgtgc atgcctgtga 1583

tattcatcat caaaatatac ctgtaaaaaa taaactactg cttcctctcc acagcttagg 1643

cctccctctt actaaaaaca atagtagttt ctgtagaagt ttcagtgaga aattatggtt 1703

atataaataa cagatatggc agaacaattt tgttgtagta ttttttttccg tagcatttct 1763

taataatagc tcagttttta aaggagggga acaatacccc atgagttcaa attaattttc 1823

tctactttga ggtatacctt cctaattata ttttacatag gctgtttttt ttaagtttaa 1883

attctcactg ttaagttgca ttgagagaca attagaaatg ttgtaattgt catatcttta 1943

catgtggatt atgaacaaat gaaagtttgc tgtgtgattg cagttttaaa ttataacatt 2003

tcataaatat gtcaatttta gaaactcaaa ctctttccca tcttttgtat ggataaagtt 2063

tatggtttca tttctgagaa tagagttggt ctgctgtgct aacttcatgt ttcttattcc 2123

aaaggcttga ttatattttt ttctccagtg attaaaaatg cagcgaaaat ccaatctaca 2183

agttcatata ttggtatttc tagacatagt ctagttctaa aagaatgtac ttggtgtgca 2243

tttttaagtg tttcatgtag acagattaat atatttttgt acaacattgt atttctacat 2303

ttatttcaag actgtacttt tcagtgactt tttcaagtgc atgtgttaac agaagattgt 2363

ttggaacgag agtgcagtgg cttctttact agcaaagaga agtgtaatac aagtgatcat 2423

agaaggtgag aatgtgttta tactgtatat ggaaacctaa tgcctctttt ctaaagcttt 2483

gtacattttt ttcgtgaaat agattaaata ttttctctct aaaaaaaaaa aa 2535

<210> 170
<211> 2191
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (451)..(846)

<400> 170
tgacaggtct ccactgatcc agcctctgat gatctgtcct ctggtgatct atcctctagt 60

gaatctggcc tctgtatgta tctggccact ggttgaactg gcctctgaat gagctgactt 120

ctgaatcaac ctttgatcgt acctttgaac cacattctgt accagtttgt gagccagttt 180

cctgtaatat tgacaatata gaaccaagta gcaataaaga tgatgatttt cttgaaaaaa 240

atggagctga tgaaaaatta gagcaaattt cagagtaaag actcattgga tgagaaaaat 300

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aaagctgata ataatattga tgctaatgaa gaaactctag aaacagatta tacaactatt    360

tgttcagatc gacctcctga aaatgaaaag aaggtagagg aagatattat cacagagctt    420

gctcttggag aagatgctat atctagcagt    atg gaa att gac caa ggt gaa      471
                                    Met Glu Ile Asp Gln Gly Glu
                                     1               5

aag aat gaa gat gaa act tct gca gat ctt gta gaa acg att aat gaa      519
Lys Asn Glu Asp Glu Thr Ser Ala Asp Leu Val Glu Thr Ile Asn Glu
        10                  15                  20

aat gtt att gaa gat aac aaa agt gag aat atc tta gaa aat aca gac      567
Asn Val Ile Glu Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp
    25                  30                  35

tct atg gag aca gat gaa atc att cct att ttg gaa aag ctt gca cct      615
Ser Met Glu Thr Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro
40                  45                  50                  55

tct gag gat gaa ctt act tgc ttt tct aaa aca tct ctc ctt cca atc      663
Ser Glu Asp Glu Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile
                60                  65                  70

gat gag aca aat cca gat ttg gaa gag aaa atg gaa agt tct ttt ggt      711
Asp Glu Thr Asn Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly
            75                  80                  85

tca cca tct aaa caa gaa agt agt gag agt ttg cca aaa gaa gcc ttt      759
Ser Pro Ser Lys Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe
        90                  95                  100

ctg gtc ctc tct gat gaa gag gat att tcg ggt gaa aaa gat gag tct      807
Leu Val Leu Ser Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser
    105                 110                 115

gaa gtt ata tcg caa aat gaa acg tgc tct cca ggt tag catataactt       856
Glu Val Ile Ser Gln Asn Glu Thr Cys Ser Pro Gly  *
120                 125                 130

aaatgttaaa gatttttat tgactttgat gaactgttta ataaaacatt atcataatgt     916

tttaaattta ttttagctgc agagaaagtt gagaatagtg atgactctat agaaagatgt    976

cttaacttca tagaattcag aattagtgtg tgtactctgt gagtagcatt gtactaaata   1036

ctaagaaggg agataaaata agtagaaaat atgcccttat agtctggaaa tagagatgaa   1096

gtagagcacc ataacactga gataacagct taagttagta cataattgac tagagttgta   1156

gcagttcttt cttgctatca cttagcgaac aaataactta gaactaaaag cctaatagtt   1216

taatctattt gcttcaagtg taacaaatta tattttcaat taatattccc aatgaaatcc   1276

tgttctttaa tattctttgt ccaggaatga cagcaccatt gttgtaagcc agaaacctta   1336

aagcttgatt atccatttga taaagacttt acccatttgc tccctcagcc cttttgattc   1396
```

```
tacccagcct attctcttcc tcattttctg aatgagctcc ctgtaaccca attctcttat   1456

ttgatattgt ccgtctatgt cttagatctc tgttactttt aggttgattt caaactcctt   1516

atgtaaaagg tacattaact ttatgatttg ttcagtacct atctctccca tctcttttat   1576

tttatttatt attcctagag aaaaagaatg agaaaaattc taccttcttt tatggtcaaa   1636

ctgaaaaaca ttattcctct atgaaacttt ctcagcctgt ggaagactga gaaaagcatg   1696

aatacctttc ttttcccatt atatcacatt cttttagatt tagacatctc tgagagaagt   1756

gaccttgcta gcataaaaca ccatctaatt tcttcaaaga aaaaaaaatg gaggcaggtc   1816

taagagacag agacaacttt tttccccaat atatcatacc agcttttgga ggtagagatt   1876

tttttcttat taaaaaatgg cttttctttt ttttttggcc aggtaaggtg gctcacgcct   1936

gtggtcctag gactttggga ggctgaggca ggcagattgc ttgagctcag gagttcgaga   1996

ccagcctggg caacatggtg agaccccgtc tctacaaagg tacaaaaatt ggccaggcgt   2056

ggtggcactt gtctgtagtc cagggtactt gagggcctga ggtgggggga tcacttgaac   2116

ctgggtggtc gaggctgcag tgagccgaga tcgcgccact actccagcct gggtgacaaa   2176

gtaagaccct gcctc                                                    2191



      <210> 171
      <211> 874
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (141)..(401)

      <400> 171
gtagttcgcg acctcggatt cgatacgcgg gtgcaagggc gcacctgctt cacccaggcg     60

cccaacgtag aggttgagca tcagcggcag catggccgac ccttccgcga agtgcagcca    120

ttgcacgtat tcgtcatagg    atg ctg tgg ccc ggc gca gga ttg gag gga      170
                         Met Leu Trp Pro Gly Ala Gly Leu Glu Gly
                          1               5                   10

cat aga cct ggt gga agg cgt ggg gct gcc ctg acc cag gga ttt ggc      218
His Arg Pro Gly Gly Arg Arg Gly Ala Ala Leu Thr Gln Gly Phe Gly
                15                  20                  25

tcc tgt agc gct gct ggg cag agg tcc gca gga gct gca ggt act tct      266
Ser Cys Ser Ala Ala Gly Gln Arg Ser Ala Gly Ala Ala Gly Thr Ser
            30                  35                  40
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tgg cca act cta gct gct gct tct tgc act gct tcc ggc ggg gtg agg        314
Trp Pro Thr Leu Ala Ala Ala Ser Cys Thr Ala Ser Gly Gly Val Arg
        45                  50                  55

acc cac agc tct gat gtg ggc gct tca ggc cat ggt gga gct gag att        362
Thr His Ser Ser Asp Val Gly Ala Ser Gly His Gly Gly Ala Glu Ile
    60                  65                  70

cag gtt ggc ttt tcc cct cag ctc cca gct ggc tgg tga acccatcatc         411
Gln Val Gly Phe Ser Pro Gln Leu Pro Ala Gly Trp  *
75                  80                  85

atagccaaaa gtactcagca gcagcacctc caggtccaga ggcacctcca gctgcatgca      471

cacacaatga atgaaagact gccaggtgtc cgaaccctgg acatgcagct tgttgagttg      531

caggatgact ctctgttcag ggtccaaggt ctcgttcctg gaatccaggt ccgtgttggg      591

gaggaagaac ttcatcttgg cgttcagcca ttctgggtct ttggtgagca gcctcacaag      651

acagctccac aggttcttgt tgccgagctg gaggccaacg ggtccatga ggagccagcc       711

ttggtctcct cgttcatgat aggtgctcta gggtccccac ggagagggtc tcatgggtgt      771

ctgggctatg tgtgccttga gctggattga caggttgttt ccatagtgca gactccctca      831

gagctcccgg cactcaccct cagcgctcgc ggctcctccg cgc                        874



     <210> 172
     <211> 1297
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (15)..(1052)

     <400> 172
agccagaggc cccg atg gca aag ggt aaa agc acc acc tta acg cag gac         50
                Met Ala Lys Gly Lys Ser Thr Thr Leu Thr Gln Asp
                 1               5                  10

atg agc acc agc ctc cag gaa ggc cag gag gac ggg ccg gca gga tgg         98
Met Ser Thr Ser Leu Gln Glu Gly Gln Glu Asp Gly Pro Ala Gly Trp
        15                  20                  25

aga gcg aat ctg aag ccc gtg gac agg aga agc cca gct gag agg act        146
Arg Ala Asn Leu Lys Pro Val Asp Arg Arg Ser Pro Ala Glu Arg Thr
    30                  35                  40

ctg aag ccc aag gaa cca cgg gcc ctg gca gag ccg agg gcg ggg gag        194
Leu Lys Pro Lys Glu Pro Arg Ala Leu Ala Glu Pro Arg Ala Gly Glu
45                  50                  55                  60
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gcc ccc agg aag gtc tca ggc agc ttt gct ggg agt gtc cac atc acc         242
Ala Pro Arg Lys Val Ser Gly Ser Phe Ala Gly Ser Val His Ile Thr
                 65                  70                  75

ctg acc ccc gtg agg cct gac agg acc cca cgc cca gcc agc cca gga         290
Leu Thr Pro Val Arg Pro Asp Arg Thr Pro Arg Pro Ala Ser Pro Gly
             80                  85                  90

ccc agc ctc cca gcc agg tcc ccc tcc cca ccc cgc cgc agg aga ctg         338
Pro Ser Leu Pro Ala Arg Ser Pro Ser Pro Pro Arg Arg Arg Arg Leu
         95                 100                 105

gcc gtc cct gcc agc ctc gac gtt tgt gac aac tgg ctt cgg ccg gag         386
Ala Val Pro Ala Ser Leu Asp Val Cys Asp Asn Trp Leu Arg Pro Glu
    110                 115                 120

ccc cct ggc cag gaa gcc cga gtg cag agc tgg aag gag gag gag aag         434
Pro Pro Gly Gln Glu Ala Arg Val Gln Ser Trp Lys Glu Glu Glu Lys
125                 130                 135                 140

aaa cct cac ctt cag ggc aaa cca ggg aga ccc ttg tcc ccg gcc aat         482
Lys Pro His Leu Gln Gly Lys Pro Gly Arg Pro Leu Ser Pro Ala Asn
                145                 150                 155

gtc cct gct ctg cct ggc gag acg gtg acc tcc cca gtc agg ctg cac         530
Val Pro Ala Leu Pro Gly Glu Thr Val Thr Ser Pro Val Arg Leu His
            160                 165                 170

ccc gac tac ctc tcc ccg gag gag ata cag agg cag ctg cag gac atc         578
Pro Asp Tyr Leu Ser Pro Glu Glu Ile Gln Arg Gln Leu Gln Asp Ile
        175                 180                 185

gag agg cgg ctg gac gcc ctg gag ctc cgc ggc gtg gag ctg gag aag         626
Glu Arg Arg Leu Asp Ala Leu Glu Leu Arg Gly Val Glu Leu Glu Lys
    190                 195                 200

cga ctg cgg gcg gcc gag gga gat gac gct gag gat agc ctc atg gtg         674
Arg Leu Arg Ala Ala Glu Gly Asp Asp Ala Glu Asp Ser Leu Met Val
205                 210                 215                 220

gac tgg ttc tgg ctc att cac gag aag cag ctt ctg ctg aga cag gag         722
Asp Trp Phe Trp Leu Ile His Glu Lys Gln Leu Leu Leu Arg Gln Glu
                225                 230                 235

tca gag ctg atg tac aag tcc aag gcc cag cgt ctg gag gag cag cag         770
Ser Glu Leu Met Tyr Lys Ser Lys Ala Gln Arg Leu Glu Glu Gln Gln
            240                 245                 250

ctg gac atc gag ggc gag ctg cgc cgg ctc atg gcc aag ccc gag gct         818
Leu Asp Ile Glu Gly Glu Leu Arg Arg Leu Met Ala Lys Pro Glu Ala
        255                 260                 265

ctg aag tca ctg cag gag cgg cgg cgg gag cag gag ctg ctg gag cag         866
Leu Lys Ser Leu Gln Glu Arg Arg Arg Glu Gln Glu Leu Leu Glu Gln
    270                 275                 280
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tac gtg agc acc gtg aac gac cgc agt gac atc gtg gac tcg ctg gac      914
Tyr Val Ser Thr Val Asn Asp Arg Ser Asp Ile Val Asp Ser Leu Asp
285                 290                 295                 300

gag gac cgg ctc cgg gaa caa gag gag gat cag atg ctg cgg gac atg      962
Glu Asp Arg Leu Arg Glu Gln Glu Glu Asp Gln Met Leu Arg Asp Met
                305                 310                 315

att gag aag ctg ggc ctc cag agg aag aag tcc aag ttc cgc ttg tcc     1010
Ile Glu Lys Leu Gly Leu Gln Arg Lys Lys Ser Lys Phe Arg Leu Ser
            320                 325                 330

aag atc tgg tca cca aaa agc aaa agc agc ccc tcc cag tag tagccag     1059
Lys Ile Trp Ser Pro Lys Ser Lys Ser Ser Pro Ser Gln  *
        335                 340                 345

tagggccgtg ggctcggccc ggacctggca tccggacttg gactcggggc catgggcttg   1119

gcccggaccc ggaacccgga cttgtactcg ggccgtgggg ctcggcccgg acccggcatt   1179

cggacttgga ctcgggaagg gcctcctgtc cctacaaggg gcatgtggac agcagggacc   1239

tgcgctaccg tctgtggtct caataaagaa accgaccaca tggaaaaaaa aaaaaaaa     1297




     <210> 173
     <211> 546
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (131)..(502)

     <400> 173
ctgccgtgag aaaattagcc tctggggtac ggccgacttt tgtccactgg gtgtcgcaga     60

tcccagtcct cagggcctca agacagctct gcaatccgcc gcacagaatt caagttcgga    120

ttcggctttg   atg acc tta atc cag gca aat cct aaa tcc tat cca gtc     169
             Met Thr Leu Ile Gln Ala Asn Pro Lys Ser Tyr Pro Val
               1               5                  10

ggc agc atc cag atg aac cac aac tcc ttc ctc agc gca acc agg cca      217
Gly Ser Ile Gln Met Asn His Asn Ser Phe Leu Ser Ala Thr Arg Pro
    15                  20                  25

agg gag tgc tcc atc ccc tgc ctc gca gtt act gat tct cca agc cgg      265
Arg Glu Cys Ser Ile Pro Cys Leu Ala Val Thr Asp Ser Pro Ser Arg
30                  35                  40                  45

gcg ccg ccc agt cct ggc ggg gct tcc ccc acc cct ctc cgc gcc ggg      313
Ala Pro Pro Ser Pro Gly Gly Ala Ser Pro Thr Pro Leu Arg Ala Gly
                50                  55                  60
```

```
caa tcg cgc gtt ctt tct tta ctt gtg ctc cac tgg tgg gca gca tgt       361
Gln Ser Arg Val Leu Ser Leu Leu Val Leu His Trp Trp Ala Ala Cys
            65                  70                  75

gct ccc gcg tcc aca gct ctg ttt cgc ctt ccg gtc ccc gta gct ctg       409
Ala Pro Ala Ser Thr Ala Leu Phe Arg Leu Pro Val Pro Val Ala Leu
        80                  85                  90

cag ggg aac ggg atc tct gcc gcc tcc tcg gcc gct aag cga ccc ggg       457
Gln Gly Asn Gly Ile Ser Ala Ala Ser Ser Ala Ala Lys Arg Pro Gly
    95                  100                 105

gct gcc cga cct agc gag tgc gca cga ccg ccc agc gag ggg tag ccg       505
Ala Ala Arg Pro Ser Glu Cys Ala Arg Pro Pro Ser Glu Gly  *
110                 115                 120

agtcgaggca gcacggttcc caaggcagcc aaggctgcgc c                         546



     <210> 174
     <211> 1009
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (50)..(793)

     <400> 174
gcacgagggc acgagctgta tgagtggtag cctttcccct caaccagca    atg gag       55
                                                          Met Glu
                                                           1

gag cag ccc cag atg caa gac gcc gac gag ccc gcg gac tcc gga ggg      103
Glu Gln Pro Gln Met Gln Asp Ala Asp Glu Pro Ala Asp Ser Gly Gly
        5                   10                  15

gaa ggc cgg gca ggc ggg cca ccg cag gtc gcc ggc gcc cag gcg gcg      151
Glu Gly Arg Ala Gly Gly Pro Pro Gln Val Ala Gly Ala Gln Ala Ala
    20                  25                  30

tgc agc gag gac cgc atg acc ctg ctc ctc agg ctg aga gca cag aca      199
Cys Ser Glu Asp Arg Met Thr Leu Leu Leu Arg Leu Arg Ala Gln Thr
 35                 40                  45                  50

aaa caa caa ctc tta gaa tat aaa tca atg gtt gat gca agt gaa gaa      247
Lys Gln Gln Leu Leu Glu Tyr Lys Ser Met Val Asp Ala Ser Glu Glu
                55                  60                  65

aaa act cca gaa caa att atg caa gaa aag caa atc gaa gct aaa att      295
Lys Thr Pro Glu Gln Ile Met Gln Glu Lys Gln Ile Glu Ala Lys Ile
            70                  75                  80

gaa gac ctg gaa aat gaa att gaa gag gta aaa gtt gct ttt gag ata      343
Glu Asp Leu Glu Asn Glu Ile Glu Glu Val Lys Val Ala Phe Glu Ile
```

```
         85                  90                  95

aaa aag ctt gca tta gac agg atg aga ctt tca act gca ctt aaa aaa      391
Lys Lys Leu Ala Leu Asp Arg Met Arg Leu Ser Thr Ala Leu Lys Lys
    100                 105                 110

aac ctg gag aaa att agc aga cag tct agt gtg ctc atg gat aac atg      439
Asn Leu Glu Lys Ile Ser Arg Gln Ser Ser Val Leu Met Asp Asn Met
115                 120                 125             130

aaa cac cta tta gag cta aat aaa tta ata atg aaa tca cag cag gaa      487
Lys His Leu Leu Glu Leu Asn Lys Leu Ile Met Lys Ser Gln Gln Glu
                135                 140                 145

tct tgg gat tta gag gaa aaa ctg ctt gat att aga aag aag aga ttg      535
Ser Trp Asp Leu Glu Glu Lys Leu Leu Asp Ile Arg Lys Lys Arg Leu
            150                 155                 160

caa tta aaa caa gct tca gaa agt aag ctt tta gaa ata cag act gaa      583
Gln Leu Lys Gln Ala Ser Glu Ser Lys Leu Leu Glu Ile Gln Thr Glu
        165                 170                 175

aag aac aaa cag aag att gat ttg gac agt atg gaa aac tca gag agg      631
Lys Asn Lys Gln Lys Ile Asp Leu Asp Ser Met Glu Asn Ser Glu Arg
    180                 185                 190

ata aag atc ata cga caa aac cta cag atg gag ata aaa att act act      679
Ile Lys Ile Ile Arg Gln Asn Leu Gln Met Glu Ile Lys Ile Thr Thr
195                 200                 205             210

gtt att caa cat gtg ttc cag aac ctt att ttg ggg agt aaa gtc aat      727
Val Ile Gln His Val Phe Gln Asn Leu Ile Leu Gly Ser Lys Val Asn
                215                 220                 225

tgg gca gag gat cct gcc ctt aag gaa att gtt ctg cag ctt gag aag      775
Trp Ala Glu Asp Pro Ala Leu Lys Glu Ile Val Leu Gln Leu Glu Lys
            230                 235                 240

aat gtt gac atg atg taa taagaa ttcatttctg acatatttta catttctggc      829
Asn Val Asp Met Met  *
        245

aatctcaact cttatttgga atacttctgt gcatttgtct gtccaccgta attttagaaa    889

agcatatcca taacgtttac agttgtagta cagttgtggt tagttatttg tagtgggatt    949

gaaagtaatt tttttctttt tatatttcta tattcaggtt ggtttttggg tgccgttcgc   1009
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<210> 175
<211> 834
<212> DNA
<213> Homo sapiens

<220>

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      <221> CDS
      <222> (12)..(833)

      <400> 175
tttcgtcaag g atg aca tcc att cga gct gta ttt ata ttc ctg tgg ctg       50
             Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu
              1               5                  10

cag ctg gac ttg gtg aat gga gag aat gtg gag cag cat cct tca acc        98
Gln Leu Asp Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr
     15                  20                  25

ctg agt gtc cag gag gga gac agc gct gtt atc aag tgt act tat tca       146
Leu Ser Val Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser
 30                  35                  40                  45

gac agt gcc tca aac tac ttc cct tgg tat aag caa gaa ctt gga aaa       194
Asp Ser Ala Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys
                 50                  55                  60

aga cct cag ctt att ata gac att cgt tca aat gtg ggc gaa aag aaa       242
Arg Pro Gln Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys
             65                  70                  75

gac caa cga att gct gtt aca ttg aac aag aca gcc aaa cat ttc tcc       290
Asp Gln Arg Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser
         80                  85                  90

ctg cac atc aca gag acc caa cct gaa gac tcg gct gtc tac ttc tgt       338
Leu His Ile Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys
     95                 100                 105

gca gca agt aac ggc cag gca gga act gct ctg atc ttt ggg aag gga       386
Ala Ala Ser Asn Gly Gln Ala Gly Thr Ala Leu Ile Phe Gly Lys Gly
110                 115                 120                 125

acc acc tta tca gtg agt tcc aat atc cag aac cct gac cct gcc gtg       434
Thr Thr Leu Ser Val Ser Ser Asn Ile Gln Asn Pro Asp Pro Ala Val
                130                 135                 140

tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc cta ttc       482
Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
            145                 150                 155

acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat tct gat       530
Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
        160                 165                 170

gtg tat atc aca gac aaa act gtg cta gac atg agg tct atg gac ttc       578
Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
    175                 180                 185

aag agc aac agt gct gtg gcc tgg agc aac aaa tct gac ttt gca tgt       626
Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys
190                 195                 200                 205

gca aac gcc ttc aac aac agc att att cca gaa gac acc ttc ttc ccc       674
```

```
Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
                210                 215                 220

agc cca gaa agt tcc tgt gat gtc aag ctg gtc gag aaa agc ttt gaa      722
Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
            225                 230                 235

aca gat acg aac cta aac ttt caa aac ctg tca gtg att ggg ttc cga      770
Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
        240                 245                 250

atc ctc ctc ctg aaa gtg gcc ggg ttt aat ctg ctc atg acg ctg cgg      818
Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
    255                 260                 265

ctg tgg tcc agc tga g                                                834
Leu Trp Ser Ser  *
270




     <210> 176
     <211> 778
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (34)..(576)

     <220>
     <221> misc_feature
     <222> (1)...(778)
     <223> n = a,t,c or g

     <400> 176
tttcgtagac ctctctgtct tgtagcatct gcc atg aga atc agg ctc ctg tgc      54
                                     Met Arg Ile Arg Leu Leu Cys
                                       1               5

tgt gtg gcc ttt tct ctc ctg tgg gca ggt cca gtg att gct ggg atc      102
Cys Val Ala Phe Ser Leu Leu Trp Ala Gly Pro Val Ile Ala Gly Ile
         10                  15                  20

acc cag gca cca aca tct cag atc ctg gca gca gga cgg cgc atg aca      150
Thr Gln Ala Pro Thr Ser Gln Ile Leu Ala Ala Gly Arg Arg Met Thr
     25                  30                  35

ctg aga tgt acc cag gat atg aga cat aat gcc atg tac tgg tat aga      198
Leu Arg Cys Thr Gln Asp Met Arg His Asn Ala Met Tyr Trp Tyr Arg
 40                  45                  50                  55

caa gat cta gga ctg ggg cta agg ctc atc cat tat tca aat act gca      246
Gln Asp Leu Gly Leu Gly Leu Arg Leu Ile His Tyr Ser Asn Thr Ala
                 60                  65                  70
```

```
ggt acc act ggc aaa gga gaa gtc cct gat ggt tat agt gtc tcc aga      294
Gly Thr Thr Gly Lys Gly Glu Val Pro Asp Gly Tyr Ser Val Ser Arg
             75                  80                  85

gca aac aca gat gat ttc ccc ctc acg ttg gcg tct gct gta ccc tct      342
Ala Asn Thr Asp Asp Phe Pro Leu Thr Leu Ala Ser Ala Val Pro Ser
         90                  95                 100

cag aca tct gtg tac ttc tgt gcc agc agt gac ggg gct agc ggg agt      390
Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Asp Gly Ala Ser Gly Ser
    105                 110                 115

ccc cac acc ggg gag ctg ttt ttt gga gaa ggc tct agg ctg acc gta      438
Pro His Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val
120                 125                 130                 135

ctg gag gac ctg aaa aac gtg ttc cca ccc gag gtc gct gtg ttt gag      486
Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu
                140                 145                 150

cca tca gaa gca gag atc tcc cac acc caa aag gcc aca ctg gtg tgc      534
Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys
            155                 160                 165

ctg gcc aca ggc ttc tac ccc gac cac gtg gag ctg agc tga tttttc       583
Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser  *
        170                 175                 180

atagactatg agcttctaaa aaatcatccc catattcgtc attacattct tgggatcaaa    643

tatactgcat gaaaaaagat gctcagaaaa gtctatgtta agttaatgta gaatatatga    703

atgagtgaag gaaagtgttt tgaaaccatc atagggaata taataagata anattacact    763

agaataaaat gaaac                                                     778



      <210> 177
      <211> 708
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (176)..(493)

      <400> 177
gagggcggga gaggcagatg agtaaatgga tccttacact aagtgtgatg agcagaaacc     60

caggcgctct ggggcatgag cagggatacc taacccagcc ctgggggctc aatctctccc    120

cacccctgca ggagaggctt ggggtgagtt ttgggaataa ggaccatcca gccac atg     178
                                                             Met
                                                              1
```

```
acg aag ggg aag gaa aat ccc cat caa ggc aaa aac aca gtc caa ggc      226
Thr Lys Gly Lys Glu Asn Pro His Gln Gly Lys Asn Thr Val Gln Gly
              5                  10                  15

tct gag gcc caa att ccg ggg aga ggg gtg aag gtt gtt tgt cgc acc      274
Ser Glu Ala Gln Ile Pro Gly Arg Gly Val Lys Val Val Cys Arg Thr
         20                  25                  30

tgg gtt aaa ggg tgg ggg tgg aga gta gga gaa gag gct aca cag gtg      322
Trp Val Lys Gly Trp Gly Trp Arg Val Gly Glu Glu Ala Thr Gln Val
     35                  40                  45

aga agg tgt cag atc aca aag ggc ctt gta tgc caa act aag aag act      370
Arg Arg Cys Gln Ile Thr Lys Gly Leu Val Cys Gln Thr Lys Lys Thr
 50                  55                  60                  65

gaa ctt gac cat gaa gtt agg cag acc ctc tgg aga gtt tta aag caa      418
Glu Leu Asp His Glu Val Arg Gln Thr Leu Trp Arg Val Leu Lys Gln
                 70                  75                  80

gga gtc gtg tgg atg aac aaa cct gtg atg ggc tgg ggt tac caa gga      466
Gly Val Val Trp Met Asn Lys Pro Val Met Gly Trp Gly Tyr Gln Gly
             85                  90                  95

ggg ctt cct gga gga ggt cag act tga gctga gggaaggata ggatttggag      518
Gly Leu Pro Gly Gly Gly Gln Thr  *
        100                 105

agctgacatt ctgatgagcg gcttcggtta aagctcacaa aaacccttcc ctcccccatg    578

ccctttgaaa tcatttgaat caaagattgc gtgtgttaaa gacatgtttg tctgttatct    638

gaaagctgtg gtttctcttt aacagattca gggcctcatc ctttgactcg gaccaagaag    698

gaattatgag                                                           708



     <210> 178
     <211> 1463
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (120)..(1175)

     <220>
     <221> misc_feature
     <222> (1)...(1463)
     <223> n = a,t,c or g

     <400> 178
tttcgtgcaa agaaaactgt gagagagaga atttttaaaa agcagctggg gcctgaggtt     60
```

```
tctcccccag taccctgggt cacctcagcc cagagctggc ggcaggcccc cagcccctc      119
atg tca gag ccc cct gtg tac tgt aac ctg gtg gac ctt cgc cgc tgt       167
Met Ser Glu Pro Pro Val Tyr Cys Asn Leu Val Asp Leu Arg Arg Cys
  1               5                  10                  15

cct cgg tcc cca ccc cca ggc cct gca tgc ccc ctg ctg cag agg ctg       215
Pro Arg Ser Pro Pro Pro Gly Pro Ala Cys Pro Leu Leu Gln Arg Leu
             20                  25                  30

gat gcc tgg gag cag cac ctg gac ccc aac tct gga cgc tgc ttc tac       263
Asp Ala Trp Glu Gln His Leu Asp Pro Asn Ser Gly Arg Cys Phe Tyr
         35                  40                  45

ata aat tca ctg act ggc tgc aag tcc tgg aag ccc ccg cgc cgc agt       311
Ile Asn Ser Leu Thr Gly Cys Lys Ser Trp Lys Pro Pro Arg Arg Ser
     50                  55                  60

cgc agc gag acg aac cct ggc tcc atg gag ggg aca cag acc ctg aag       359
Arg Ser Glu Thr Asn Pro Gly Ser Met Glu Gly Thr Gln Thr Leu Lys
 65                  70                  75                  80

agg aac aat gat gtc ctg caa cct cag gca aag ggc ttc aga tct gac       407
Arg Asn Asn Asp Val Leu Gln Pro Gln Ala Lys Gly Phe Arg Ser Asp
                 85                  90                  95

aca ggg acc cca gaa ccg ctt gac cca cag ggt tca ctc agc ctc agc       455
Thr Gly Thr Pro Glu Pro Leu Asp Pro Gln Gly Ser Leu Ser Leu Ser
            100                 105                 110

caa cgc acc tcg cag ctt gac cct cca gcc ttg cag gcc cct cga cct       503
Gln Arg Thr Ser Gln Leu Asp Pro Pro Ala Leu Gln Ala Pro Arg Pro
        115                 120                 125

ctg ccg cag ctc ctg gac gac ccc cat gag gtg gaa aag tcg ggt ctg       551
Leu Pro Gln Leu Leu Asp Asp Pro His Glu Val Glu Lys Ser Gly Leu
    130                 135                 140

ctc aac atg acc aag att gcc caa ggg ggg cgc aag ctc agg aag aac       599
Leu Asn Met Thr Lys Ile Ala Gln Gly Gly Arg Lys Leu Arg Lys Asn
145                 150                 155                 160

tgg ggc ccg tct tgg gtg gtg tta acg ggt aac agc ctg gtg ttc tac       647
Trp Gly Pro Ser Trp Val Val Leu Thr Gly Asn Ser Leu Val Phe Tyr
                165                 170                 175

cga gag cca ccg ccg aca gcg ccc tcc tca ggc tgg gga cca gcg ggt       695
Arg Glu Pro Pro Pro Thr Ala Pro Ser Ser Gly Trp Gly Pro Ala Gly
            180                 185                 190

agc cgg ccc gaa agt agc gtg gac ctg cgc ggg gcg gcc ctg gcg cac       743
Ser Arg Pro Glu Ser Ser Val Asp Leu Arg Gly Ala Ala Leu Ala His
        195                 200                 205

ggc cgc cac ctg tcc agc cgc cgc aac gtc ctg cac atc cgc acg atc       791
Gly Arg His Leu Ser Ser Arg Arg Asn Val Leu His Ile Arg Thr Ile
    210                 215                 220
```

```
cct ggc cac gag ttc ctg ctg cag tcg gac cac gag aca gag ctg cga      839
Pro Gly His Glu Phe Leu Leu Gln Ser Asp His Glu Thr Glu Leu Arg
225                 230                 235                 240

gcc tgg cac cgc gcg ctg cgg act gtc atc gag cgg ctg gat cgg gag      887
Ala Trp His Arg Ala Leu Arg Thr Val Ile Glu Arg Leu Asp Arg Glu
                245                 250                 255

aac ccc ctg gag ctg cgt ctg tcg ggc tct gga ccc gcg gag ctg agc      935
Asn Pro Leu Glu Leu Arg Leu Ser Gly Ser Gly Pro Ala Glu Leu Ser
            260                 265                 270

gcc ggg gag gac gaa gaa gag gag tcg gag ctg gtg tcc aag ccg ctg      983
Ala Gly Glu Asp Glu Glu Glu Glu Ser Glu Leu Val Ser Lys Pro Leu
        275                 280                 285

ctg cgc ctc agc agc cgc cgg agc tcc att cgg ggg ccc gaa ggc acc     1031
Leu Arg Leu Ser Ser Arg Arg Ser Ser Ile Arg Gly Pro Glu Gly Thr
    290                 295                 300

gag cag aac cgc gtg cgc aac aaa cta aag cgg ctc atc gcg aag aga     1079
Glu Gln Asn Arg Val Arg Asn Lys Leu Lys Arg Leu Ile Ala Lys Arg
305                 310                 315                 320

ccg ccc tta caa agc ctg cag gag cgg ggt ctg ctc cga ggt gag ggg     1127
Pro Pro Leu Gln Ser Leu Gln Glu Arg Gly Leu Leu Arg Gly Glu Gly
                325                 330                 335

gct ggg cca ggt tca tgg ata aga aaa ctc cag cga ggc tca gag tag     1175
Ala Gly Pro Gly Ser Trp Ile Arg Lys Leu Gln Arg Gly Ser Glu  *
            340                 345                 350

agcttcccag aactagacca caaccttctg tgactgctgc tttcccacta ccccagattg   1235

tttaggggag aagctggggt gacctgtacc cctttgccag attgtttgaa gcangggaag   1295

ggaggtggag tgtatttcct tgcccaggcc tggcacaggc agccaggagg accagcctca   1355

cttaaggata aagacctatg ctgagaagag ctcctgtgag tgacgctggc acttggcttc   1415

cgcctcactc tacttcccca gaccaggtgt tcggctggca gatggaat                1463



      <210> 179
      <211> 678
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (122)..(478)

      <400> 179
agtgcggtgg aattctggtt aaaaaaagta cagaatgcaa aaggatatgg cataaaaggc     60
```

```
caagtccgaa aagggctact agtgttctag gtgtctttcc agaaagatta tgcgcatata      120

a    atg tgc aca ctt gca tgt gtg cac aca cat aca cac act ctc ata      166
     Met Cys Thr Leu Ala Cys Val His Thr His Thr His Thr Leu Ile
      1               5                  10                  15

tac cta aaa tac gaa tgg gag cac atg aca cac aca ttc tgc ctg ctg      214
Tyr Leu Lys Tyr Glu Trp Glu His Met Thr His Thr Phe Cys Leu Leu
                20                  25                  30

ctt tgt ctg tgc ata att tta tct tcc agg tca tct gtg ctg gtg tct      262
Leu Cys Leu Cys Ile Ile Leu Ser Ser Arg Ser Ser Val Leu Val Ser
            35                  40                  45

atc agt ctg cta gtc ttt ccc cgc cat gtg gcc att gtt cca gtc ccc      310
Ile Ser Leu Leu Val Phe Pro Arg His Val Ala Ile Val Pro Val Pro
        50                  55                  60

tcc tat gca cac cca ggt ttc tct agg acc atg tta tcc cag agc cag      358
Ser Tyr Ala His Pro Gly Phe Ser Arg Thr Met Leu Ser Gln Ser Gln
    65                  70                  75

gtg gac agg aca caa agg gct agg ggt caa tgg ggg tgt tct cgc ctc      406
Val Asp Arg Thr Gln Arg Ala Arg Gly Gln Trp Gly Cys Ser Arg Leu
80                  85                  90                  95

cag tct gcc ctg cca gcc ccc agt cgt ggg tgg acc tgc cat cag ctt      454
Gln Ser Ala Leu Pro Ala Pro Ser Arg Gly Trp Thr Cys His Gln Leu
                100                 105                 110

gct ctg ccc act ccc cag gcc tga gctgctggcg aaacaggcaa gtgactgcac      508
Ala Leu Pro Thr Pro Gln Ala  *
            115

tgcccatggc cggtcaccag cctcaggtga accccaggag gggttcctac ctagcactca      568

tcatttcctc aacttcacta ctgtgtcgcc ctgtgggaca gggaagtcca agtcggggaa      628

aaagcctgtg gggaggggtt ggtgggagat ggggagccca tatggcccag                 678




     <210> 180
     <211> 599
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (189)..(512)

     <400> 180
accgaaagct gtaggagttt ataccagtac ttccaattcc aaccttattc tagttttcac       60

cctttccaaa tttgtaattc tctgactata agaaatctgg ctcctgctct ttccctgctg      120
```

```
ccactgaatt gtatagaggc ggagtctcgg gtgcattcaa gatccggctt cactcgtaac     180

ccactgcc atg gcc gag gaa ggc agt gct gct gga ggt gta atg gac att      230
         Met Ala Glu Glu Gly Ser Ala Ala Gly Gly Val Met Asp Ile
           1               5                  10

aat act gtt tta cag gag gtg ctg aag acc gcc ctc atc cat gat ggc       278
Asn Thr Val Leu Gln Glu Val Leu Lys Thr Ala Leu Ile His Asp Gly
 15                  20                  25                  30

cta gca tat gaa att tgc aaa gct gcc aaa gcc tca gac aag tgc caa       326
Leu Ala Tyr Glu Ile Cys Lys Ala Ala Lys Ala Ser Asp Lys Cys Gln
                 35                  40                  45

gcc cat ctt tgt gtg ctg tgt gtg ctt gca tcc aac tgt gat gag cct       374
Ala His Leu Cys Val Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro
             50                  55                  60

atg tat gtc aag ttg gtg gag gcc ctt tgt gct gaa cac caa atc aac       422
Met Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn
         65                  70                  75

cta att aag gtt gat gac cag aaa cta ggg gaa tcg gta ggc ctc tgt       470
Leu Ile Lys Val Asp Asp Gln Lys Leu Gly Glu Ser Val Gly Leu Cys
     80                  85                  90

aaa act gac aga gag ggg aaa ccg tgt aaa gtg gtt ggt tga agttgta       519
Lys Thr Asp Arg Glu Gly Lys Pro Cys Lys Val Val Gly  *
 95                 100                 105

tagtagttac gaactatggc aaggagtctc aggccaagga tatcattgaa gagtacttca     579

aatgcaagaa atgaacaagt                                                 599




     <210> 181
     <211> 1396
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (68)..(1039)

     <400> 181
tttcgtagtt cttagtccgt gcggtggaat tcccggccgc gctccgaacg gcgcctcccg      60

ccccacc  atg ggc aac agc gcg agc cgc aac gac ttc gag tgg gtc tac      109
         Met Gly Asn Ser Ala Ser Arg Asn Asp Phe Glu Trp Val Tyr
           1               5                  10

acc gac cag ccg cac acg cag cgg cgc aag gag ata ctg gcc aag tac       157
Thr Asp Gln Pro His Thr Gln Arg Arg Lys Glu Ile Leu Ala Lys Tyr
 15                  20                  25                  30
```

```
ccg gcc atc aag gcc ctg atg cgg cca gac ccg cgc ctc aag tgg gcg       205
Pro Ala Ile Lys Ala Leu Met Arg Pro Asp Pro Arg Leu Lys Trp Ala
                 35                  40                  45

gtg ctg gtg ctg gtg ctg gtg cag atg ctg gcc tgc tgg ctg gtg cgc       253
Val Leu Val Leu Val Leu Val Gln Met Leu Ala Cys Trp Leu Val Arg
             50                  55                  60

ggg ctg gcc tgg cgc tgg ctg ctg ttc tgg gcc tac gcc ttt ggt ggc       301
Gly Leu Ala Trp Arg Trp Leu Leu Phe Trp Ala Tyr Ala Phe Gly Gly
         65                  70                  75

tgc gtg aac cac tcg ctg acg ctg gcc atc cac gac atc tcg cac aac       349
Cys Val Asn His Ser Leu Thr Leu Ala Ile His Asp Ile Ser His Asn
     80                  85                  90

gcg gcc ttc ggc acg ggc cgt gcg gca cgc aac cgc tgg ctg gcc gtg       397
Ala Ala Phe Gly Thr Gly Arg Ala Ala Arg Asn Arg Trp Leu Ala Val
 95                 100                 105                 110

ttc gcc aac ctg ccc gtg ggt gtg ccc tac gcc gcc tcc ttc aag aag       445
Phe Ala Asn Leu Pro Val Gly Val Pro Tyr Ala Ala Ser Phe Lys Lys
                115                 120                 125

tac cac gtg gac cac cac cgc tac ctg ggc ggc gac ggg ctg gac gtg       493
Tyr His Val Asp His His Arg Tyr Leu Gly Gly Asp Gly Leu Asp Val
            130                 135                 140

gac gtg ccc acg cgt ctg gag ggc tgg ttc ttc tgc acg ccc gcc cgc       541
Asp Val Pro Thr Arg Leu Glu Gly Trp Phe Phe Cys Thr Pro Ala Arg
        145                 150                 155

aag ctg ctc tgg ctg gtg ctg cag ccc ttc ttc tac tca cta cgg ccg       589
Lys Leu Leu Trp Leu Val Leu Gln Pro Phe Phe Tyr Ser Leu Arg Pro
    160                 165                 170

ctc tgc gtc cac ccc aag gcc gtg acc cgc atg gag gtg ctc aac acg       637
Leu Cys Val His Pro Lys Ala Val Thr Arg Met Glu Val Leu Asn Thr
175                 180                 185                 190

ctg gtg cag ctg gcg gcc gac ctg gcc atc ttt gcc ctt tgg ggg ctc       685
Leu Val Gln Leu Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu
                195                 200                 205

aag ccc gtg gtc tac ctg ctg gcc agc tcc ttc ctg ggc ctg ggc ctg       733
Lys Pro Val Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu
            210                 215                 220

cac ccc atc tcg ggc cac ttc gtg gcc gag cac tac atg ttc ctc aag       781
His Pro Ile Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys
        225                 230                 235

ggc cac gag acc tac tcc tac tat ggg cct ctc aac tgg atc acc ttc       829
Gly His Glu Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe
    240                 245                 250

aat gtg ggc tac cac gtg gag cac cac gac ttc ccc agc atc ccg ggc       877
```

```
Asn Val Gly Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly
255                 260                 265                 270

tac aac ctg ccg ctg gtg cgg aag atc gcg ccc gag tac tac gac cac      925
Tyr Asn Leu Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His
                275                 280                 285

ctg ccg cag cac cac tcc tgg gtg aag gtg ctc tgg gat ttt gtg ttt      973
Leu Pro Gln His His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe
            290                 295                 300

gag gac tcc ctg ggg ccc tat gcc agg gtg aag cgg gtg tac agg ctg     1021
Glu Asp Ser Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr Arg Leu
        305                 310                 315

gca aaa gat ggt ctg tga gcccgg gctgcctcct ggtggtggcc attgtccccc     1075
Ala Lys Asp Gly Leu  *
    320

atcggcccct cagccttgca ccccagcact gagaagctac atttccttcc tgtgctctgg   1135

actgctgccc ttgtccccga ggagtgtccc gcgcagccac acctggcaac agcagtgtgg   1195

gctgcagggc tccgtctgca cgtggacttg ccctggacct tgagtgtggc cctccctttc   1255

tgggcctccc caggtgaggc ctggccctgc cccaccatga cctgggtgct ctgagcccac   1315

ggttcccacg gagctgactt ctccggggtg cctgtgccct acattaaacc cggcgtttgt   1375

ttcacagcca aaaaaaaaaa a                                              1396



     <210> 182
     <211> 2728
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (22)..(2688)

     <400> 182
ctggatggac tagccggggc c atg gcc ggc gcg gcg gcg gag tca ggg cgg       51
                        Met Ala Gly Ala Ala Ala Glu Ser Gly Arg
                         1               5                  10

gag ctg tgg acc ttc gcg ggt tcc cgg gac ccg agc gca ccg cgg cta       99
Glu Leu Trp Thr Phe Ala Gly Ser Arg Asp Pro Ser Ala Pro Arg Leu
                15                  20                  25

gcc tac ggc tac ggc ccg ggc agc ctg cgc gag ctg cgg gcg cgc gag      147
Ala Tyr Gly Tyr Gly Pro Gly Ser Leu Arg Glu Leu Arg Ala Arg Glu
            30                  35                  40

ttc agc cgc ctg gca gga act gtc tat ctt gac cat gca ggt gcc acc      195
```

```
Phe Ser Arg Leu Ala Gly Thr Val Tyr Leu Asp His Ala Gly Ala Thr
        45                  50                  55

ttg ttc tcc cag agc cag ctc gaa agc ttc act agt gat ctc atg gaa       243
Leu Phe Ser Gln Ser Gln Leu Glu Ser Phe Thr Ser Asp Leu Met Glu
    60              65                  70

aac act tat ggt aat cct cac agc cag aac atc agc agc aag ctc acc       291
Asn Thr Tyr Gly Asn Pro His Ser Gln Asn Ile Ser Ser Lys Leu Thr
75                  80                  85                  90

cat gac act gtg gag cag gtg cgc tac aga atc ctg gcg cac ttc cac       339
His Asp Thr Val Glu Gln Val Arg Tyr Arg Ile Leu Ala His Phe His
                95                  100                 105

acc acc gca gaa gac tac act gtg atc ttc act gcc ggg agc acg gct       387
Thr Thr Ala Glu Asp Tyr Thr Val Ile Phe Thr Ala Gly Ser Thr Ala
            110                 115                 120

gct ctc aaa ctg gtg gca gag gcc ttt cca tgg gtg tcc cag ggc cca       435
Ala Leu Lys Leu Val Ala Glu Ala Phe Pro Trp Val Ser Gln Gly Pro
        125                 130                 135

gag agc agt ggg agt cgc ttc tgt tac ctc acc gac agc cac acc tcc       483
Glu Ser Ser Gly Ser Arg Phe Cys Tyr Leu Thr Asp Ser His Thr Ser
    140                 145                 150

gta gtg ggt atg agg aac gtg acc atg gct ata aat gtc ata tcc atc       531
Val Val Gly Met Arg Asn Val Thr Met Ala Ile Asn Val Ile Ser Ile
155                 160                 165                 170

ccg gtc agg cca gag gac ctg tgg tct gca gag gaa cgt ggt gct tca       579
Pro Val Arg Pro Glu Asp Leu Trp Ser Ala Glu Glu Arg Gly Ala Ser
                175                 180                 185

gcc agc aac cca gac tgc cag ctg ccg cat ctc ttc tgc tac cca gct       627
Ala Ser Asn Pro Asp Cys Gln Leu Pro His Leu Phe Cys Tyr Pro Ala
            190                 195                 200

cag agt aac ttt tct gga gtc aga tac ccc ctg tcc tgg ata gaa gag       675
Gln Ser Asn Phe Ser Gly Val Arg Tyr Pro Leu Ser Trp Ile Glu Glu
        205                 210                 215

gtc aag tct ggg cgg ttg cgc cct gtg agc acg cct ggg aag tgg ttt       723
Val Lys Ser Gly Arg Leu Arg Pro Val Ser Thr Pro Gly Lys Trp Phe
    220                 225                 230

gtg ctg ctg gat gca gcc tcc tac gtg agc acc tcg cct ttg gac ctg       771
Val Leu Leu Asp Ala Ala Ser Tyr Val Ser Thr Ser Pro Leu Asp Leu
235                 240                 245                 250

tca gct cac cag gcc gac ttt gtc ccc atc tcc ttc tat aag atc ttc       819
Ser Ala His Gln Ala Asp Phe Val Pro Ile Ser Phe Tyr Lys Ile Phe
                255                 260                 265

ggg ttt cct aca ggc ctg ggc gct ctg ctg gtc cat aat cgt gcg gct       867
Gly Phe Pro Thr Gly Leu Gly Ala Leu Leu Val His Asn Arg Ala Ala
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            270                 275                 280

cct cta ctg agg aag acc tac ttt gga gga ggg aca gcc tct gcg tac        915
Pro Leu Leu Arg Lys Thr Tyr Phe Gly Gly Gly Thr Ala Ser Ala Tyr
        285                 290                 295

cta gca gga gaa gac ttc tac atc ccg agg cag tcg gta gct cag agg        963
Leu Ala Gly Glu Asp Phe Tyr Ile Pro Arg Gln Ser Val Ala Gln Arg
    300                 305                 310

ttt gaa gat ggc acc atc tca ttc ctt gat gtt atc gcg cta aaa cat       1011
Phe Glu Asp Gly Thr Ile Ser Phe Leu Asp Val Ile Ala Leu Lys His
315                 320                 325                 330

gga ttt gac acc cta gag cgc ctc aca ggt gga atg gag aat ata aag       1059
Gly Phe Asp Thr Leu Glu Arg Leu Thr Gly Gly Met Glu Asn Ile Lys
                335                 340                 345

cag cac acc ttc acc ttg gct cag tat acc tac atg gcc ctg tcc tct       1107
Gln His Thr Phe Thr Leu Ala Gln Tyr Thr Tyr Met Ala Leu Ser Ser
            350                 355                 360

ctc cag tac ccc aat gga gcc cct gtg gtg cgg att tac agc gat tct       1155
Leu Gln Tyr Pro Asn Gly Ala Pro Val Val Arg Ile Tyr Ser Asp Ser
        365                 370                 375

gag ttc agc agc cct gag gtt cag ggc ccg atc atc aat ttt aat gtg       1203
Glu Phe Ser Ser Pro Glu Val Gln Gly Pro Ile Ile Asn Phe Asn Val
    380                 385                 390

ctg gat gac aaa ggg aac atc att ggt tac tcc cag gtg gac aaa atg       1251
Leu Asp Asp Lys Gly Asn Ile Ile Gly Tyr Ser Gln Val Asp Lys Met
395                 400                 405                 410

gcc agt ctt tac aac atc cac ctg cga act ggc tgc ttc tgt aac act       1299
Ala Ser Leu Tyr Asn Ile His Leu Arg Thr Gly Cys Phe Cys Asn Thr
                415                 420                 425

ggg gcc tgc cag agg cac ctg ggc ata agc aac gag atg gtc agg aag       1347
Gly Ala Cys Gln Arg His Leu Gly Ile Ser Asn Glu Met Val Arg Lys
            430                 435                 440

cat ttt cag gct ggt cat gtc tgt ggg gac aat atg gac ctc ata gat       1395
His Phe Gln Ala Gly His Val Cys Gly Asp Asn Met Asp Leu Ile Asp
        445                 450                 455

ggg cag ccc aca gga tct gtg agg att tca ttt gga tac atg tcg acg       1443
Gly Gln Pro Thr Gly Ser Val Arg Ile Ser Phe Gly Tyr Met Ser Thr
    460                 465                 470

ctg gat gat gtc cag gcc ttt ctt agg ttc atc ata gac act cgc ctg       1491
Leu Asp Asp Val Gln Ala Phe Leu Arg Phe Ile Ile Asp Thr Arg Leu
475                 480                 485                 490

cac tca tca ggg gac tgg cct gtc cct cag gcc cat gct gac acc ggg       1539
His Ser Ser Gly Asp Trp Pro Val Pro Gln Ala His Ala Asp Thr Gly
                495                 500                 505
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gag act gga gcc cca tca gca gac agc cag gct gat gtt ata cct gct     1587
Glu Thr Gly Ala Pro Ser Ala Asp Ser Gln Ala Asp Val Ile Pro Ala
            510                 515                 520

gtc atg ggc aga cgt agc ctc tcg cct cag gaa gat gcc ctc aca ggc     1635
Val Met Gly Arg Arg Ser Leu Ser Pro Gln Glu Asp Ala Leu Thr Gly
        525                 530                 535

tcc agg gtt tgg aac aac tcg tct act gtg aat gct gtg cct gtg gcc     1683
Ser Arg Val Trp Asn Asn Ser Ser Thr Val Asn Ala Val Pro Val Ala
    540                 545                 550

cca cct gtg tgt gat gtc gcc aga acc cag ccg act cct tca gag aaa     1731
Pro Pro Val Cys Asp Val Ala Arg Thr Gln Pro Thr Pro Ser Glu Lys
555                 560                 565                 570

gct gca gga gtc ctg gag ggg gcc ctt ggg cca cat gtt gtc act aac     1779
Ala Ala Gly Val Leu Glu Gly Ala Leu Gly Pro His Val Val Thr Asn
                575                 580                 585

ctt tat ctc tat cca atc aaa tcc tgt gct gca ttt gag gtg acc agg     1827
Leu Tyr Leu Tyr Pro Ile Lys Ser Cys Ala Ala Phe Glu Val Thr Arg
            590                 595                 600

tgg cct gta gga aac caa ggg ctg cta tat gac cgg agc tgg atg gtt     1875
Trp Pro Val Gly Asn Gln Gly Leu Leu Tyr Asp Arg Ser Trp Met Val
        605                 610                 615

gtg aat cac aat ggt gtt tgc ctg agt cag aag cag gaa ccc cgg ctc     1923
Val Asn His Asn Gly Val Cys Leu Ser Gln Lys Gln Glu Pro Arg Leu
    620                 625                 630

tgc ctg atc cag ccc ttc atc gac ttg cgg caa agg atc atg gtc atc     1971
Cys Leu Ile Gln Pro Phe Ile Asp Leu Arg Gln Arg Ile Met Val Ile
635                 640                 645                 650

aaa gcc aaa ggg atg gag cct ata gag gtg cct ctt gag gaa aat agt     2019
Lys Ala Lys Gly Met Glu Pro Ile Glu Val Pro Leu Glu Glu Asn Ser
                655                 660                 665

gaa cgg act cag att cgc caa agc agg gtc tgt gct gac aga gta agt     2067
Glu Arg Thr Gln Ile Arg Gln Ser Arg Val Cys Ala Asp Arg Val Ser
            670                 675                 680

act tat gat tgt gga gaa aaa att tca agc tgg ttg tca aca ttt ttt     2115
Thr Tyr Asp Cys Gly Glu Lys Ile Ser Ser Trp Leu Ser Thr Phe Phe
        685                 690                 695

ggc cgt cct tgt aat ttg atc aaa caa agt tca aac tct caa agg aat     2163
Gly Arg Pro Cys Asn Leu Ile Lys Gln Ser Ser Asn Ser Gln Arg Asn
    700                 705                 710

gca aag aag aaa cat gga aaa gat caa ctt cct ggt aca atg gcc acc     2211
Ala Lys Lys Lys His Gly Lys Asp Gln Leu Pro Gly Thr Met Ala Thr
715                 720                 725                 730
```

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ctt tct ctg gtg aat gag gca cag tat ctg ctg atc aac aca tcc agt       2259
Leu Ser Leu Val Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser
                735                 740                 745

att ttg gaa ctt cac cgg caa cta aac acc agt gat gag aat gga aag       2307
Ile Leu Glu Leu His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys
            750                 755                 760

gag gaa tta ttc tca ctg aag gat ctc agc ttg cgt ttt cgt gcc aat       2355
Glu Glu Leu Phe Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn
        765                 770                 775

att att atc aat gga aaa agg gct ttt gaa gaa gag aaa tgg gat gag       2403
Ile Ile Ile Asn Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu
    780                 785                 790

att tca att ggc tct ttg cgt ttc cag gtt ttg ggg cct tgt cac aga       2451
Ile Ser Ile Gly Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg
795                 800                 805                 810

tgc cag atg att tgc atc gac cag caa act ggg caa cga aac cag cat       2499
Cys Gln Met Ile Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His
                815                 820                 825

gtt ttc caa aaa ctt tct gag agt cgt gaa aca aag gtg aac ttt ggc       2547
Val Phe Gln Lys Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly
            830                 835                 840

atg tac ctg atg cat gca tca ttg gat tta tcc tcc cca tgt ttc ctg       2595
Met Tyr Leu Met His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu
        845                 850                 855

tct gta gga tct cag gtg ctc cct gtg ttg aaa gag aat gtg gaa ggt       2643
Ser Val Gly Ser Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly
    860                 865                 870

cat gat tta cct gca tct gag aaa cac cag gat gtt acc tcc taa aaa       2691
His Asp Leu Pro Ala Ser Glu Lys His Gln Asp Val Thr Ser  *
875                 880                 885

aaatttttag catacattaa agtttctctt ttaaaaa                              2728




<210> 183
<211> 1265
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (546)..(857)

<400> 183
cttcgacatt cgtatagcag acccaagctg gctagcgttt aaacttaagc ttggtaccga      60
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gctcggatcc actagtccag tgtggtggaa ttcggcagtc cccaaggggc gcagactctg    120

ctgtgaggtg tgcgaagccc cagccgagcg ggtgtgcgcg gcctgcacag tcacttatta    180

ctggtctggg ccgaatcgtt caggctgaag aatatctatt ccaagcccag tggacagtcc    240

tcaaatcaac tgactgtagt aatgccaccc actctttact gcatcggaat ctgggacttc    300

tctatatagc taagaaaaac tatgaagagg cccgttatca tctggccaat gatatttatt    360

ttgccagttg tgcatttgga acagaggaca ttaggacttc aggaggctac ttccacctgg    420

ctaatatatt ctatgacctt aaaaagttgg acctggcaga cacattgtac accaaggtct    480

ctgagatctg gcatgcatat ttgaacaatc actatcaagt cctctcacag gctcacatcc    540

aacaa    atg gat tta ctg ggc aaa cta ttt gag aat gac act ggc ttg     587
         Met Asp Leu Leu Gly Lys Leu Phe Glu Asn Asp Thr Gly Leu
           1               5                  10

gat gaa gcc caa gaa gca gaa gcc att cgc atc ctg act tca atc ttg      635
Asp Glu Ala Gln Glu Ala Glu Ala Ile Arg Ile Leu Thr Ser Ile Leu
 15                  20                  25                  30

aac att cga gaa tct aca tct gac aaa gcc ccc caa aaa acc atc ttt      683
Asn Ile Arg Glu Ser Thr Ser Asp Lys Ala Pro Gln Lys Thr Ile Phe
                 35                  40                  45

gtt ctg aag atc ctg gtc atg ctt tac tac ctg atg atg aat tct tca      731
Val Leu Lys Ile Leu Val Met Leu Tyr Tyr Leu Met Met Asn Ser Ser
             50                  55                  60

aag gca cag gaa tat ggc atg agg gcc ctc agt cta gcc aaa gaa caa      779
Lys Ala Gln Glu Tyr Gly Met Arg Ala Leu Ser Leu Ala Lys Glu Gln
         65                  70                  75

cag ctt gat gtc cat gag caa agc acc att caa gag tta tta agt ctc      827
Gln Leu Asp Val His Glu Gln Ser Thr Ile Gln Glu Leu Leu Ser Leu
     80                  85                  90

att tca act gaa gac cat ccc att act tag t gacccatgag ctctgcatca      878
Ile Ser Thr Glu Asp His Pro Ile Thr  *
 95                 100

agggttattc caggggctac tgaagatcta atatattcca gccttgcaca actgctttga    938

ggtactgtag actgctgaag tttccaccct cttcccctgg gattgcacac atagctgtta    998

tttttttctt acacagcata ttaagggaat ataaagcttt aggcatagaa atcactaaaa   1058

actgtgtttg tcatgacctt tgtacttgat ttatcatgac tttgtatgac tgagtaatat   1118

gtagtcagat cactaatatg gtatttgtaa ttaaactaca aatagtttgt catttcccag   1178

aagtcttcca acgatgcatg tttcatacac ttttgctaaa ggaggggtaa aggagggggt   1238

agggaataaa gctatattgg aacaaaa                                       1265
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<211> 1288
<212> DNA
<213> Homo sapiens

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<222> (251)..(1246)

<400> 184
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aactacagct tcttggcagc gtcggtgttg gccgcgggag aaggggagac cgcggcggcc     120

cccagtgaga gcggctttcc aggacggtgc gatgtgctgc gcagcgaaga ggcaggaggc     180

cggcttcctg ggtagcggt acaggcgggc gcttactctg tgcgcttgct tccccaaccc      240

tgcaccggcc  atg cgc ccg gcc ttg gcg gtg ggc ctg gtg ttc gca ggc      289
            Met Arg Pro Ala Leu Ala Val Gly Leu Val Phe Ala Gly
              1               5                  10

tgc tgc agt aac gtg atc ttc cta gag ctc ctg gcc cgg aag cat cca      337
Cys Cys Ser Asn Val Ile Phe Leu Glu Leu Leu Ala Arg Lys His Pro
     15                  20                  25

gga tgt ggg aac att gtg aca ttt gca caa ttt tta ttt att gct gtg      385
Gly Cys Gly Asn Ile Val Thr Phe Ala Gln Phe Leu Phe Ile Ala Val
 30                  35                  40                  45

gaa ggc ttc ctc ttt gaa gct gat ttg gga agg aag cca cca gct atc      433
Glu Gly Phe Leu Phe Glu Ala Asp Leu Gly Arg Lys Pro Pro Ala Ile
                 50                  55                  60

cca ata agg tac tat gcc ata atg gtg acc atg ttc ttc acc gtg agc      481
Pro Ile Arg Tyr Tyr Ala Ile Met Val Thr Met Phe Phe Thr Val Ser
             65                  70                  75

gtg gtg aac aac tat gcc ctg aat ctc aac att gcc atg ccc ctg cat      529
Val Val Asn Asn Tyr Ala Leu Asn Leu Asn Ile Ala Met Pro Leu His
         80                  85                  90

atg ata ttt aga tcc ggt tct cta att gcc aac acg att cta gga att      577
Met Ile Phe Arg Ser Gly Ser Leu Ile Ala Asn Thr Ile Leu Gly Ile
     95                 100                 105

atc att ttg aag aaa aga tac agt ata ttc aaa tat acc tcc att gcc      625
Ile Ile Leu Lys Lys Arg Tyr Ser Ile Phe Lys Tyr Thr Ser Ile Ala
110                 115                 120                 125

ctg gtg tct gtg ggg ata ttt att tgc act ttt atg tca gca aag cag      673
Leu Val Ser Val Gly Ile Phe Ile Cys Thr Phe Met Ser Ala Lys Gln
                130                 135                 140
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gtg act tcc cag tcc agc ttg agt gag aat gat gga ttc cag gca ttt        721
Val Thr Ser Gln Ser Ser Leu Ser Glu Asn Asp Gly Phe Gln Ala Phe
            145                 150                 155

gtg tgg tgg tta cta ggt att ggg gca ttg act ttt gct ctt ctg atg        769
Val Trp Trp Leu Leu Gly Ile Gly Ala Leu Thr Phe Ala Leu Leu Met
        160                 165                 170

tca gca agg atg ggg ata ttc caa gag act ctc tac aaa cga ttt ggg        817
Ser Ala Arg Met Gly Ile Phe Gln Glu Thr Leu Tyr Lys Arg Phe Gly
    175                 180                 185

aaa cac tcc aag gag gct ttg ttt tat aat cac gcc ctt cca ctt ccg        865
Lys His Ser Lys Glu Ala Leu Phe Tyr Asn His Ala Leu Pro Leu Pro
190                 195                 200                 205

ggt ttc gtc ttc ttg gct tct gat att tat gac cat gca gtt cta ttc        913
Gly Phe Val Phe Leu Ala Ser Asp Ile Tyr Asp His Ala Val Leu Phe
                210                 215                 220

aat aag tct gag tta tat gaa att ccc gtc atc gga gtg acc ctg ccc        961
Asn Lys Ser Glu Leu Tyr Glu Ile Pro Val Ile Gly Val Thr Leu Pro
            225                 230                 235

atc atg tgg ttc tac ctc ctc atg aac atc atc act cag tac gtg tgc       1009
Ile Met Trp Phe Tyr Leu Leu Met Asn Ile Ile Thr Gln Tyr Val Cys
        240                 245                 250

atc cgg ggt gtg ttt atc ctc acc aca gaa tgc gcc tcc ctc acc gtc       1057
Ile Arg Gly Val Phe Ile Leu Thr Thr Glu Cys Ala Ser Leu Thr Val
    255                 260                 265

acg ctc gtc gtg acc cta cgc aaa ttt gtg agc ctc atc ttt tcc atc       1105
Thr Leu Val Val Thr Leu Arg Lys Phe Val Ser Leu Ile Phe Ser Ile
270                 275                 280                 285

ttg tac ttc cag aac ccc ttc acc ctg tgg cac tgg ctg ggc acc ttg       1153
Leu Tyr Phe Gln Asn Pro Phe Thr Leu Trp His Trp Leu Gly Thr Leu
                290                 295                 300

ttt gtc ttc att ggg acc tta atg tac aca gag gtg tgg aac aac cta       1201
Phe Val Phe Ile Gly Thr Leu Met Tyr Thr Glu Val Trp Asn Asn Leu
            305                 310                 315

ggg acc aca aaa agt gag cct cag aag gac agc aag aag aac tga ggc       1249
Gly Thr Thr Lys Ser Glu Pro Gln Lys Asp Ser Lys Lys Asn  *
        320                 325                 330

ctgtgctgga gtacgtagac cagtgtcgtc gtgagggtg                            1288


    <210> 185
    <211> 3956
    <212> DNA
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<213> Homo sapiens

<220>
<221> CDS
<222> (837)..(3743)

<400> 185
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tcggattgcc catgcacttg ttgcagaaac agccaaggcc ctggctgtgg agaatgctga     120

aggaagaaga cgcagaagca ggacgaccct gaaagattca gcctcttcat cctcaaacag     180

gtcgcttctc gggagttctt ggtgttggaa tattttacag caaagcagtc gaccaggcct     240

cctcttccca cctgtccagc agcatgaaag cagcatgatt ggccgaccgc aggagaagcc     300

cccagaacca ggcccccaac tcagccatct gcggaggtca aggtgtgagc gacgtctcct     360

caccacagtg ctgtgtggtc tatacctcag ccagggagag gatgtgaaac cccccgccct     420

gcacatgagt ggtacaggcc aacaggaaca cctggctcca gccacgttca cagacatgtc     480

agccgtggag tagtgctgac acttttctct cagcttctca gggtttcagt ccttttgggt     540

ttggtttatt tacctttttt atggttttgt ggctggacgt tcacaaccaa ggcagacagc     600

atgggtgacc agcaactgta caagaccaac catgtggccc atggtagtga gaacctttc      660

taccaacagc caccacttgg cgtccacagc gggctgagcc cactgatggc taccaataca     720

cctactccca ggccagcgag atccggaccc agaagcttac cagcggtgtc ttacacaagc     780

tggactcttt cacccaggtg tttgccaacc aaaacctgcg aattcaggtc aacaat         836
atg gcc cag gtg ctg cac act cag tca gca gtg atg gat gga gcc cct       884
Met Ala Gln Val Leu His Thr Gln Ser Ala Val Met Asp Gly Ala Pro
1               5                   10                  15

gac agt gct ctc cgc cag ctg ctg tct cag aag ccc atg gag ccc cca       932
Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
            20                  25                  30

gca ccg gct atc cct tcc cgc tac cag cag gtg ccc cag cag cct cac       980
Ala Pro Ala Ile Pro Ser Arg Tyr Gln Gln Val Pro Gln Gln Pro His
        35                  40                  45

cct ggt ttc act ggt ggg ctg tcc aaa cca gct ctt cag gtc ggg cag      1028
Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
    50                  55                  60

cac cct acc caa ggg cac ctg tat tat gac tac cag cag cct ctg gct      1076
His Pro Thr Gln Gly His Leu Tyr Tyr Asp Tyr Gln Gln Pro Leu Ala
65                  70                  75                  80

cag gtg cca gtg cag gga gga cag cca ctg cag gcc cca cag atg ctg      1124
Gln Val Pro Val Gln Gly Gly Gln Pro Leu Gln Ala Pro Gln Met Leu
                85                  90                  95
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tca cag cac atg caa cag atg cag cag cac cag tat tac cca ccg cag      1172
Ser Gln His Met Gln Gln Met Gln Gln His Gln Tyr Tyr Pro Pro Gln
            100                 105                 110

caa cag cag caa gcc ggg caa cag cgt atc tcc atg caa gaa ata cag      1220
Gln Gln Gln Gln Ala Gly Gln Gln Arg Ile Ser Met Gln Glu Ile Gln
        115                 120                 125

acg cag ccg caa caa att cgc cca tca cag cca cag ccg ccg cca cag      1268
Thr Gln Pro Gln Gln Ile Arg Pro Ser Gln Pro Gln Pro Pro Pro Gln
    130                 135                 140

cag cag cag ccg cag cag cta cag ctg cag cag cgg cag ggt tca atg      1316
Gln Gln Gln Pro Gln Gln Leu Gln Leu Gln Gln Arg Gln Gly Ser Met
145                 150                 155                 160

cag ata cct cag tat tat cag ccc caa ccc atg atg cag cac ttg caa      1364
Gln Ile Pro Gln Tyr Tyr Gln Pro Gln Pro Met Met Gln His Leu Gln
                165                 170                 175

gag cag cag cag caa cag atg cac ctg cag cct cct tct tat cac agg      1412
Glu Gln Gln Gln Gln Gln Met His Leu Gln Pro Pro Ser Tyr His Arg
            180                 185                 190

gac cct cac cag tat acc cca gag cag gca cac act gtc cag ctg att      1460
Asp Pro His Gln Tyr Thr Pro Glu Gln Ala His Thr Val Gln Leu Ile
        195                 200                 205

ccc ctg ggc tcc atg tcc cag tac tac tac cag gag ccc cag cag ccc      1508
Pro Leu Gly Ser Met Ser Gln Tyr Tyr Tyr Gln Glu Pro Gln Gln Pro
    210                 215                 220

tac agc cac ccc ctc tac cag cag agc cac ctg tcc cag cac cag cag      1556
Tyr Ser His Pro Leu Tyr Gln Gln Ser His Leu Ser Gln His Gln Gln
225                 230                 235                 240

cgt gag gac agt cag ctg aag acc tac tct agt gac aga cag gcc cag      1604
Arg Glu Asp Ser Gln Leu Lys Thr Tyr Ser Ser Asp Arg Gln Ala Gln
                245                 250                 255

gcc atg ctg agc tcc cat ggg gac ctg ggg cct cct gac aca gga atg      1652
Ala Met Leu Ser Ser His Gly Asp Leu Gly Pro Pro Asp Thr Gly Met
            260                 265                 270

gga gac cca gcg agc tca gat ctg acc cgg gtc agc agc acc ctc ccc      1700
Gly Asp Pro Ala Ser Ser Asp Leu Thr Arg Val Ser Ser Thr Leu Pro
        275                 280                 285

cat cgc ccc ctc cta tcc ccc agt ggg atc cac ctc aac aac atg ggg      1748
His Arg Pro Leu Leu Ser Pro Ser Gly Ile His Leu Asn Asn Met Gly
    290                 295                 300

cct cag cat cag cag ctg tct ccc agt gcc atg tgg ccc cag atg cac      1796
Pro Gln His Gln Gln Leu Ser Pro Ser Ala Met Trp Pro Gln Met His
305                 310                 315                 320
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cta cct gat ggg aga gcc cag cca ggg tcc cct gag tca agt ggc caa      1844
Leu Pro Asp Gly Arg Ala Gln Pro Gly Ser Pro Glu Ser Ser Gly Gln
                325                 330                 335

ccc aaa gga gcg ttt ggg gag cag ttt gat gcc aag aac aag ctg aca      1892
Pro Lys Gly Ala Phe Gly Glu Gln Phe Asp Ala Lys Asn Lys Leu Thr
        340                 345                 350

tgc tcc atc tgc ctg aag gag ttc aag aac ctg cct gcc ctg aat ggc      1940
Cys Ser Ile Cys Leu Lys Glu Phe Lys Asn Leu Pro Ala Leu Asn Gly
    355                 360                 365

cac atg cgg tcc cac ggg gga atg agg gcc tcc ccc aac ctc aaa cag      1988
His Met Arg Ser His Gly Gly Met Arg Ala Ser Pro Asn Leu Lys Gln
370                 375                 380

gaa atc ccc agg aag cat cag ccg agt gtg ccc aaa gcc gag gag ccc      2036
Glu Ile Pro Arg Lys His Gln Pro Ser Val Pro Lys Ala Glu Glu Pro
385                 390                 395                 400

ctc aag acc gtg cag gag aag aaa aag ttc cgg cac cgg tcg gaa cct      2084
Leu Lys Thr Val Gln Glu Lys Lys Lys Phe Arg His Arg Ser Glu Pro
                405                 410                 415

ctc ttc atc ccg ccg ccg ccc tcc tac aac ccg aac ccc gct gcc tcc      2132
Leu Phe Ile Pro Pro Pro Pro Ser Tyr Asn Pro Asn Pro Ala Ala Ser
            420                 425                 430

tac tcg ggc gcc acc ctg tac cag agc cag ctg cgc tcc ccg cgc gtc      2180
Tyr Ser Gly Ala Thr Leu Tyr Gln Ser Gln Leu Arg Ser Pro Arg Val
        435                 440                 445

ctc ggg gac cac ctg ctc ctg gac ccc acc cac gag ctg ccc cct tac      2228
Leu Gly Asp His Leu Leu Leu Asp Pro Thr His Glu Leu Pro Pro Tyr
    450                 455                 460

acg ccc cca ccc atg ctg agc ccg gtg cgc cag ggc tcg ggg ctc ttc      2276
Thr Pro Pro Pro Met Leu Ser Pro Val Arg Gln Gly Ser Gly Leu Phe
465                 470                 475                 480

agc aat gtc ctc atc tcc ggc cac ggc cct ggc gcc cac ccg cag ctg      2324
Ser Asn Val Leu Ile Ser Gly His Gly Pro Gly Ala His Pro Gln Leu
                485                 490                 495

ccc ctg acg ccc ctg acg ccc aca cca cgg gtg ctg ctg tgt cgc tcc      2372
Pro Leu Thr Pro Leu Thr Pro Thr Pro Arg Val Leu Leu Cys Arg Ser
            500                 505                 510

aac agc atc gat ggc agc aac gtg acg gtc acc cca ggg cct gga gag      2420
Asn Ser Ile Asp Gly Ser Asn Val Thr Val Thr Pro Gly Pro Gly Glu
        515                 520                 525

cag act gta gat gtt gaa cca cgc atc aac att ggc ttg aga ttc caa      2468
Gln Thr Val Asp Val Glu Pro Arg Ile Asn Ile Gly Leu Arg Phe Gln
    530                 535                 540

gca gaa atc cct gaa ctc caa gat atc tct gcc ctg gcc cag gac aca      2516
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Ala Glu Ile Pro Glu Leu Gln Asp Ile Ser Ala Leu Ala Gln Asp Thr
545                 550                 555                 560

cac aag gcc aca ctg gta tgg aag ccc tgg cca gaa cta gaa aac cat      2564
His Lys Ala Thr Leu Val Trp Lys Pro Trp Pro Glu Leu Glu Asn His
                565                 570                 575

gac ctc cag caa aga gtg gag aat ctt ctg aat ttg tgc tgt tcc agt      2612
Asp Leu Gln Gln Arg Val Glu Asn Leu Leu Asn Leu Cys Cys Ser Ser
            580                 585                 590

gca ttg cca ggt gga ggg acc aat tct gaa ttt gct ttg cac tct ctg      2660
Ala Leu Pro Gly Gly Gly Thr Asn Ser Glu Phe Ala Leu His Ser Leu
        595                 600                 605

ttt gag gcc aaa ggt gat gtg atg gtt gct ctg gaa atg ctg cta ctg      2708
Phe Glu Ala Lys Gly Asp Val Met Val Ala Leu Glu Met Leu Leu Leu
    610                 615                 620

cgg aag cct gtc agg tta aaa tgt cat cct tta gca aat tac cac tat      2756
Arg Lys Pro Val Arg Leu Lys Cys His Pro Leu Ala Asn Tyr His Tyr
625                 630                 635                 640

gcc ggt tcg gac aag tgg acc tcc cta gaa aga aaa ctg ttt aac aaa      2804
Ala Gly Ser Asp Lys Trp Thr Ser Leu Glu Arg Lys Leu Phe Asn Lys
                645                 650                 655

gca cta gcc act tac agc aaa gac ttt att ttt gta cag aag atg gtg      2852
Ala Leu Ala Thr Tyr Ser Lys Asp Phe Ile Phe Val Gln Lys Met Val
            660                 665                 670

aag tcc aag acg gtg gct cag tgc gtg gag tac tac tac acg tgg aaa      2900
Lys Ser Lys Thr Val Ala Gln Cys Val Glu Tyr Tyr Tyr Thr Trp Lys
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aag atc atg cgg ctg ggg cgg aaa cac cgg aca cgc ctg gca gaa atc      2948
Lys Ile Met Arg Leu Gly Arg Lys His Arg Thr Arg Leu Ala Glu Ile
    690                 695                 700

atc gac gat tgt gtg aca agt gaa gaa gaa gaa gag tta gag gag gag      2996
Ile Asp Asp Cys Val Thr Ser Glu Glu Glu Glu Glu Leu Glu Glu Glu
705                 710                 715                 720

gag gag gag gac ccg gaa gaa gat agg aaa tcc aca aaa gaa gaa gag      3044
Glu Glu Glu Asp Pro Glu Glu Asp Arg Lys Ser Thr Lys Glu Glu Glu
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agt gag gtg ccg aag tcc ccg gag cca cca ccc gtc ccc gtc ctg gct      3092
Ser Glu Val Pro Lys Ser Pro Glu Pro Pro Pro Val Pro Val Leu Ala
            740                 745                 750

ccc acg gag ggg ccg ccc ctg cag gcc ctg ggc cag ccc tca ggc tcc      3140
Pro Thr Glu Gly Pro Pro Leu Gln Ala Leu Gly Gln Pro Ser Gly Ser
        755                 760                 765

ttc atc tgt gaa atg ccc aac tgt ggg gct gac tgt aga tgt cat gtc      3188
Phe Ile Cys Glu Met Pro Asn Cys Gly Ala Asp Cys Arg Cys His Val
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act ccc ttt ctt ccc cag gtg ttc agc tcc cga cag gca ctg aat ggc     3236
Thr Pro Phe Leu Pro Gln Val Phe Ser Ser Arg Gln Ala Leu Asn Gly
785                 790                 795                 800

cat gcc cgc atc cac ggg ggc acc aac cag gtg acc aag gcc cga ggt     3284
His Ala Arg Ile His Gly Gly Thr Asn Gln Val Thr Lys Ala Arg Gly
                805                 810                 815

gcc atc ccc tct ggg aag cag aag cct ggt ggc acc cag agt ggg tac     3332
Ala Ile Pro Ser Gly Lys Gln Lys Pro Gly Gly Thr Gln Ser Gly Tyr
            820                 825                 830

tgt tcg gta aag agc tca ccc tct cac agc acc acc agc ggc gag aca     3380
Cys Ser Val Lys Ser Ser Pro Ser His Ser Thr Thr Ser Gly Glu Thr
        835                 840                 845

gac ccc acc acc atc ttc ccc tgc aag gag tgt ggc aaa gtc ttc ttc     3428
Asp Pro Thr Thr Ile Phe Pro Cys Lys Glu Cys Gly Lys Val Phe Phe
    850                 855                 860

aag atc aaa agc cga aat gca cac atg aaa act cac atg cag cag gag     3476
Lys Ile Lys Ser Arg Asn Ala His Met Lys Thr His Met Gln Gln Glu
865                 870                 875                 880

gaa caa cag agg caa aag gct cag aag gcg gct ttt gca gct gag atg     3524
Glu Gln Gln Arg Gln Lys Ala Gln Lys Ala Ala Phe Ala Ala Glu Met
                885                 890                 895

gca gcc acg att gag agg act acg ggg ccc gtg ggg gcg ccg ggg ctg     3572
Ala Ala Thr Ile Glu Arg Thr Thr Gly Pro Val Gly Ala Pro Gly Leu
            900                 905                 910

ctg ccc ctg gac cag ctg agt ctg atc aaa ccc atc aag gat gtg gac     3620
Leu Pro Leu Asp Gln Leu Ser Leu Ile Lys Pro Ile Lys Asp Val Asp
        915                 920                 925

atc ctc gac gac gac gtc gtc cag cag ttg gga ggt gtc atg gaa gag     3668
Ile Leu Asp Asp Asp Val Val Gln Gln Leu Gly Gly Val Met Glu Glu
    930                 935                 940

gct gaa gtt gtg gac acc gat ctt ctc ttg gat gat caa gat tca gtc     3716
Ala Glu Val Val Asp Thr Asp Leu Leu Leu Asp Asp Gln Asp Ser Val
945                 950                 955                 960

ttg ctt cag ggt gac gca gaa cta taa agccc tgtgtgtcac ttagagacag     3768
Leu Leu Gln Gly Asp Ala Glu Leu  *
                965

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aacccttttta aactacctgt tttaaaagtg gtcattttat tcaggtttag aaaaaaaaat  3888

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gtcgcttctc gggagttctt ggtgttggaa tattttacag caaagcagtc gaccaggcct     240

cctcttccca cctgtccagc agcatgaaag cagcatgatt ggccgaccgc aggagaagcc     300

cccagaacca ggcccccaac tcagccatct gcggaggtca aggtgtgagc gacgtctcct     360

caccacagtg ctgtgtggtc tatacctcag ccagggagag gatgtgaaac cccccgccct     420

gcacatgagt ggtacaggcc aacaggaaca cctggctcca gccacgttca cagacatgtc     480

agccgtggag tagtgctgac acttttctct cagcttctca gggtttcagt ccttttgggt     540

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atgggtgacc agcaactgta caagaccaac catgtggccc atggtagtga gaacctttc      660

taccaacagc caccacttgg cgtccacagc gggctgagcc cactgatggc taccaataca     720

cctactccca ggccagcgag atccggaccc agaagcttac cagcggtgtc ttacacaagc     780

tggactcttt cacccaggtg tttgccaacc aaaacctgcg aattcaggtc aacaat         836
atg gcc cag gtg ctg cac act cag tca gca gtg atg gat gga gcc cct       884
Met Ala Gln Val Leu His Thr Gln Ser Ala Val Met Asp Gly Ala Pro
1               5                   10                  15

gac agt gct ctc cgc cag ctg ctg tct cag aag ccc atg gag ccc cca       932
Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
            20                  25                  30

gca ccg gct atc cct tcc cgc tac cag cag gtg ccc cag cag cct cac       980
Ala Pro Ala Ile Pro Ser Arg Tyr Gln Gln Val Pro Gln Gln Pro His
        35                  40                  45

cct ggt ttc act ggt ggg ctg tcc aaa cca gct ctt cag gtc ggg cag      1028
Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
    50                  55                  60
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cac cct acc caa ggg cac ctg tat tat gac tac cag cag cct ctg gct      1076
His Pro Thr Gln Gly His Leu Tyr Tyr Asp Tyr Gln Gln Pro Leu Ala
 65                  70                  75                  80

cag gtg cca gtg cag gga gga cag cca ctg cag gcc cca cag atg ctg      1124
Gln Val Pro Val Gln Gly Gly Gln Pro Leu Gln Ala Pro Gln Met Leu
                 85                  90                  95

tca cag cac atg caa cag atg cag cag cac cag tat tac cca ccg cag      1172
Ser Gln His Met Gln Gln Met Gln Gln His Gln Tyr Tyr Pro Pro Gln
            100                 105                 110

caa cag cag caa gcc ggg caa cag cgt atc tcc atg caa gaa ata cag      1220
Gln Gln Gln Gln Ala Gly Gln Gln Arg Ile Ser Met Gln Glu Ile Gln
        115                 120                 125

acg cag ccg caa caa att cgc cca tca cag cca cag ccg ccg cca cag      1268
Thr Gln Pro Gln Gln Ile Arg Pro Ser Gln Pro Gln Pro Pro Pro Gln
    130                 135                 140

cag cag cag ccg cag cag cta cag ctg cag cag cgg cag ggt tca atg      1316
Gln Gln Gln Pro Gln Gln Leu Gln Leu Gln Gln Arg Gln Gly Ser Met
145                 150                 155                 160

cag ata cct cag tat tat cag ccc caa ccc atg atg cag cac ttg caa      1364
Gln Ile Pro Gln Tyr Tyr Gln Pro Gln Pro Met Met Gln His Leu Gln
                165                 170                 175

gag cag cag cag caa cag atg cac ctg cag cct cct tct tat cac agg      1412
Glu Gln Gln Gln Gln Gln Met His Leu Gln Pro Pro Ser Tyr His Arg
            180                 185                 190

gac cct cac cag tat acc cca gag cag gca cac act gtc cag ctg att      1460
Asp Pro His Gln Tyr Thr Pro Glu Gln Ala His Thr Val Gln Leu Ile
        195                 200                 205

ccc ctg ggc tcc atg tcc cag tac tac tac cag gag ccc cag cag ccc      1508
Pro Leu Gly Ser Met Ser Gln Tyr Tyr Tyr Gln Glu Pro Gln Gln Pro
    210                 215                 220

tac agc cac ccc ctt tac cag cag agc cac ctg tcc cag cac cag cag      1556
Tyr Ser His Pro Leu Tyr Gln Gln Ser His Leu Ser Gln His Gln Gln
225                 230                 235                 240

cgt gag gac agt cag ctg aag acc tac tct agt gac aga cag gcc cag      1604
Arg Glu Asp Ser Gln Leu Lys Thr Tyr Ser Ser Asp Arg Gln Ala Gln
                245                 250                 255

gcc atg ctg agc tcc cat ggg gac ctg ggg cct cct gac aca gga atg      1652
Ala Met Leu Ser Ser His Gly Asp Leu Gly Pro Pro Asp Thr Gly Met
            260                 265                 270

gga gac cca gcg agc tca gat ctg acc cgg gtc agc agc acc ctc ccc      1700
Gly Asp Pro Ala Ser Ser Asp Leu Thr Arg Val Ser Ser Thr Leu Pro
        275                 280                 285

cat cgc ccc ctc cta tcc ccc agt ggg atc cac ctc aac aac atg ggg      1748
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His Arg Pro Leu Leu Ser Pro Ser Gly Ile His Leu Asn Asn Met Gly
    290                 295                 300

cct cag cat cag cag ctg tct ccc agt gcc atg tgg ccc cag atg cac      1796
Pro Gln His Gln Gln Leu Ser Pro Ser Ala Met Trp Pro Gln Met His
305                 310                 315                 320

cta cct gat ggg aga gcc cag cca ggg tcc cct gag tca agt ggc caa      1844
Leu Pro Asp Gly Arg Ala Gln Pro Gly Ser Pro Glu Ser Ser Gly Gln
                325                 330                 335

ccc aaa gga gcg ttt ggg gag cag ttt gat gcc aag aac aag ctg aca      1892
Pro Lys Gly Ala Phe Gly Glu Gln Phe Asp Ala Lys Asn Lys Leu Thr
            340                 345                 350

tgc tcc atc tgc ctg aag gag ttc aag aac ctg cct gcc ctg aat ggc      1940
Cys Ser Ile Cys Leu Lys Glu Phe Lys Asn Leu Pro Ala Leu Asn Gly
        355                 360                 365

cac atg cgg tcc cac ggg gga atg agg gcc tcc ccc aac ctc aaa cag      1988
His Met Arg Ser His Gly Gly Met Arg Ala Ser Pro Asn Leu Lys Gln
    370                 375                 380

gaa atc ccc agg aag cat cag ccg agt gtg ccc aaa gcc gag gag ccc      2036
Glu Ile Pro Arg Lys His Gln Pro Ser Val Pro Lys Ala Glu Glu Pro
385                 390                 395                 400

ctc aag acc gtg cag gag aag aaa aag ttc cgg cac cgg tcg gaa cct      2084
Leu Lys Thr Val Gln Glu Lys Lys Lys Phe Arg His Arg Ser Glu Pro
                405                 410                 415

ctc ttc atc ccg ccg ccg ccc tcc tac aac ccg aac ccc gct gcc tcc      2132
Leu Phe Ile Pro Pro Pro Pro Ser Tyr Asn Pro Asn Pro Ala Ala Ser
            420                 425                 430

tac tcg ggc gcc acc ctg tac cag agc cag ctg cgc tcc ccg cgc gtc      2180
Tyr Ser Gly Ala Thr Leu Tyr Gln Ser Gln Leu Arg Ser Pro Arg Val
        435                 440                 445

ctc ggg gac cac ctg ctc ctg gac ccc acc cac gag ctg ccc cct tac      2228
Leu Gly Asp His Leu Leu Leu Asp Pro Thr His Glu Leu Pro Pro Tyr
    450                 455                 460

acg ccc cca ccc atg ctg agc ccg gtg cgc cag ggc tcg ggg ctc ttc      2276
Thr Pro Pro Pro Met Leu Ser Pro Val Arg Gln Gly Ser Gly Leu Phe
465                 470                 475                 480

agc aat gtc ctc atc tcc ggc cac ggc cct ggc gcc cac ccg cag ctg      2324
Ser Asn Val Leu Ile Ser Gly His Gly Pro Gly Ala His Pro Gln Leu
                485                 490                 495

ccc ctg acg ccc ctg acg ccc aca cca cgg gtg ctg ctg tgt cgc tcc      2372
Pro Leu Thr Pro Leu Thr Pro Thr Pro Arg Val Leu Leu Cys Arg Ser
            500                 505                 510

aac agc atc gat ggc agc aac gtg acg gtc acc cca ggg cct gga gag      2420
Asn Ser Ile Asp Gly Ser Asn Val Thr Val Thr Pro Gly Pro Gly Glu
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        515                 520                 525

cag act gta gat gtt gaa cca cgc atc aac att ggc ttg aga ttc caa      2468
Gln Thr Val Asp Val Glu Pro Arg Ile Asn Ile Gly Leu Arg Phe Gln
    530                 535                 540

gca gaa atc cct gaa ctc caa gat atc tct gcc ctg gcc cag gac aca      2516
Ala Glu Ile Pro Glu Leu Gln Asp Ile Ser Ala Leu Ala Gln Asp Thr
545                 550                 555                 560

cac aag gcc aca ctg gta tgg aag ccc tgg cca gaa cta gaa aac cat      2564
His Lys Ala Thr Leu Val Trp Lys Pro Trp Pro Glu Leu Glu Asn His
            565                 570                 575

gac ctc cag caa aga gtg gag aat ctt ctg aat ttg tgc tgt tcc agt      2612
Asp Leu Gln Gln Arg Val Glu Asn Leu Leu Asn Leu Cys Cys Ser Ser
        580                 585                 590

gca ttg cca ggt gga ggg acc aat tct gaa ttt gct ttg cac tct ctg      2660
Ala Leu Pro Gly Gly Gly Thr Asn Ser Glu Phe Ala Leu His Ser Leu
        595                 600                 605

ttt gag gcc aaa ggt gat gtg atg gtt gct ctg gaa atg ctg cta ctg      2708
Phe Glu Ala Lys Gly Asp Val Met Val Ala Leu Glu Met Leu Leu Leu
    610                 615                 620

cgg aag cct gtc agg tta aaa tgt cat cct tta gca aat tac cac tat      2756
Arg Lys Pro Val Arg Leu Lys Cys His Pro Leu Ala Asn Tyr His Tyr
625                 630                 635                 640

gcc ggt tcg gac aag tgg acc tcc cta gaa aga aaa ctg ttt aac aaa      2804
Ala Gly Ser Asp Lys Trp Thr Ser Leu Glu Arg Lys Leu Phe Asn Lys
            645                 650                 655

gca cta gcc act tac agc aaa gac ttt att ttt gta cag aag atg gtg      2852
Ala Leu Ala Thr Tyr Ser Lys Asp Phe Ile Phe Val Gln Lys Met Val
        660                 665                 670

aag tcc aag acg gtg gct cag tgc gtg gag tac tac tac acg tgg aaa      2900
Lys Ser Lys Thr Val Ala Gln Cys Val Glu Tyr Tyr Tyr Thr Trp Lys
        675                 680                 685

aag atc atg cgg ctg ggg cgg aaa cac cgg aca cgc ttg gca gaa atc      2948
Lys Ile Met Arg Leu Gly Arg Lys His Arg Thr Arg Leu Ala Glu Ile
    690                 695                 700

atc gac gat tgt gtg aca agt gaa gaa gaa gaa gag tta gag gag gag      2996
Ile Asp Asp Cys Val Thr Ser Glu Glu Glu Glu Glu Leu Glu Glu Glu
705                 710                 715                 720

gag gag gag gac ccg gaa gaa gat agg aaa tcc aca aaa gaa gaa gag      3044
Glu Glu Glu Asp Pro Glu Glu Asp Arg Lys Ser Thr Lys Glu Glu Glu
            725                 730                 735

agt gag gtg ccg aag tcc ccg gag cca cca ccc gtc ccc gtc ctg gct      3092
Ser Glu Val Pro Lys Ser Pro Glu Pro Pro Pro Val Pro Val Leu Ala
        740                 745                 750
```

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ccc acg gag ggg ccg ccc ctg cag gcc ctg ggc cag ccc tca ggc tcc      3140
Pro Thr Glu Gly Pro Pro Leu Gln Ala Leu Gly Gln Pro Ser Gly Ser
        755                 760                 765

ttc atc tgt gaa atg ccc aac tgt ggg gct gtg ttc agc tcc cga cag      3188
Phe Ile Cys Glu Met Pro Asn Cys Gly Ala Val Phe Ser Ser Arg Gln
    770                 775                 780

gca ctg aat ggc cat gcc cgc atc cac ggg ggc acc aac cag gtg acc      3236
Ala Leu Asn Gly His Ala Arg Ile His Gly Gly Thr Asn Gln Val Thr
785                 790                 795                 800

aag gcc cga ggt gcc atc ccc tct ggg aag cag aag cct ggt ggc acc      3284
Lys Ala Arg Gly Ala Ile Pro Ser Gly Lys Gln Lys Pro Gly Gly Thr
                805                 810                 815

cag agt ggg tac tgt tcg gta aag agc tca ccc tct cac agc acc acc      3332
Gln Ser Gly Tyr Cys Ser Val Lys Ser Ser Pro Ser His Ser Thr Thr
            820                 825                 830

agc ggc gag aca gac ccc acc acc atc ttc ccc tgc aag gag tgt ggc      3380
Ser Gly Glu Thr Asp Pro Thr Thr Ile Phe Pro Cys Lys Glu Cys Gly
        835                 840                 845

aaa gtc ttc ttc aag atc aaa agc cga aat gca cac atg aaa act cac      3428
Lys Val Phe Phe Lys Ile Lys Ser Arg Asn Ala His Met Lys Thr His
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agg cag cag gag gaa caa cag agg caa aag gct cag aag gcg gct ttt      3476
Arg Gln Gln Glu Glu Gln Gln Arg Gln Lys Ala Gln Lys Ala Ala Phe
865                 870                 875                 880

gca gct gag atg gca gcc acg att gag agg act acg ggg ccc gtg ggg      3524
Ala Ala Glu Met Ala Ala Thr Ile Glu Arg Thr Thr Gly Pro Val Gly
                885                 890                 895

gcg ccg ggg ctg ctg ccc ctg gac cag ctg agt ctg atc aaa ccc atc      3572
Ala Pro Gly Leu Leu Pro Leu Asp Gln Leu Ser Leu Ile Lys Pro Ile
            900                 905                 910

aag gat gtg gac atc ctc gac gac gac gtc gtc cag cag ttg gga ggt      3620
Lys Asp Val Asp Ile Leu Asp Asp Asp Val Val Gln Gln Leu Gly Gly
        915                 920                 925

gtc atg gaa gag gct gaa gtt gtg gac acc gat ctt ctc ttg gat gat      3668
Val Met Glu Glu Ala Glu Val Val Asp Thr Asp Leu Leu Leu Asp Asp
    930                 935                 940

caa gat tca gtc ttg ctt cag ggt gac gca gaa cta taa agccctgtgt       3717
Gln Asp Ser Val Leu Leu Gln Gly Asp Ala Glu Leu  *
945                 950                 955

gtcacttaga gacagtgaaa acccacggcc tccatcttca ttaatcagga aacctggact    3777

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ccttgcagca ctgctggacc aggttacaag atgttcacct aagattgaga cctagtgact    180

acatttccta cgggaacaaa taaatggttt ttcatctccc ggagatacat tacaaacaaa    240

tatggtgcta aaagaactcc ttacctttct ctgactacaa tttatttgga catacttttg    300

tattgaagag aggtatacat actgaagcta cttgctgtac tataggagac tctgtcctgt    360

aggatc   atg gac cat cct agt agg gaa aag gat gaa aga caa cgg aca    408
         Met Asp His Pro Ser Arg Glu Lys Asp Glu Arg Gln Arg Thr
           1               5                  10

act aaa ccc atg gca caa agg agt gca cac tgc tct cga cca tct ggc      456
Thr Lys Pro Met Ala Gln Arg Ser Ala His Cys Ser Arg Pro Ser Gly
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Ser Ser Ser Ser Ser Gly Val Leu Met Val Gly Pro Asn Phe Arg Val
                 35                  40                  45

ggc aag aag ata gga tgt ggg aac ttc gga gag ctc aga tta ggt gaa       552
Gly Lys Lys Ile Gly Cys Gly Asn Phe Gly Glu Leu Arg Leu Gly Glu
             50                  55                  60

ggt ctc cca cag gtg tat tac ttt gga cca tgt ggg aaa tat aat gcc       600
Gly Leu Pro Gln Val Tyr Tyr Phe Gly Pro Cys Gly Lys Tyr Asn Ala
         65                  70                  75

atg gtg ctg gag ctc ctt ggc cct agc ttg gag gac ttg ttt gac ctc       648
Met Val Leu Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asp Leu
     80                  85                  90

tgt gac cga aca ttt act ttg aag acg gtg tta atg ata gcc atc cag       696
Cys Asp Arg Thr Phe Thr Leu Lys Thr Val Leu Met Ile Ala Ile Gln
 95                 100                 105                 110

ctg ctt tct cga atg gaa tac gtg cac tca aag aac ctc att tac cga       744
Leu Leu Ser Arg Met Glu Tyr Val His Ser Lys Asn Leu Ile Tyr Arg
                115                 120                 125

gat gtc aag cca gag aac ttc ctg att ggt cga caa ggc aat aag aaa       792
Asp Val Lys Pro Glu Asn Phe Leu Ile Gly Arg Gln Gly Asn Lys Lys
            130                 135                 140

gag cat gtt ata cac att ata gac ttt gga ctg gcc aag gaa tac att       840
Glu His Val Ile His Ile Ile Asp Phe Gly Leu Ala Lys Glu Tyr Ile
        145                 150                 155

gac ccc gaa acc aaa aaa cac ata cct tat agg gaa cac aaa agt tta       888
Asp Pro Glu Thr Lys Lys His Ile Pro Tyr Arg Glu His Lys Ser Leu
    160                 165                 170

act gga act gca aga tat atg tct atc aac acg cat ctt ggc aaa gag       936
Thr Gly Thr Ala Arg Tyr Met Ser Ile Asn Thr His Leu Gly Lys Glu
175                 180                 185                 190

caa agc cgg aga gat gat ttg gaa gcc cta ggc cat atg ttc atg tat       984
Gln Ser Arg Arg Asp Asp Leu Glu Ala Leu Gly His Met Phe Met Tyr
                195                 200                 205

ttc ctt cga ggc agc ctc ccc tgg caa gga ctc aag gct gac aca tta      1032
Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Asp Thr Leu
            210                 215                 220

aaa gag aga tat caa aaa att ggt gac acc aaa agg aat act ccc att      1080
Lys Glu Arg Tyr Gln Lys Ile Gly Asp Thr Lys Arg Asn Thr Pro Ile
        225                 230                 235

gaa gct ctc tgt gag aac ttt cca gag gag atg gca acc tac ctt cga      1128
Glu Ala Leu Cys Glu Asn Phe Pro Glu Glu Met Ala Thr Tyr Leu Arg
    240                 245                 250
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tat gtc agg cga ctg gac ttc ttt gaa aaa cct gat tat gag tat tta      1176
Tyr Val Arg Arg Leu Asp Phe Phe Glu Lys Pro Asp Tyr Glu Tyr Leu
255                 260                 265                 270

cgg acc ctc ttc aca gac ctc ttt gaa aag aaa ggc tac acc ttt gac      1224
Arg Thr Leu Phe Thr Asp Leu Phe Glu Lys Lys Gly Tyr Thr Phe Asp
                275                 280                 285

tat gcc tat gat tgg gtt ggg aga cct att cct act cca gta ggg tca      1272
Tyr Ala Tyr Asp Trp Val Gly Arg Pro Ile Pro Thr Pro Val Gly Ser
            290                 295                 300

gtt cac gta gat tct ggt gca tct gca ata act cga gaa agc cac aca      1320
Val His Val Asp Ser Gly Ala Ser Ala Ile Thr Arg Glu Ser His Thr
        305                 310                 315

cat agg gat cgg cca tca caa cag cag cct ctt cga aat cag gtg gtt      1368
His Arg Asp Arg Pro Ser Gln Gln Gln Pro Leu Arg Asn Gln Val Val
    320                 325                 330

agc tca acc aat gga gag ctg aat gtt gat gat ccc acg gga gcc cac      1416
Ser Ser Thr Asn Gly Glu Leu Asn Val Asp Asp Pro Thr Gly Ala His
335                 340                 345                 350

tcc aat gca cca atc aca gct cat gcc gag gtg gag gta gtg gag gaa      1464
Ser Asn Ala Pro Ile Thr Ala His Ala Glu Val Glu Val Val Glu Glu
                355                 360                 365

gct aag tgc tgc tgt ttc ttt aag agg aaa agg aag aag act gct cag      1512
Ala Lys Cys Cys Cys Phe Phe Lys Arg Lys Arg Lys Lys Thr Ala Gln
            370                 375                 380

cgc cac aag tga cca gtgcctccca ggagtcctca ggccctgggg actctgactc      1567
Arg His Lys  *
        385

aattgtacct gcagctcctg ccatttctca ttggaaggga ctcctctttg ggggagggtg    1627

gatatccaaa ctaaaaagaa gaaaacagat gcccccagaa ggggccagtg cgggcagcca    1687

gggcctagtg ggtcattggc catctccgcc tgcctaaggc tctgagcagg tcccagagct    1747

gctgttcctc cactgcttgc ccatagggct gcctggttga ctctccttcc cattgtttac    1807

agtgaaggtg tcattcacaa aaactcaagg actgctattc tccttcttcc ccttagttta    1867

ctcctggttt ttaccccacc ctcaaccctc tccagcataa aacctagtga gctaaaggct    1927

ttgtctgcag aaggagatca agaggctggg ggtaaggcca agaaggtagg aggaaaatgg    1987

cagacctggg ctggagaaga accttctccg tatcccaggt gtgcctggca gtatggtttc    2047

ctcttcctct gtgcctgtgc agcattcatc ccagctggcc ttggggttca ggttccttct    2107

tccctccctc ctgtgaagtt acactgtagg acacaagctg tgagcaatct gcagtctact    2167
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gtccctgtgt gttggcgttc ttagcttttt tgacaaactc ttttctccag gtagtaggac   2227

aatgaaaatt gttttaagca aaggaaagaa aactgacttt gttgcacttt tagttttttt   2287

aaaaaaaaca aaaacaaaaa catgaaaaaa a                                  2318




      <210> 188
      <211> 1335
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (505)..(1119)

      <400> 188
cgacgatttc gtgcgccccc gagcgggccg ccggggcgct gcgagactgg agaagttggc     60

gaggaggcct ggagaaccca ggagtttcca agctgtgctg ccacccgagc tctggatcca    120

cctggctgtg gtggcctgtg gcaatcggct ggaggagacg ctggtcatgc tcaaatcagc    180

tgtgcttttt agccacagga agatccaatt ccacatcttc actgaagact ctctgaagcc    240

cgagtttgat aagcagttac gccatggcct gactcatata caaagaagtt tgagcacaga    300

atctacccca tcacattttc tgttggaaac cctcaggagt ggaagaaatt gttcaaaccc    360

tgtgctgccc agagactctt tcttccggtg attttaaagg atgtggactc acttctctac    420

gtggacaccg atgtcctctt tctgagacct gttgatgaca tctggaagct tctgaggctg    480

tttaattcca cccagcttgc agcc   atg gcc cct gag cac gaa atc ccc aag     531
                             Met Ala Pro Glu His Glu Ile Pro Lys
                              1               5

att ggc tgg tac agc cgc ttt gct agg cat cct ttc tat ggc tct gca      579
Ile Gly Trp Tyr Ser Arg Phe Ala Arg His Pro Phe Tyr Gly Ser Ala
 10                  15                  20                  25

gga gtt aat tca gga gtc atg tta atg aat tta act cgg ata aga agt      627
Gly Val Asn Ser Gly Val Met Leu Met Asn Leu Thr Arg Ile Arg Ser
                30                  35                  40

acc cag ttc aag aac agc atg att cca aca ggc ctg gct tgg gag gac      675
Thr Gln Phe Lys Asn Ser Met Ile Pro Thr Gly Leu Ala Trp Glu Asp
            45                  50                  55

atg ttg tac cct ctg tac cag aag tac aag aat gcc atc acg tgg gga      723
Met Leu Tyr Pro Leu Tyr Gln Lys Tyr Lys Asn Ala Ile Thr Trp Gly
        60                  65                  70

gac cag gat tta tta aat att att ttt tat ttc aac cca gag tgt ctc      771
Asp Gln Asp Leu Leu Asn Ile Ile Phe Tyr Phe Asn Pro Glu Cys Leu
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     75                  80                  85

tat gta ttc ccc tgc cag tgg aac tac cgt ccc gat cac tgc atg tac      819
Tyr Val Phe Pro Cys Gln Trp Asn Tyr Arg Pro Asp His Cys Met Tyr
 90                 95                 100                 105

gga agc aac tgc aga gag gct gag cat gaa ggt gtg tct gtt ctg cat      867
Gly Ser Asn Cys Arg Glu Ala Glu His Glu Gly Val Ser Val Leu His
                110                 115                 120

gga aac cga ggc gtc tac cat gac gat aag caa cca acg ttc aga gca      915
Gly Asn Arg Gly Val Tyr His Asp Asp Lys Gln Pro Thr Phe Arg Ala
            125                 130                 135

ctc tat gaa gca ata cgg gat ttt ccc ttt caa gac aat ctc ttt caa      963
Leu Tyr Glu Ala Ile Arg Asp Phe Pro Phe Gln Asp Asn Leu Phe Gln
        140                 145                 150

tcc atg tat tac ccc ctt cag ctg aag ttt ttg gag act gtg cac act     1011
Ser Met Tyr Tyr Pro Leu Gln Leu Lys Phe Leu Glu Thr Val His Thr
    155                 160                 165

tta tgt gga cga atc ccg caa gtt ttt ctg aag caa att gag aaa aca     1059
Leu Cys Gly Arg Ile Pro Gln Val Phe Leu Lys Gln Ile Glu Lys Thr
170                 175                 180                 185

atg aaa agg gct tat gag aaa cac gtc atc atc cat gtt ggc ccc aac     1107
Met Lys Arg Ala Tyr Glu Lys His Val Ile Ile His Val Gly Pro Asn
                190                 195                 200

cag atg cac tga ata ttttgtcttg ttgcaagtca attaggtgtc ttgtgaacaa     1162
Gln Met His  *
            205

ggaaatacta atctctaagc tgcctgggtc tttttgtgtg aatatttaat ggtgctccat   1222

gactgttgag ttttaaaaac ctcgttaaat tttgccaaat cagttgcccc caaaagggaa   1282

tatgcttttc cttatttttt tttctaaaat gctatttatc tctaaggaaa aaa           1335




     <210> 189
     <211> 1685
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (126)..(770)

     <400> 189
gcacgagcgc aggcagggct ctggggcacc tagagaccgg ggccggagac gtggcagccg     60

ccctgcccgc cagaaagttt cctagaagtt tgctgggcgc gggcgcacga ctgactggct    120
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ggacc    atg aac gtg ttc cga atc ctc ggc gac ctg agc cac ctc ctg      167
         Met Asn Val Phe Arg Ile Leu Gly Asp Leu Ser His Leu Leu
          1               5                  10

gcc atg atc ttg ctg ctg ggg aag atc tgg agg tcc aag tgc tgc aag       215
Ala Met Ile Leu Leu Leu Gly Lys Ile Trp Arg Ser Lys Cys Cys Lys
 15                  20                  25                  30

ggc atc tct ggg aag agc cag atc ctg ttt gct ctc gtc ttc acc acc       263
Gly Ile Ser Gly Lys Ser Gln Ile Leu Phe Ala Leu Val Phe Thr Thr
                 35                  40                  45

agg tac ctg gac ctg ttc acc aac ttc atc tcc atc tac aac aca gta       311
Arg Tyr Leu Asp Leu Phe Thr Asn Phe Ile Ser Ile Tyr Asn Thr Val
             50                  55                  60

atg aag gtg gtt ttt ctc ctc tgt gcc tat gtt aca gtg tac atg ata       359
Met Lys Val Val Phe Leu Leu Cys Ala Tyr Val Thr Val Tyr Met Ile
         65                  70                  75

tat ggg aaa ttc cgt aaa act ttt gac agt gag aat gac aca ttc cgc       407
Tyr Gly Lys Phe Arg Lys Thr Phe Asp Ser Glu Asn Asp Thr Phe Arg
     80                  85                  90

ctg gag ttt ctt ctg gtc cca gtc att ggc ctt tcc ttc ctt gaa aac       455
Leu Glu Phe Leu Leu Val Pro Val Ile Gly Leu Ser Phe Leu Glu Asn
 95                 100                 105                 110

tac agt ttc act ctg ctg gag atc ctc tgg act ttc tct atc tat ctg       503
Tyr Ser Phe Thr Leu Leu Glu Ile Leu Trp Thr Phe Ser Ile Tyr Leu
                115                 120                 125

gaa tca gtg gct atc ctg ccc cag ctc ttc atg atc agc aag act gga       551
Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys Thr Gly
            130                 135                 140

gag gct gag acc ata act act cac tac ctg ttc ttt ctg ggt ctg tac       599
Glu Ala Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly Leu Tyr
        145                 150                 155

cgg gca ctc tac ctg gct aac tgg atc agg cgg tac cag act gag aat       647
Arg Ala Leu Tyr Leu Ala Asn Trp Ile Arg Arg Tyr Gln Thr Glu Asn
    160                 165                 170

ttc tat gac caa att gca gtc gtg tct gga gta gta caa acc atc ttc       695
Phe Tyr Asp Gln Ile Ala Val Val Ser Gly Val Val Gln Thr Ile Phe
175                 180                 185                 190

tac tgt gac ttc ttc tac ttg tat gtg acc aaa gtc ctt aag gga aag       743
Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys Gly Lys
                195                 200                 205

aag tta agt ctt cca atg cca atc tga ggacc ttcagagaca gtctacgcct       795
Lys Leu Ser Leu Pro Met Pro Ile  *
            210                 215

taacaagcac atgaaggaaa ctattctgaa tgttctcttt ggcaacttat ccataatttg     855
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ggatcaaatg ttaaaaccag aaaagtgttt agtgtggatt tcagcaaaac ctgatcatcc     915

cacccagaag accttctcat caatagatcg cccttaaaga cccattgtaa ggtcataaaa     975

aacctcggcc aactgcacaa agatggtgcc tcactgcaac aagaaacctt aaggtgtctt    1035

accgacgaaa taaaaaacat aaatgattgt tctccaaggc ctgagggcaa gactcatgat    1095

gagcaagtca accccaatct ggaacaatgt ccctcctctt agaatgtccc aactaaagac    1155

cagttaaaat attagggtac gttcttgtga atttccactt tccaggtaga tgaccaaatt    1215

taggtggtca agatataaag gtgtcagcta gttttaagtg tgaaacttat ttcactttca    1275

cactgccttc aggccagaag caaaccaaat ttaccaggtt tggctggagg agttttgtga    1335

ctcatctttt actggtttga attttttcaa accagtggct gatacctgcc ttgtacttag    1395

taccttaata ccaataacct aatggtactt aggcgagtac catttgcaca atcactgttt    1455

tacttatgag cagatacaga tatatccaaa cccttaccta ctaggtatcc tgctagggtt    1515

ttcaattcca attcttgtat taagtttttt cctttcagtt ttaggtgcga aagtaatcag    1575

tcaatccaat atcccccatc tttgtcttga aacaaaaact gttttaagac gtctacgttg    1635

aattattcag agaattaagc aataaaagct cacaccttat tgtcaaaaaa               1685



      <210> 190
      <211> 716
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (151)..(636)

      <400> 190
atttggccct cgaggccaag aattcggcac gaggcaggca gggctctggg gcacctagag      60

accggggccg gagacgtggc agccgccctg cccgccagaa agtttcctag aagtttgctg     120

ggcgcgggcg cacgactgac tggctggacc    atg aac gtg ttc cga atc ctc       171
                                    Met Asn Val Phe Arg Ile Leu
                                    1               5

ggc gac ctg agc cac ctc ctg gcc atg atc ttg ctg ctg ggg aag atc       219
Gly Asp Leu Ser His Leu Leu Ala Met Ile Leu Leu Leu Gly Lys Ile
        10                  15                  20

tgg agg tcc aag tgc tgc aag ggc atc tct ggg aag agc cag atc ctg       267
Trp Arg Ser Lys Cys Cys Lys Gly Ile Ser Gly Lys Ser Gln Ile Leu
    25                  30                  35
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ttt gct ctc gtc ttc acc acc agg tac ctg gac ctg ttc acc aac ttc      315
Phe Ala Leu Val Phe Thr Thr Arg Tyr Leu Asp Leu Phe Thr Asn Phe
 40                 45                  50                  55

atc tcc atc tac aac aca gta atg aag atc ctc tgg act ttc tct atc      363
Ile Ser Ile Tyr Asn Thr Val Met Lys Ile Leu Trp Thr Phe Ser Ile
                60                  65                  70

tat ctg gaa tca gtg gct atc ctg ccc cag ctc ttc atg atc agc aag      411
Tyr Leu Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys
            75                  80                  85

act gga gag gct gag acc ata act act cac tac ctg ttc ttt ctg ggt      459
Thr Gly Glu Ala Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly
        90                  95                 100

ctg tac cgg gca ctc tac ctg gct aac tgg atc aag cgg tac cag act      507
Leu Tyr Arg Ala Leu Tyr Leu Ala Asn Trp Ile Lys Arg Tyr Gln Thr
    105                 110                 115

gag aat ttc tat gac caa att gca gtc ggg tct gga gta gta caa acc      555
Glu Asn Phe Tyr Asp Gln Ile Ala Val Gly Ser Gly Val Val Gln Thr
120                 125                 130                 135

atc ttc tac tgt gac ttc ttc tac ttg tat gtg acc aaa gtc ctt aag      603
Ile Phe Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys
                140                 145                 150

gga aag aag tta agt ctt cca atg cca atc tga ggaccttc agagacagtc      654
Gly Lys Lys Leu Ser Leu Pro Met Pro Ile  *
            155                 160

tacgccttaa caagcacatg aaggaaacta ttttgaatgt tctctttggc aacttatcca    714

ta                                                                   716


     <210> 191
     <211> 948
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (380)..(706)

     <400> 191
tgagatggag tctcactctg tcgctcaggc tggagtgcag tgggaagatc tcagcttact     60

gtaacctcca cctcccgggt tcaagcgact ctcgtgcctc agcctcctga gtagctggga    120

ttacaggcac ctgccaccat gcccagctaa tttttatatt tttaagagat gggggttcac    180

catgttggcc aggctggtct caaactcctg acctcaggcg atccgcccac cttggcctcc    240
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caaagtgctg gttttgcaga tgggagccac catgcccagc ctagtctcac tttataggct    300

cccaaaccac agcagaacac ctggctgcct catccctctg cacccatcac gccagtgggc    360

atgctggctg taggtgggg atg gcc ttt gcc cgg gtt cct ggg agc acc tgg     412
                     Met Ala Phe Ala Arg Val Pro Gly Ser Thr Trp
                      1               5                  10

tgt ttt atg gtc acc tac cca ctt aca cct gac cct ggg gcc tct gca      460
Cys Phe Met Val Thr Tyr Pro Leu Thr Pro Asp Pro Gly Ala Ser Ala
            15                  20                  25

gtt ttc ttg gcg ttg tca cca caa aag gaa gaa gcc cac ctg tgg ctg      508
Val Phe Leu Ala Leu Ser Pro Gln Lys Glu Glu Ala His Leu Trp Leu
        30                  35                  40

gct ggc tgg ccg cca ggt cag agc caa ggc agg cag ggc ctt cct gtc      556
Ala Gly Trp Pro Pro Gly Gln Ser Gln Gly Arg Gln Gly Leu Pro Val
    45                  50                  55

tgg ctt ctt gaa ggc aga cac aag tct gca ggc tgc tca cgt cat ctc      604
Trp Leu Leu Glu Gly Arg His Lys Ser Ala Gly Cys Ser Arg His Leu
60                  65                  70                  75

att atc ttt tct cac gag gac tac ttc gga tac aat cac agc aac cct      652
Ile Ile Phe Ser His Glu Asp Tyr Phe Gly Tyr Asn His Ser Asn Pro
                80                  85                  90

ggc ctt ggc cct gcc ctg tcc ctg cca tgc aac ttc aca act cag ctg      700
Gly Leu Gly Pro Ala Leu Ser Leu Pro Cys Asn Phe Thr Thr Gln Leu
            95                 100                 105

gcc tag acccctggga ggcctccaag tccctaaggt tagacatctc ctggggtgct        756
Ala  *


atggactgtc ggggctccaa ggagccgagt gtgggggaaa ctcactgtgg gaggcgctcc    816

tgacctgcag ggagctggaa tgctgtggga gggccctgac cccggggccc atggagctcc    876

ctaggctcct ctggccacac ggacgcgtgg gtcgacccgg gaattccggg ccggtaccga    936

aggcgatcaa gg                                                         948



     <210> 192
     <211> 1152
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (47)..(943)
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     <400> 192
agaacaagca cagcccaagc cagatgtaca gcacacacag catccc   atg gtg gcc        55
                                                      Met Val Ala
                                                       1

aaa gac agg cag ctt cct acc tta atg gca cag ccc ccg caa act gta        103
Lys Asp Arg Gln Leu Pro Thr Leu Met Ala Gln Pro Pro Gln Thr Val
    5                   10                  15

gta cag gtg ctt gca gtg aaa acc acg cag cag ctc cct aaa ctg cag        151
Val Gln Val Leu Ala Val Lys Thr Thr Gln Gln Leu Pro Lys Leu Gln
 20                  25                  30                  35

cag gct ccg aac caa cca aaa atc tac gtg caa ccc caa acc ccc cag        199
Gln Ala Pro Asn Gln Pro Lys Ile Tyr Val Gln Pro Gln Thr Pro Gln
                 40                  45                  50

agc caa atg tcg ctc cca gct tct tca gag aaa cag acg gca agc cag        247
Ser Gln Met Ser Leu Pro Ala Ser Ser Glu Lys Gln Thr Ala Ser Gln
             55                  60                  65

gtg gag cag cca att ata acc caa gga tcc tct gtt aca aag ata act        295
Val Glu Gln Pro Ile Ile Thr Gln Gly Ser Ser Val Thr Lys Ile Thr
         70                  75                  80

ttt gag ggg cgc cag cct ccc aca gtt aca aag ata act ggt ggc agt        343
Phe Glu Gly Arg Gln Pro Pro Thr Val Thr Lys Ile Thr Gly Gly Ser
     85                  90                  95

tct gtg cct aag ctg aca tca cca gtt aca agc ata tct ccc att cag        391
Ser Val Pro Lys Leu Thr Ser Pro Val Thr Ser Ile Ser Pro Ile Gln
100                 105                 110                 115

gcc tct gag aag aca gca gtg tct gac att ttg aaa atg tct ttg atg        439
Ala Ser Glu Lys Thr Ala Val Ser Asp Ile Leu Lys Met Ser Leu Met
                120                 125                 130

gaa gct cag att gat aca aat gta gaa cat atg ata gtg gat ccc cca        487
Glu Ala Gln Ile Asp Thr Asn Val Glu His Met Ile Val Asp Pro Pro
            135                 140                 145

aag aag gct ctt gcc act agc atg ctc act ggt gaa gca gga tca tta        535
Lys Lys Ala Leu Ala Thr Ser Met Leu Thr Gly Glu Ala Gly Ser Leu
        150                 155                 160

ccc tcc acc cac atg gtg gtg gca ggg atg gcg aat tcc act ccc cag        583
Pro Ser Thr His Met Val Val Ala Gly Met Ala Asn Ser Thr Pro Gln
    165                 170                 175

caa cag aaa tgt aga gag tcc tgt tcg agt cca tcc act gtt ggc tct        631
Gln Gln Lys Cys Arg Glu Ser Cys Ser Ser Pro Ser Thr Val Gly Ser
180                 185                 190                 195

tcc cta acg aca agg aaa att gat cca cca gca gtg cct gcg aca ggc        679
Ser Leu Thr Thr Arg Lys Ile Asp Pro Pro Ala Val Pro Ala Thr Gly
                200                 205                 210
```

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cag ttc atg cgt att cag aat gta ggc caa aag aaa gct gaa gag agt       727
Gln Phe Met Arg Ile Gln Asn Val Gly Gln Lys Lys Ala Glu Glu Ser
            215                 220                 225

cca gca gaa att atc atc cag gct att cct cag tat gct att cct tgt       775
Pro Ala Glu Ile Ile Ile Gln Ala Ile Pro Gln Tyr Ala Ile Pro Cys
        230                 235                 240

cac tcc agc tcc aat gtg gtg gtg gag ccc agt ggg ctt ctt gag cta       823
His Ser Ser Ser Asn Val Val Val Glu Pro Ser Gly Leu Leu Glu Leu
    245                 250                 255

aac aac ttc act agt caa cag ctg gat gat gag gag aca gca atg gag       871
Asn Asn Phe Thr Ser Gln Gln Leu Asp Asp Glu Glu Thr Ala Met Glu
260                 265                 270                 275

cag gac ata gac agt agc acg gag gat gga act gaa ccc agc cct tct       919
Gln Asp Ile Asp Ser Ser Thr Glu Asp Gly Thr Glu Pro Ser Pro Ser
                280                 285                 290

cag agc tct gct gaa cgg tcc tag tgtttggaca caatagtgca ctttaaaacc      973
Gln Ser Ser Ala Glu Arg Ser  *
            295

tgcttggtta ccaagtgtcc agggaaaccc ttgtattttg atgactaaaa agagcacttt    1033

gcccgtactt aggctgtgga ccctaaaaca gcagtgtttc aacaagatgt tgctgcagga    1093

gcagcttttt aaaacaagat aaaactcaca ggggaatgta cttttttaaa aaaaaaaaa     1152



    <210> 193
    <211> 2582
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (195)..(1436)

    <400> 193
ctcgtgagac gtgggacttc tcgcgggaac tgcattcaaa tatcccaggc gcttactcga      60

gagctagctg agcgaatggg ccggcgactg tggagttagc gtcctcaatg tggacgccct     120

gagctcccat taggagccgc tggctgcggc agcaggggac tagcgtgaga gttggctaaa     180

aaaaagaaaa gaac  atg gag gca gat ata atc aca aat ctt cga tgc agg      230
                 Met Glu Ala Asp Ile Ile Thr Asn Leu Arg Cys Arg
                   1               5                  10

ctc aaa gag gct gaa gaa gag cga cta aaa gct gca cag tat ggt tta       278
Leu Lys Glu Ala Glu Glu Glu Arg Leu Lys Ala Ala Gln Tyr Gly Leu
         15                  20                  25
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```
caa cta gta gag agt caa aat gaa tta cag aat caa ttg gat aaa tgt       326
Gln Leu Val Glu Ser Gln Asn Glu Leu Gln Asn Gln Leu Asp Lys Cys
     30                  35                  40

cgt aat gaa atg atg acc atg act gag agt tat gaa caa gaa aaa tat       374
Arg Asn Glu Met Met Thr Met Thr Glu Ser Tyr Glu Gln Glu Lys Tyr
 45                  50                  55                  60

acc ctt caa aga gaa gtt gaa ctc aag agt cga atg tta gaa agt ttg       422
Thr Leu Gln Arg Glu Val Glu Leu Lys Ser Arg Met Leu Glu Ser Leu
                 65                  70                  75

agc tgc gaa tgt gaa gct att aaa caa caa caa aaa atg cac ctg gag       470
Ser Cys Glu Cys Glu Ala Ile Lys Gln Gln Gln Lys Met His Leu Glu
             80                  85                  90

aaa ttg gaa gaa caa cta agc aga agc cat gga cag gaa gtg aat gaa       518
Lys Leu Glu Glu Gln Leu Ser Arg Ser His Gly Gln Glu Val Asn Glu
         95                 100                 105

cta aaa act aag ata gaa aaa ctg aaa gtg gaa tta gat gaa gcc agg       566
Leu Lys Thr Lys Ile Glu Lys Leu Lys Val Glu Leu Asp Glu Ala Arg
    110                 115                 120

ctt agt gaa aag cag ctg aag cac caa gta gat cat cag aag gaa ctc       614
Leu Ser Glu Lys Gln Leu Lys His Gln Val Asp His Gln Lys Glu Leu
125                 130                 135                 140

ctc tct tgt aaa tca gag gaa ctg cgc gta atg tct gaa cgt gtg cag       662
Leu Ser Cys Lys Ser Glu Glu Leu Arg Val Met Ser Glu Arg Val Gln
                145                 150                 155

gaa agc atg tct tca gag atg ctg gct ctt caa att gag ctg aca gaa       710
Glu Ser Met Ser Ser Glu Met Leu Ala Leu Gln Ile Glu Leu Thr Glu
            160                 165                 170

atg gag agt atg aag acc acc ctc aaa gaa gaa gtg aat gaa cta caa       758
Met Glu Ser Met Lys Thr Thr Leu Lys Glu Glu Val Asn Glu Leu Gln
        175                 180                 185

tac aga caa gaa cag cta gaa ctt ctt att act aac cta atg cgc cag       806
Tyr Arg Gln Glu Gln Leu Glu Leu Leu Ile Thr Asn Leu Met Arg Gln
    190                 195                 200

gta gac cgg ctt aaa gag gaa aaa gaa gag cga gag aaa gaa gca gtt       854
Val Asp Arg Leu Lys Glu Glu Lys Glu Glu Arg Glu Lys Glu Ala Val
205                 210                 215                 220

tct tac tat aat gcc cta gag aaa gct cgt gta gca aat caa gat ctt       902
Ser Tyr Tyr Asn Ala Leu Glu Lys Ala Arg Val Ala Asn Gln Asp Leu
                225                 230                 235

cag gta cag ttg gac cag gca ctc cag caa gcc ttg gat ccc aat agt       950
Gln Val Gln Leu Asp Gln Ala Leu Gln Gln Ala Leu Asp Pro Asn Ser
            240                 245                 250

aaa ggc aac tct ttg ttt gca gag gtg gaa gat cga agg gca gca atg       998
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Lys Gly Asn Ser Leu Phe Ala Glu Val Glu Asp Arg Arg Ala Ala Met
        255                 260                 265

gaa cgt cag ctt atc agt atg aaa gtc aag tat cag tca cta aag aag      1046
Glu Arg Gln Leu Ile Ser Met Lys Val Lys Tyr Gln Ser Leu Lys Lys
    270                 275                 280

caa aat gta ttt aac aga gaa cag atg cag aga atg aag tta caa att      1094
Gln Asn Val Phe Asn Arg Glu Gln Met Gln Arg Met Lys Leu Gln Ile
285                 290                 295                 300

gcc acg ttg cta cag atg aaa ggg tct caa act gaa ttt gag cag cag      1142
Ala Thr Leu Leu Gln Met Lys Gly Ser Gln Thr Glu Phe Glu Gln Gln
                305                 310                 315

gaa cgg ttg ctt gcc atg ttg gag cag aag aat ggt gaa ata aaa cat      1190
Glu Arg Leu Leu Ala Met Leu Glu Gln Lys Asn Gly Glu Ile Lys His
            320                 325                 330

ctt tta ggt gaa att aga aat ctg gag aaa ttt aag aat tta tat gac      1238
Leu Leu Gly Glu Ile Arg Asn Leu Glu Lys Phe Lys Asn Leu Tyr Asp
        335                 340                 345

agt atg gaa tcc aag cct tca gtc gac tct ggt act ctg gaa gat aac      1286
Ser Met Glu Ser Lys Pro Ser Val Asp Ser Gly Thr Leu Glu Asp Asn
    350                 355                 360

acc tat tat aca gat tta ctt cag atg aag ctg gat aac tta aac aaa      1334
Thr Tyr Tyr Thr Asp Leu Leu Gln Met Lys Leu Asp Asn Leu Asn Lys
365                 370                 375                 380

gaa att gaa agc act aaa ggt gaa ttg tcc ata cag cga atg aaa gca      1382
Glu Ile Glu Ser Thr Lys Gly Glu Leu Ser Ile Gln Arg Met Lys Ala
                385                 390                 395

tta ttt gag agc cag cgg gct cta gat att gag cga aaa ctt ttt tgc      1430
Leu Phe Glu Ser Gln Arg Ala Leu Asp Ile Glu Arg Lys Leu Phe Cys
            400                 405                 410

aaa tga aagatgcctc cagctttcag aaagtgaaaa tatgaaactg agagctaaac      1486
Lys  *

tagatgaatt gaaactaaaa tatgaacctg aagagacagt tgaagtgcct gtactgaaaa   1546

agaggcgtga ggtgctccct gtggatataa ccaccgctaa agatgcatgt gtcaacaaca   1606

gtgctctcgg gggagaagtt tatcgattac cgcctcagaa agaggagaca cagtcctgcc   1666

ctaacagttt agaagataac aacttgcaat tagaaaaatc agtttctata cacacaccag   1726

tagtcagtct ctctcctcac aaaaatctgc ccgtggatat gcagctgaag aaggaaaaga   1786

aatgtgtgaa actcatagga gttcccgctg acgctgaggc cttaagtgaa agaagtggaa   1846

acaccccaaa ctctcccagg ttagctgctg aatcaaagct tcaaacagaa gttaaagaag   1906
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gaaaagaaac ttcaagcaaa ttggaaaaag aaacttgtaa gaaatcacac cctattctat   1966

atgtgtcttc taaatctact ccagagaccc agtgccctca acagtaaaga cttttcttta   2026

agtaagagta cggtgccact tgcctcaaaa gttactatgg tgcttaagat tgtcttgatc   2086

tgacatatat caccttctgg gttatttact cattgtgcca ggacctggca ttttcatgtg   2146

cctttgacca agtgttcaga atttgcttga ctctaacctg gagagcttct taagtgatgc   2206

cccttcatgg agcttctatg acagtgaata aactattaat tgaaggaaaa tgttataatt   2266

aatgtatcta tttgctgcat tgtatatgga ttaaatgata aaaaacaagt aatctaccct   2326

cagagccatg tatttgagaa tgcttcaatc atattttcct atgtactttt ttttataaac   2386

ttagttttag actatgttgt aaaaatggga aggttgtaaa ctatgttgta aaaataggaa   2446

atgtggctta aaatatatac attatattgt ttcaggattt tgtcagtgtt taaagaacca   2506

tgttcatctt tgtatttata tacatgattt aaattttgtc taaaatttta aataaaactg   2566

ccagtgattt atcctt                                                   2582




      <210> 194
      <211> 1042
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (528)..(953)

      <400> 194
cgaagacatc tcctattagc tgtgtgactg tttataggca ggttcttgtg ccccggttgg     60

tgcttcacaa aaggaagctt ataacaacag tacttgtctc acagttttag gataattaaa    120

ttatggtata tgcaaagcaa ttaaaacagc tcctgccaaa gagtaaacac catataaata    180

ttcattaaat aacatacaaa cataccaggt tgggaaaaat cagtaagcat aggagtcagg    240

aaattccaag ttggttatca caactcttgg cccacagggc tttaatccag gtgcccttgt    300

ctcctaccct tgttgccatc ccagtgtctc cagggagtaa gtagaaataa agatcctatc    360

tcacctcttg ggcattttcc cctgccctga aagcgtataa tcgcttagca cagtcggtgc    420

ttaaggggcc aggctccaaa gaagattaaa ggaacagttt gtggggtgca ctgggcagca    480

gtactctcct ctgagttcaa tcatcttgca ctctaagaat caccacc  atg gcc ctt    536
                                                     Met Ala Leu
                                                       1
```

```
gtg cca ggg aga agc aag gag gat ggg ctt tgg act aga aat agc cca      584
Val Pro Gly Arg Ser Lys Glu Asp Gly Leu Trp Thr Arg Asn Ser Pro
      5                  10                  15

ggc tcc tcc cag cat cca gaa agt ccc agg ctg ccc aac cct ctc tgg      632
Gly Ser Ser Gln His Pro Glu Ser Pro Arg Leu Pro Asn Pro Leu Trp
 20                  25                  30                  35

gac aga gga aaa att ggc aag gtt gaa ggt cac cag cac att cag gtt      680
Asp Arg Gly Lys Ile Gly Lys Val Glu Gly His Gln His Ile Gln Val
                 40                  45                  50

agt act tcc tca gcc tgt gtc tgg cag ctg gct tac cct cca gtt tgg      728
Ser Thr Ser Ser Ala Cys Val Trp Gln Leu Ala Tyr Pro Pro Val Trp
             55                  60                  65

ccc aac ctc cct gct gtc cct att cag gat ttc tct caa aag tcc cat      776
Pro Asn Leu Pro Ala Val Pro Ile Gln Asp Phe Ser Gln Lys Ser His
         70                  75                  80

ctg ccg tct att gtg gtg gaa tcc agt gag gtg aat gaa gag agt ggg      824
Leu Pro Ser Ile Val Val Glu Ser Ser Glu Val Asn Glu Glu Ser Gly
     85                  90                  95

gat ctc cat ttg ccc cat gag gag ctg ctg ctg ctc act gat ggt gag      872
Asp Leu His Leu Pro His Glu Glu Leu Leu Leu Leu Thr Asp Gly Glu
100                 105                 110                 115

gaa gag gat gct gag gcc ttc ttc caa gac caa agt gaa gag cca ggt      920
Glu Glu Asp Ala Glu Ala Phe Phe Gln Asp Gln Ser Glu Glu Pro Gly
                120                 125                 130

gag gga ggt ggc tca ttc agg ggg cca ctg tga gctgaatg ttctgggcag      971
Glu Gly Gly Gly Ser Phe Arg Gly Pro Leu  *
            135                 140

agccaagatg gaagtcagtt acggcccctg cattcagcag taaaaggcac acagcaggtg   1031

ctcaataaat g                                                        1042



     <210> 195
     <211> 903
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (17)..(739)

     <400> 195
ggctccagaa agcggc    atg tcc cct ttg ctc ttt ggg gct ggg ctg gtc       49
                     Met Ser Pro Leu Leu Phe Gly Ala Gly Leu Val
                       1               5                  10
```

```
gtt ctg aat cta gtg acg tct gcc agg agc cag aag aca gaa cct cta        97
Val Leu Asn Leu Val Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu
             15                  20                  25

agt ggc tct ggg gac cag cca ctc ttc cgt gga gct gat cga tat gac       145
Ser Gly Ser Gly Asp Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp
         30                  35                  40

ttt gcc atc atg ata cct cca gga ggc acg gaa tgc ttt tgg caa ttt       193
Phe Ala Ile Met Ile Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe
     45                  50                  55

gcc cac cag act gga tac ttc tat ttc agt tac gag gtt cag cgg aca       241
Ala His Gln Thr Gly Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr
 60                  65                  70                  75

gtg ggg atg tca cat gac cgg cat gtt gct gcc acg gca cat aac cca       289
Val Gly Met Ser His Asp Arg His Val Ala Ala Thr Ala His Asn Pro
                 80                  85                  90

cag gga ttt ctc ata gac acc tcc cag ggt gtt cgg ggc cag att aac       337
Gln Gly Phe Leu Ile Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn
             95                 100                 105

ttc tct acc caa gag aca ggt ttt tat cag ctt tgt cta agt aat cag       385
Phe Ser Thr Gln Glu Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln
        110                 115                 120

cat aat cac ttc ggt tct gtg caa gtg tac ctc aac ttt ggg gtc ttc       433
His Asn His Phe Gly Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe
    125                 130                 135

tat gag ggg cct gag act gat cac aaa cag aag gaa aga aaa caa ctg       481
Tyr Glu Gly Pro Glu Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu
140                 145                 150                 155

aat gat act ctg gat gca att gag gac ggc aca caa aag gtg cag aac       529
Asn Asp Thr Leu Asp Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn
                160                 165                 170

aat atc ttt cac atg tgg cga tac tac aac ttt gcc cgg atg agg aaa       577
Asn Ile Phe His Met Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys
            175                 180                 185

atg gct gac ttt ttc ctt atc caa tca aac tat aac tac gtg aac tgg       625
Met Ala Asp Phe Phe Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp
        190                 195                 200

tgg tcg aca gcc cag agc ctt gtt att att ctt tct ggg atc ctg caa       673
Trp Ser Thr Ala Gln Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln
    205                 210                 215

ctg tat ttc ttg aag cgt ctc ttc aat gtt cca aca act aca gat aca       721
Leu Tyr Phe Leu Lys Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr
220                 225                 230                 235

aag aag cca aga tgc taa gctaag gtgactatag caccctggct gttttcttct       775
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Lys Lys Pro Arg Cys  *
                240

ggggcttagt cgaatcagct ttgtaatgtt atgggacaaa aatcaattat ctcattaatg    835

ttttagtctg ctgcacacat ctaaaaaagc aaaatggcaa taaaatcata acagtgaaaa    895

aaaaaaaa                                                             903
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<210> 196
<211> 649
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (19)..(312)

<400> 196
ccgggagctt ggtgcgct atg gcg aca ccc agc ctg cgg ggt cgt ctg gcg       51
                    Met Ala Thr Pro Ser Leu Arg Gly Arg Leu Ala
                     1               5                  10

cgg ttt ggg aac ccg cgg aag cct gtg ctg aag ccc aat aaa cct ctc       99
Arg Phe Gly Asn Pro Arg Lys Pro Val Leu Lys Pro Asn Lys Pro Leu
            15                  20                  25

att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag gcg      147
Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala
        30                  35                  40

act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag aat      195
Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln Asn
    45                  50                  55

gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc gat      243
Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu Asp
60                  65                  70                  75

tgt gcc gcg agg gct cag gtg acc gat ggc tcc tgg ggt gct ttc tca      291
Cys Ala Ala Arg Ala Gln Val Thr Asp Gly Ser Trp Gly Ala Phe Ser
                80                  85                  90

gga aaa gaa tgg ggg aga tag aa gtaatgattc tccctgcctt ttgctaggaa      344
Gly Lys Glu Trp Gly Arg  *
            95

aggccctttc attcatttgg gaggtatatt attcacgcca aagtgggaaa ggttacagtt    404

ttgaaggctg tgtgatcttg acggatttat tcattgctct gaactttcga gttactgtac    464

gtaaaatgag gctaaccaat accaccttaa agaatgttgt gagtgtcaga tgaagtaatg    524

aatgggaaaa tcattttgaa aaatgtaaat tgctgctcaa gtagacatta ttgtgtgaaa    584
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tagaactaaa gagactaaac taaataatga caatagtttg gttcctgtct aggctaattg    644

ctagg                                                                 649




      <210> 197
      <211> 360
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (36)..(275)

      <400> 197
agacgtatag ctgagcgacc cagcccgcga gcgag   atg ccg gtg gcc gtg ggt        53
                                         Met Pro Val Ala Val Gly
                                         1               5

ccc tac gga cag tcc cag cca agc tgc ttc tac cgt gta aaa atg ggc      101
Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Tyr Arg Val Lys Met Gly
            10                  15                  20

ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc gag gcg ctc ttc ggc      149
Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Glu Ala Leu Phe Gly
        25                  30                  35

acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc      197
Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
    40                  45                  50

ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc      245
Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
55                  60                  65                  70

atg gcc att ggg atg ggc atc cga tgc taa c catggttgcc aactacatct      296
Met Ala Ile Gly Met Gly Ile Arg Cys  *
                75                  80

gtcccttccc atcaatccca gcccatgtac taataaaaga aagtctttga gtaaaaaaaa    356

aaaa                                                                  360




      <210> 198
      <211> 1280
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (206)..(535)
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     <400> 198
gggggttctag aaaatatatt tcctataata aaatggcacc ttcccccttt caagaagggt      60

gattctgggg ccgactcagg gtttaggtgc cccctggtgt ggcctaaatg tccccacctg     120

ggccatcttt ctggggagga ctctcccagg tagggaaggc cagaggtggc ccagtgcctg     180

gagggttagg gtctctgcct gggat  atg caa gag gaa gta gga aag gga ggt      232
                             Met Gln Glu Glu Val Gly Lys Gly Gly
                              1               5

ctc atg gat gat cct agg ctg cta gaa gtc ctt aag gcc cca tct agt       280
Leu Met Asp Asp Pro Arg Leu Leu Glu Val Leu Lys Ala Pro Ser Ser
 10                  15                  20                  25

cca ttc cac tcc cta ccc cca ttc cag agc cga gta gta agt tta cag       328
Pro Phe His Ser Leu Pro Pro Phe Gln Ser Arg Val Val Ser Leu Gln
                 30                  35                  40

atg ttt ccc cca tta cgt acc ccc acc cat ccc tgc tgc agc gag cct       376
Met Phe Pro Pro Leu Arg Thr Pro Thr His Pro Cys Cys Ser Glu Pro
             45                  50                  55

gag agc cag gca gag cca ggc aca gct cct cag tct tct cac aca gtc       424
Glu Ser Gln Ala Glu Pro Gly Thr Ala Pro Gln Ser Ser His Thr Val
         60                  65                  70

ctg ccg gtg gcc ttc cct cat gac cct tgc ttg gga ggg tgg agc act       472
Leu Pro Val Ala Phe Pro His Asp Pro Cys Leu Gly Gly Trp Ser Thr
     75                  80                  85

ggc tcc ttg acc cta aaa ggt agc tgg cag ggg caa gat ggg ggc cag       520
Gly Ser Leu Thr Leu Lys Gly Ser Trp Gln Gly Gln Asp Gly Gly Gln
 90                  95                 100                 105

cta cct aat gga tga aagccacaag tgaatacagt tcttgtcacc agggttgccc       575
Leu Pro Asn Gly  *
                110

tgccctcact cggcagggag ttctgacacc ccagggcccg tgagctacct gcttgagccc     635

ctgtttctgg ggcaccttcg aggaggcgtt gtggagggca tcgccccctg tttattcaca     695

acaccctcag gggcaaacag gcctgggacc cgctgacacc attttgggta gctggatgca     755

cccgacagca gtggggtcca cacactgagc tccagctggc actgcccact caagggctga     815

gtggaggggc ccctccggcc agctctgctc caccagccct gcaagctgat gcagggcggg     875

ggaagggctg ggtgttgcac tattgctgcg ctgccttaag gcatctgtcc tctggtggtg     935

cacccgtgca cacaggtaca gtgcatctgg gcacagcttt tggatccaca cctctgcaca     995

agtgtgaata cctctgcaca tatgggtgta tctgtgtgtg ctcgtgtata tggggtgggg    1055

aacatgagac ttcctgtgac cagtccaccc tggctcccag ctgtctgtat cctcctgccc    1115
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cgccctggcg agtgcctacc ctggcagaac ccagggagga gtggaggctg cctctgcctg   1175

ggcctccaca cagcatcctg tacatacgcc acctgggctg ggggtgggga ggcagggcca   1235

ggagcatcga ttaaagatca catcctgggg cttccaggga gctca                   1280




      <210> 199
      <211> 2549
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (284)..(1741)

      <400> 199
cggtctggat ttaccgggcc gacgatttcg tgtagtatcc tgggagctgc gggctactgg     60

gcctgcgctg ccgggctttg ggttctgggc ctctgccgct ctctggccct aagtgctgag    120

ctgccgggaa cggcagcttc tgacgctggg ccattggacg ctgcggaacc aggcttcttc    180

actttgagtt tccgccgcga agcgccagtc cgggccgagg agggagcctt tactacttct    240

ccctggtttc attcatgttc tgaggagggt gtgagaagga acc  atg gat ccc aca    295
                                                 Met Asp Pro Thr
                                                 1

gcc ttg gtg gaa gcc att gtg gaa gaa gtg gcc tgt ccc atc tgt atg      343
Ala Leu Val Glu Ala Ile Val Glu Glu Val Ala Cys Pro Ile Cys Met
5                   10                  15                  20

acc ttc ctg agg gag ccc atg agc att gac tgt ggc cac agc ttc tgc      391
Thr Phe Leu Arg Glu Pro Met Ser Ile Asp Cys Gly His Ser Phe Cys
                25                  30                  35

cac agc tgt ctc tct gga ctc tgg gag atc cca gga gaa tcc cag aac      439
His Ser Cys Leu Ser Gly Leu Trp Glu Ile Pro Gly Glu Ser Gln Asn
            40                  45                  50

tgg ggt tac acc tgt ccc ctc tgt cga gct cct gtc cag cca agg aac      487
Trp Gly Tyr Thr Cys Pro Leu Cys Arg Ala Pro Val Gln Pro Arg Asn
        55                  60                  65

ctg cgg cct aat tgg cag ctg gcc aat gtt gta gaa aaa gtc cgt ctg      535
Leu Arg Pro Asn Trp Gln Leu Ala Asn Val Val Glu Lys Val Arg Leu
    70                  75                  80

cta agg cta cat cca gga atg ggg ctg aag ggt gac ctg tgt gag cgc      583
Leu Arg Leu His Pro Gly Met Gly Leu Lys Gly Asp Leu Cys Glu Arg
85                  90                  95                  100

cat ggg gaa aag ctg aag atg ttc tgc aaa gag gat gtc ttg ata atg      631
```

```
His Gly Glu Lys Leu Lys Met Phe Cys Lys Glu Asp Val Leu Ile Met
                105                 110                 115

tgt gag gcc tgc agc cag tcc cca gag cat gag gcc cac agt gtt gtg       679
Cys Glu Ala Cys Ser Gln Ser Pro Glu His Glu Ala His Ser Val Val
            120                 125                 130

cca atg gag gat gtt gcc tgg gag tac aag tgg gaa ctt cat gag gcc       727
Pro Met Glu Asp Val Ala Trp Glu Tyr Lys Trp Glu Leu His Glu Ala
        135                 140                 145

ctc gaa cat ctg aag aaa gag caa gaa gag gcc tgg aag ctt gaa gtt       775
Leu Glu His Leu Lys Lys Glu Gln Glu Glu Ala Trp Lys Leu Glu Val
    150                 155                 160

ggt gaa agg aaa cga act gcc acc tgg aag ata cag gtg gaa acc cga       823
Gly Glu Arg Lys Arg Thr Ala Thr Trp Lys Ile Gln Val Glu Thr Arg
165                 170                 175                 180

aaa cag agt att gta tgg gag ttt gaa aaa tac cag cga tta cta gag       871
Lys Gln Ser Ile Val Trp Glu Phe Glu Lys Tyr Gln Arg Leu Leu Glu
                185                 190                 195

aaa aag cag cca cca cat cgg cag ctg ggg gca gag gta gca gca gct       919
Lys Lys Gln Pro Pro His Arg Gln Leu Gly Ala Glu Val Ala Ala Ala
            200                 205                 210

ctg gcc agc cta cag cgg gag gca gcg gag acc atg cag aaa ctg gag       967
Leu Ala Ser Leu Gln Arg Glu Ala Ala Glu Thr Met Gln Lys Leu Glu
        215                 220                 225

ttg aac cat agc gag ctc atc cag cag agc cag gtc ctg tgg agg atg      1015
Leu Asn His Ser Glu Leu Ile Gln Gln Ser Gln Val Leu Trp Arg Met
    230                 235                 240

att gca gag ttg aaa gag agg tcg cag agg cct gtc cgc tgg atg ttg      1063
Ile Ala Glu Leu Lys Glu Arg Ser Gln Arg Pro Val Arg Trp Met Leu
245                 250                 255                 260

cag gat att cag gaa gtg tta aac agg agc aaa tct tgg agc ttg cag      1111
Gln Asp Ile Gln Glu Val Leu Asn Arg Ser Lys Ser Trp Ser Leu Gln
                265                 270                 275

cag cca gaa cca atc tcc ctg gag ttg aag aca gat tgc cgt gtg ctg      1159
Gln Pro Glu Pro Ile Ser Leu Glu Leu Lys Thr Asp Cys Arg Val Leu
            280                 285                 290

ggg cta aga gag atc ctg aag act tat gca gct gat gtg cgc ttg gat      1207
Gly Leu Arg Glu Ile Leu Lys Thr Tyr Ala Ala Asp Val Arg Leu Asp
        295                 300                 305

cca gat act gct tac tcc cgt ctc atc gtg tct gag gac aga aaa cgt      1255
Pro Asp Thr Ala Tyr Ser Arg Leu Ile Val Ser Glu Asp Arg Lys Arg
    310                 315                 320

gtg cac tat gga gac acc aac cag aaa ctg cca gac aat cct gag aga      1303
Val His Tyr Gly Asp Thr Asn Gln Lys Leu Pro Asp Asn Pro Glu Arg
```

```
325                 330                 335                 340

ttt tac cgc tat aat atc gtc ctg gga agc cag tgc atc tcc tca ggc      1351
Phe Tyr Arg Tyr Asn Ile Val Leu Gly Ser Gln Cys Ile Ser Ser Gly
                345                 350                 355

cgg cac tac tgg gag gtg gag gtg gga gac agg tct gag tgg ggc ctg      1399
Arg His Tyr Trp Glu Val Glu Val Gly Asp Arg Ser Glu Trp Gly Leu
            360                 365                 370

gga gta tgt aag caa aat gta gac cgg aag gag gtg gtc tac tta tcc      1447
Gly Val Cys Lys Gln Asn Val Asp Arg Lys Glu Val Val Tyr Leu Ser
        375                 380                 385

ccc cac tat gga ttc tgg gtg ata agg ctg agg aag gga aat gag tac      1495
Pro His Tyr Gly Phe Trp Val Ile Arg Leu Arg Lys Gly Asn Glu Tyr
    390                 395                 400

cga gca ggc acc gat gag tac cca atc ctg tcc ttg ccg gtc cct cct      1543
Arg Ala Gly Thr Asp Glu Tyr Pro Ile Leu Ser Leu Pro Val Pro Pro
405                 410                 415                 420

cgc cgg gtg gga atc ttc gtg gat tat gag gcc cat gac att tct ttc      1591
Arg Arg Val Gly Ile Phe Val Asp Tyr Glu Ala His Asp Ile Ser Phe
                425                 430                 435

tac aat gtg act gac tgt ggc tcc cac atc ttc act ttc ccc cgc tat      1639
Tyr Asn Val Thr Asp Cys Gly Ser His Ile Phe Thr Phe Pro Arg Tyr
            440                 445                 450

ccc ttc cct ggg cgc ctc ctg ccc tat ttt agt cct tgc tac agc att      1687
Pro Phe Pro Gly Arg Leu Leu Pro Tyr Phe Ser Pro Cys Tyr Ser Ile
        455                 460                 465

gga acc aac aac act gct cct ctg gcc atc tgc tcc ctg gat ggg gag      1735
Gly Thr Asn Asn Thr Ala Pro Leu Ala Ile Cys Ser Leu Asp Gly Glu
    470                 475                 480

gac taa gaaagctacc accctaacca cagaggcttg gaattgggcc tggcccccat      1791
Asp  *
485

ggggcttgga ggaccgagcc actgacaggt atcccctgaa actgagctga gcccagtatc    1851

caaggattcc tctgtctgat cctttggtct ttgctaccag gctgaagtct gtcatgaaac    1911

cacttatttt aaaaagcaga ggcccagtca aatgagcatt gcatcccatg agggaagcac    1971

gacagggctg atggtgagga tcagagcagt tctaaggtga ctcgttgggg taaggatcag    2031

gactttgtcc atgtagtagc caaccaccct cttccctgat tcccgtccgg tgtcacagtt    2091

cagtcagtga ggatgatgaa gtagatacag tcttcaggac accattagat gggctttccc    2151

aataggccaa aaaaatgctg cgcataccca gagctggttg ttgtgctgag gccagtcaga    2211

ggatgcttcc cctgaggttt gctataacta agcaaccttt atgtgactct caccttctga    2271
```

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cctcctggca agagaaattc agtgcagcag ggggacacag acctgcccaa gccaccccac   2331

tgccgttccc tctctgagca caagctgggc aaatcactgt cccttggact ccagtagacc   2391

agtgtcctag tcttgccttt tttctctaag tggcaggatc agaaaacctg cgagctttag   2451

tttgtatttt cactttatga atgaggaaac tgaaatggcc ttaagggagc aagttatttc   2511

ttttttttg agactcctca aaaaagaaaa aaaaaaa                             2549



     <210> 200
     <211> 1377
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (331)..(1047)

     <400> 200
ttttgaaatc ggtccactat ccgtgtggtg gaattccaac gtgtagatcc tcgagaactg      60

tggccgactg ggtgtgttcc gtagacacgc tgttggcatt tttcttactg atttgagttt     120

tctcaccagc agagaacagc tgacggtctt tccataagtg cttctaagag agatgtgtgg     180

taccccgggc taagtagaca gcaactgagc cctccctccc accccagggc tcccagagca     240

acagggagca gggagcatag gacctggccg cagccaggaa tctacactga ccggctcagc     300

ccatgaagta tcttgggctg aagtcacagg     atg aga ctg ttt gta tct gta     351
                                     Met Arg Leu Phe Val Ser Val
                                     1               5

act gtc ctt gtc atc tgt ctt gca gat tta gaa gag gaa tca gaa agc       399
Thr Val Leu Val Ile Cys Leu Ala Asp Leu Glu Glu Glu Ser Glu Ser
        10                  15                  20

tgg gac aac tct gag gct gaa gag gag gag aaa gcc cct gtg ttg cca       447
Trp Asp Asn Ser Glu Ala Glu Glu Glu Glu Lys Ala Pro Val Leu Pro
    25                  30                  35

gag agt aca gaa ggg cgg gag ctg acc cag ggc ccg gca gag tcc tcc       495
Glu Ser Thr Glu Gly Arg Glu Leu Thr Gln Gly Pro Ala Glu Ser Ser
40                  45                  50                  55

tct ctc tca ggc tgt ggg agc tgg cag ccc cgg aag ctg cca gtc ttc       543
Ser Leu Ser Gly Cys Gly Ser Trp Gln Pro Arg Lys Leu Pro Val Phe
                60                  65                  70

aag tcc ctc cgg cac atg agg cag gtc ctg ggt gcc cct tct ttc cgc       591
Lys Ser Leu Arg His Met Arg Gln Val Leu Gly Ala Pro Ser Phe Arg
            75                  80                  85
```

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atg ctg gcc tgg cac gtt ctc atg ggg aac cag gtg atc tgg aaa agc      639
Met Leu Ala Trp His Val Leu Met Gly Asn Gln Val Ile Trp Lys Ser
        90                  95                  100

aga gac gtg gac ctc gtc cag tca gct ttt gaa gta ctt cgg acc atg      687
Arg Asp Val Asp Leu Val Gln Ser Ala Phe Glu Val Leu Arg Thr Met
    105                 110                 115

ctt ccc gtg ggc tgc gtc cgc atc atc cca tac agc agc cag tac gag      735
Leu Pro Val Gly Cys Val Arg Ile Ile Pro Tyr Ser Ser Gln Tyr Glu
120                 125                 130                 135

gag gcc tat cgg tgc aac ttc ctg ggg ctc agc ccg cac gtg cag atc      783
Glu Ala Tyr Arg Cys Asn Phe Leu Gly Leu Ser Pro His Val Gln Ile
                140                 145                 150

ccc ccc cac gtg ctc tcc tca gag ttt gct gtc atc gtg gag gtc cac      831
Pro Pro His Val Leu Ser Ser Glu Phe Ala Val Ile Val Glu Val His
            155                 160                 165

gca gcc gca cgt tcc acc ctc cac cct gtg ggg tgt gag gat gac cag      879
Ala Ala Ala Arg Ser Thr Leu His Pro Val Gly Cys Glu Asp Asp Gln
        170                 175                 180

tct ctc agc aag tac gag ttt gtg gtg acc agt ggg agc cct gta gct      927
Ser Leu Ser Lys Tyr Glu Phe Val Val Thr Ser Gly Ser Pro Val Ala
    185                 190                 195

gca gac cga gtg ggc ccc acc atc ctg aat aag att gaa gcg gct ctg      975
Ala Asp Arg Val Gly Pro Thr Ile Leu Asn Lys Ile Glu Ala Ala Leu
200                 205                 210                 215

acc aac cag aac ctg tct gtg gat gtg gtg gac cag tgc ctc gtc tgc     1023
Thr Asn Gln Asn Leu Ser Val Asp Val Val Asp Gln Cys Leu Val Cys
                220                 225                 230

ctc aag gag gag tgg atg aag taa gcaacagtgt gggtgaggcc cctttgcttg     1077
Leu Lys Glu Glu Trp Met Lys  *
            235

cgaccctgga gaaaacctgg agctgtttcc aaaagaggag ctgggccgtg gccactgagg    1137

gaggagctga gagaagaggt tgggggcggg gttccaactc cacgtccgcc actgcaaagc    1197

tcaggtggcc tcgggaggcg gtcatcatgt ctgcctccgg ctcctgcatg gggaggtggg    1257

ggtctatcat gactagtgct gctgtgaaca ttcctgatcc ggtctctgac aaacacgcct    1317

gtgcacatga gtgtgtcgtg caccttagcc tagcaccgca gttgcgggac ctcaacggcc    1377



<210> 201
<211> 441
<212> DNA
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     <213> Homo sapiens

     <220>
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     <222> (90)..(416)

     <400> 201
ctctcatttt ctctctcaca caaaaatact ctggacttct ccaagtccct gaggagcctg      60

accactgaag ctgatcatga gatgactgt  atg ctg aca cac ccc ctt cag ggg      113
                                 Met Leu Thr His Pro Leu Gln Gly
                                 1               5

cct ggc ctt gac tta ggg ctg cac tgt atc ctc agc aac ggc ctt gca      161
Pro Gly Leu Asp Leu Gly Leu His Cys Ile Leu Ser Asn Gly Leu Ala
    10                  15                  20

gga gcc cct ttt gga ctg ctt tcc cta ttc agc cca aag ttg ggg tgg      209
Gly Ala Pro Phe Gly Leu Leu Ser Leu Phe Ser Pro Lys Leu Gly Trp
25                  30                  35                  40

tgg gag aag agg ggt tgg agt gaa tcc atc tct att caa att cca gct      257
Trp Glu Lys Arg Gly Trp Ser Glu Ser Ile Ser Ile Gln Ile Pro Ala
                45                  50                  55

ggg att act cta gga gtc ttc ctg gct tgt ttt ggg ctc aaa ctt agc      305
Gly Ile Thr Leu Gly Val Phe Leu Ala Cys Phe Gly Leu Lys Leu Ser
            60                  65                  70

tac att gtt tat tgg ctc cca aag tcg gga ttg aag agt gaa aag atg      353
Tyr Ile Val Tyr Trp Leu Pro Lys Ser Gly Leu Lys Ser Glu Lys Met
        75                  80                  85

cag gca atg aat cct tct gca cac tcc tcc ccc cac att cct gac act      401
Gln Ala Met Asn Pro Ser Ala His Ser Ser Pro His Ile Pro Asp Thr
    90                  95                  100

agt aag aac caa taa acacttgttg acggaaaaaa aaaaa                      441
Ser Lys Asn Gln  *
105




     <210> 202
     <211> 732
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (72)..(296)

     <400> 202
cccacgcgtc cgggcatgca taacctaaat gggaataaat atggcgcttc ggggaaggag      60
```

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ggaaaaagta a atg aag ttc cag gaa tgt cat tct gaa gta atg agg cat      110
             Met Lys Phe Gln Glu Cys His Ser Glu Val Met Arg His
              1              5                   10

gga cag aaa ata tac ccc tca cat cat cgg att gag atg gca gtc gaa       158
Gly Gln Lys Ile Tyr Pro Ser His His Arg Ile Glu Met Ala Val Glu
    15                  20                  25

ata gct tca ttg aag tgt cag cac tca tcc atc aat caa tca ccc aca       206
Ile Ala Ser Leu Lys Cys Gln His Ser Ser Ile Asn Gln Ser Pro Thr
 30                 35                  40                  45

agg aaa aat agc aac agt aca acg ggg tgg ctt tta tgg gat tta ctc       254
Arg Lys Asn Ser Asn Ser Thr Thr Gly Trp Leu Leu Trp Asp Leu Leu
                50                  55                  60

atg ggc ata ggg aat agc ggc tca aat gta gtt ctg aca tga aaagcaa       303
Met Gly Ile Gly Asn Ser Gly Ser Asn Val Val Leu Thr  *
            65                  70                  75

ggtgctgata ttattttta tgatgggagg atcataaagt gaattgagaa cagtgaggtc      363

tgtctttgct taacctattc aaccagaaat gaatggagct cgactggaaa ggaacagtct     423

tcagatgggt taagattgaa gggtggactg gactctactg agcaccgtcc ttcaacaagg     483

aaattctatt aaaggaaaat caatgcatta gtattggggt tctcgtagct gttaaaaatt     543

gtctgctcca atccagggtt attaggccaa agttacataa ttcagatctc actgcaacca     603

tccaaaagtg gattctcgag cccttgctcc aatgggggga ggagatcaat acaattccca     663

attccatgga aattgtttcc cttctaagga agaaaaaata aatcatctgc ttcaacataa     723

aaaaaaaaa                                                             732
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<210> 203
<211> 1476
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (111)..(488)

<400> 203

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ctgaaaacag tgaaactgag ttagaaagga ttttgcgtcg cagaaaggtg acagcagaag      60

cagatagcag tagtccaact gggatattag ccacctcaga gtccaaatcc    atg cca     116
                                                          Met Pro
                                                           1

gtg ttg ggt tct gta tcc agt gta aca aaa aca gcc ttg aac aag aaa       164
Val Leu Gly Ser Val Ser Ser Val Thr Lys Thr Ala Leu Asn Lys Lys
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             5                   10                  15

act ctg gag gca gaa ttc aac agc ccg tcc ccc cca aca cct gag cca      212
Thr Leu Glu Ala Glu Phe Asn Ser Pro Ser Pro Pro Thr Pro Glu Pro
     20                  25                  30

ggt gaa ggg ccc cgt aaa ttg gaa gga tgc aca agt tcc aag gtt acg      260
Gly Glu Gly Pro Arg Lys Leu Glu Gly Cys Thr Ser Ser Lys Val Thr
 35                  40                  45                  50

ttt cag cct ccc agt agc att gga tgc agg aaa aaa tac att gac ggt      308
Phe Gln Pro Pro Ser Ser Ile Gly Cys Arg Lys Lys Tyr Ile Asp Gly
                 55                  60                  65

gaa aaa caa gcc gaa cca gtt gta gtt tta gat cct gtt tct aca cat      356
Glu Lys Gln Ala Glu Pro Val Val Val Leu Asp Pro Val Ser Thr His
             70                  75                  80

gaa ccc caa acc aaa gac cag gtt gct gaa aaa gat cca act caa cac      404
Glu Pro Gln Thr Lys Asp Gln Val Ala Glu Lys Asp Pro Thr Gln His
         85                  90                  95

aag gag gat gaa ggc gaa att caa cca gaa aac aaa gaa gac agc att      452
Lys Glu Asp Glu Gly Glu Ile Gln Pro Glu Asn Lys Glu Asp Ser Ile
    100                 105                 110

gaa aac gtg aga gag aca gac agc tcc aac tgc tga tcca taaaccagaa      502
Glu Asn Val Arg Glu Thr Asp Ser Ser Asn Cys  *
115                 120                 125

gcctgacatg tttggaagtc cttttcaata agcacatgat tagtgttgtt atattggcaa    562

gggctgtaga cattctgctc tggtcactgt attcagaata caggttcttt tctggtgtca    622

cttttgtaag tagcaactat aaacataagt aagctgttta gcaaaacaca cattcctagt    682

aggttttggt tttttgatct ttataaagat gaggtttttt tcctagttac tgtattaagt    742

atgacttctt ttagaaggtt acaaaaaaat tcagatgttg atacctttttt aggaaatgtg   802

cataccactc atcaaatgga atgctgaaag tttgaggtgc ttgtatataa tcggataaac    862

aaaactgatc aacccaatgt gattttaaaa gcccccaaag aagcttctgt tttgggtctg    922

atcctcttga tggagaaact gcagcagcat ggaaattgtt gggtactgtg gcatacaagt    982

tattttctac agtagactga gataaactga aaactcagga gctggcatca aactcgtagt   1042

cccatagtca gtgttaatta cacacattgt taactattgg atgaaaaata catgctattg   1102

attgtgtcca aagcctcccg aggacctccg tggggatgct ctggtagcct gaatacagaa   1162

ctgaggtgaa agtccaaacc ttgaatttta cagtagtaag ttggtaaacc atgtgctctg   1222

tgctatgagt taattatgtt ttcccaaata ctaatgtggc acaagtacca tattttatca   1282

gagttcttat gtacagtatg gtgaagataa gtgacaagca cacatttttc ttgcttcact   1342
```

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gctgttctat attacacagg tttgttgttg ttttttttaa aaaagaaatt aagcagtagt   1402

tagtctctaa aaatacaatg tttcaggcta ccacagtgaa taaatagaaa tgtaatcagg   1462

gattaaaaaa aaaa                                                     1476



     <210> 204
     <211> 721
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (193)..(564)

     <400> 204
tgcacacacg tgcagatatg ctgtccggat acacacgcac gcacacatgc agatatgctg     60

cctgggcaca cacttccgga cacacatgca cacacaggtg cagatatgct gcctggacac    120

acgcagactg acgtgctttt gggagggtgt gccgtgaagc ctgcagtacg tgtgccgtga    180

ggctcatagt tg    atg agg gac ttt ccc tgc tcc acc gtc act ccc cca      228
                 Met Arg Asp Phe Pro Cys Ser Thr Val Thr Pro Pro
                  1               5                  10

act ctg ccc gcc tct gtc ccc gcc tca gtc ccc gcc tcc atc ccc gcc      276
Thr Leu Pro Ala Ser Val Pro Ala Ser Val Pro Ala Ser Ile Pro Ala
        15                  20                  25

tct gtc ccc tgg cct tgg cgg cta ttt ttg cca cct gcc ttg ggt gcc      324
Ser Val Pro Trp Pro Trp Arg Leu Phe Leu Pro Pro Ala Leu Gly Ala
    30                  35                  40

cag gag tcc cct act gct gtg ggc tgg ggt tgg ggg cac agc agc ccc      372
Gln Glu Ser Pro Thr Ala Val Gly Trp Gly Trp Gly His Ser Ser Pro
 45                  50                  55                  60

aag cct gag agg ctg gag ccc atg gct agt ggc tca tcc cca ctg cat      420
Lys Pro Glu Arg Leu Glu Pro Met Ala Ser Gly Ser Ser Pro Leu His
                65                  70                  75

tct ccc cct gac aca gag aag ggg cct tgg tat tta tat tta aga aat      468
Ser Pro Pro Asp Thr Glu Lys Gly Pro Trp Tyr Leu Tyr Leu Arg Asn
            80                  85                  90

gaa gat aat att aat aat gat gga agg aag act ggg ttg cag gga ctg      516
Glu Asp Asn Ile Asn Asn Asp Gly Arg Lys Thr Gly Leu Gln Gly Leu
        95                 100                 105

tgg tct ctc ctg ggg ccc ggg acc cgc ctg gtc ttt cag cca tgc tga      564
Trp Ser Leu Leu Gly Pro Gly Thr Arg Leu Val Phe Gln Pro Cys  *
    110                 115                 120
```

```
tgaccacacc ccgtccaggc cagacaccac cccccacccc actgtcgtgg tggccccaga    624

tctctgtaat tttatgtaga gtttgagctg aagccccgta tatttaattt attttgttaa    684

acatgaaagt gcatcctttc cctccaaaaa aaaaaaa                             721



     <210> 205
     <211> 3249
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (71)..(2899)

     <400> 205
catggcggcc ttagcaagct atagctgcga gatttgaatt actccactcg tagctattgc     60

attcctgacg   atg gcc tct gtg gct tcg tgc gat tcg cgt ccg agc tca     109
             Met Ala Ser Val Ala Ser Cys Asp Ser Arg Pro Ser Ser
               1               5                  10

gac gag ctc cct gga gac ccc tct tca caa gaa gaa gat gag gac tat      157
Asp Glu Leu Pro Gly Asp Pro Ser Ser Gln Glu Glu Asp Glu Asp Tyr
     15                  20                  25

gat ttt gaa gat cgg gtc agc gac tcg ggt tca tat tcc tca gcg agt      205
Asp Phe Glu Asp Arg Val Ser Asp Ser Gly Ser Tyr Ser Ser Ala Ser
 30                  35                  40                  45

agc gat tat gat gat ctt gag cct gaa tgg ctg gac agt gtg cag aaa      253
Ser Asp Tyr Asp Asp Leu Glu Pro Glu Trp Leu Asp Ser Val Gln Lys
                 50                  55                  60

aat gga gag ctg ttt tat ttg gaa ttg agt gag gat gaa gaa gaa agc      301
Asn Gly Glu Leu Phe Tyr Leu Glu Leu Ser Glu Asp Glu Glu Glu Ser
             65                  70                  75

ctc ctt cct gag aca cca act gtg aac cat gtc agg ttc agt gaa aat      349
Leu Leu Pro Glu Thr Pro Thr Val Asn His Val Arg Phe Ser Glu Asn
         80                  85                  90

gag att atc att gaa gat gac tac aaa gaa aga aaa aag tat gaa ccc      397
Glu Ile Ile Ile Glu Asp Asp Tyr Lys Glu Arg Lys Lys Tyr Glu Pro
     95                 100                 105

aaa ctc aag cag ttt acc aaa att tta aga agg aaa aga ctt tta ccc      445
Lys Leu Lys Gln Phe Thr Lys Ile Leu Arg Arg Lys Arg Leu Leu Pro
110                 115                 120                 125

aag cgc tgc aat aaa aaa aat agc aat gac aat gga cca gta tcc att      493
Lys Arg Cys Asn Lys Lys Asn Ser Asn Asp Asn Gly Pro Val Ser Ile
                130                 135                 140
```

```
cta aag cat cag tcc aat cag aag aca gga gtc att gtc caa cag cgg        541
Leu Lys His Gln Ser Asn Gln Lys Thr Gly Val Ile Val Gln Gln Arg
            145                 150                 155

tac aaa gat gtg aat gtt tat gta aac ccc aaa aag cta act gtt atc        589
Tyr Lys Asp Val Asn Val Tyr Val Asn Pro Lys Lys Leu Thr Val Ile
        160                 165                 170

aaa gcc aaa gag cag ctc aag ctt ctg gaa gtg ctg gtt gga att att        637
Lys Ala Lys Glu Gln Leu Lys Leu Leu Glu Val Leu Val Gly Ile Ile
    175                 180                 185

cat cag acc aag tgg agc tgg aga aga acc gga aag cag ggt gat gga        685
His Gln Thr Lys Trp Ser Trp Arg Arg Thr Gly Lys Gln Gly Asp Gly
190                 195                 200                 205

gag agg ctt gtg gtt cat ggc ctg ctg cca ggg gga tct gct atg aag        733
Glu Arg Leu Val Val His Gly Leu Leu Pro Gly Gly Ser Ala Met Lys
                210                 215                 220

agc ggt cag gta ctc att ggt gat gtc ctt gtt gct gtg aat gat gtc        781
Ser Gly Gln Val Leu Ile Gly Asp Val Leu Val Ala Val Asn Asp Val
            225                 230                 235

gat gtt act act gaa aac atc gag aga gtt ctg tct tgc att cct gga        829
Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly
        240                 245                 250

cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg        877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg
    255                 260                 265

gag aca tcc cat cca aga cag aaa aag aca cag tcc aac aca agt gat        925
Glu Thr Ser His Pro Arg Gln Lys Lys Thr Gln Ser Asn Thr Ser Asp
270                 275                 280                 285

tta gtc aag ctt ctc tgg gga gaa gag gtt gaa ggt atc cag cag agt        973
Leu Val Lys Leu Leu Trp Gly Glu Glu Val Glu Gly Ile Gln Gln Ser
                290                 295                 300

ggc cta aac act cct cat atc att atg tat ctc aca cta cag ctc gac       1021
Gly Leu Asn Thr Pro His Ile Ile Met Tyr Leu Thr Leu Gln Leu Asp
            305                 310                 315

tca gaa acc tca aag gaa gag cag gaa att ctt tat cat tat cca atg       1069
Ser Glu Thr Ser Lys Glu Glu Gln Glu Ile Leu Tyr His Tyr Pro Met
        320                 325                 330

tct gaa gca tct cag aaa ctt aaa agt gtg aga ggg att ttt ctc aca       1117
Ser Glu Ala Ser Gln Lys Leu Lys Ser Val Arg Gly Ile Phe Leu Thr
    335                 340                 345

ctc tgt gac atg ctg gaa aac gta act ggg aca caa gtt act agt tca       1165
Leu Cys Asp Met Leu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser
350                 355                 360                 365
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tcc ctc ctt tta aat gga aaa caa att cat gtg gct tat tgg aaa gaa      1213
Ser Leu Leu Leu Asn Gly Lys Gln Ile His Val Ala Tyr Trp Lys Glu
                370                 375                 380

tct gac aag ttg ttg cta att ggc ctg cct gct gaa gaa gtt cct ctt      1261
Ser Asp Lys Leu Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu
            385                 390                 395

cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt      1309
Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe
        400                 405                 410

atg tat ggt tct tta gat agt gcc ttt tgc cag att gag aat gtt cct      1357
Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro
    415                 420                 425

cgt ttg gat cat ttt ttt aac ttg ttc ttt caa aga gca ctt cag cct      1405
Arg Leu Asp His Phe Phe Asn Leu Phe Phe Gln Arg Ala Leu Gln Pro
430                 435                 440                 445

gcg aaa ctg cat tcc agc gcc agt ccc agt gct cag cag tac gat gct      1453
Ala Lys Leu His Ser Ser Ala Ser Pro Ser Ala Gln Gln Tyr Asp Ala
                450                 455                 460

tcc agt gca gta ctt tta gac aac ctc cct gga gtc cgg tgg ctc aca      1501
Ser Ser Ala Val Leu Leu Asp Asn Leu Pro Gly Val Arg Trp Leu Thr
            465                 470                 475

ctt cca ctg gaa atc aag atg gaa tta gac atg gca tta agt gac ttg      1549
Leu Pro Leu Glu Ile Lys Met Glu Leu Asp Met Ala Leu Ser Asp Leu
        480                 485                 490

gag gct gca gat ttt gca gaa ctg tcc gag gat tac tat gac atg agg      1597
Glu Ala Ala Asp Phe Ala Glu Leu Ser Glu Asp Tyr Tyr Asp Met Arg
    495                 500                 505

cgg ctg tat aca att ttg ggg tct tct cta ttt tac aag ggt tat ttg      1645
Arg Leu Tyr Thr Ile Leu Gly Ser Ser Leu Phe Tyr Lys Gly Tyr Leu
510                 515                 520                 525

ata tgc agt cat ttg ccc aag gat gat ctt att gat att gcc gta tac      1693
Ile Cys Ser His Leu Pro Lys Asp Asp Leu Ile Asp Ile Ala Val Tyr
                530                 535                 540

tgt cgc cac tat tgc ctg ctg cct tta gca gca aaa caa aga att ggt      1741
Cys Arg His Tyr Cys Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly
            545                 550                 555

cag ttg atc ata tgg aga gaa gtg ttt cct cag cat cac ctc cga cct      1789
Gln Leu Ile Ile Trp Arg Glu Val Phe Pro Gln His His Leu Arg Pro
        560                 565                 570

ttg gca gac tca agc act gaa gtc ttt ccg gaa cct gaa gga aga tat      1837
Leu Ala Asp Ser Ser Thr Glu Val Phe Pro Glu Pro Glu Gly Arg Tyr
    575                 580                 585

ttt ttg cta gtt gtt ggc ttg aaa cat tat atg cta tgt gta cta tta      1885
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Phe Leu Leu Val Val Gly Leu Lys His Tyr Met Leu Cys Val Leu Leu
590                 595                 600                 605

gaa gct gga ggt tgc gca tcc aaa gct att ggg agt cct gga cca gac      1933
Glu Ala Gly Gly Cys Ala Ser Lys Ala Ile Gly Ser Pro Gly Pro Asp
                610                 615                 620

tgt gta tat gtg gat caa gtc aaa aca act ctt cac cag ctg gat gga      1981
Cys Val Tyr Val Asp Gln Val Lys Thr Thr Leu His Gln Leu Asp Gly
            625                 630                 635

gta gat tct cgc ata gat gaa cgg cta gca tct tct cca gtc ccc tgt      2029
Val Asp Ser Arg Ile Asp Glu Arg Leu Ala Ser Ser Pro Val Pro Cys
        640                 645                 650

ttg tct tgt gct gac tgg ttc ctt act gga tca cgt gaa aaa aca gat      2077
Leu Ser Cys Ala Asp Trp Phe Leu Thr Gly Ser Arg Glu Lys Thr Asp
    655                 660                 665

agc ttg acc act tcg cct att ctc agt agg cta caa ggt act tcc aaa      2125
Ser Leu Thr Thr Ser Pro Ile Leu Ser Arg Leu Gln Gly Thr Ser Lys
670                 675                 680                 685

gta gca act tct cca aca tgc aga aga acg ctt ttt ggt gac tat tcc      2173
Val Ala Thr Ser Pro Thr Cys Arg Arg Thr Leu Phe Gly Asp Tyr Ser
                690                 695                 700

tta aag aca cgc aag cct agt cct tcc tgt agt agt gga gga tct gac      2221
Leu Lys Thr Arg Lys Pro Ser Pro Ser Cys Ser Ser Gly Gly Ser Asp
            705                 710                 715

aat ggt tgt gaa ggt gga gaa gat gat ggc ttt agc ccc cat act aca      2269
Asn Gly Cys Glu Gly Gly Glu Asp Asp Gly Phe Ser Pro His Thr Thr
        720                 725                 730

ccg gat gca gta cgg aag caa aga gaa tct cag ggc tct gat ggt tta      2317
Pro Asp Ala Val Arg Lys Gln Arg Glu Ser Gln Gly Ser Asp Gly Leu
    735                 740                 745

gaa gaa agt ggg acc ttg ctt aag gtc act aaa aag aag tct act ctt      2365
Glu Glu Ser Gly Thr Leu Leu Lys Val Thr Lys Lys Lys Ser Thr Leu
750                 755                 760                 765

cca aat cca ttt cat ttg gga aac ttg aaa aag gac ctt cca gaa aaa      2413
Pro Asn Pro Phe His Leu Gly Asn Leu Lys Lys Asp Leu Pro Glu Lys
                770                 775                 780

gaa tta gaa ata tat aac aca gtg aaa ctg aca tct ggt cct gag aac      2461
Glu Leu Glu Ile Tyr Asn Thr Val Lys Leu Thr Ser Gly Pro Glu Asn
            785                 790                 795

aca ctt ttc cac tac gtt gcc tta gaa aca gtg caa gga atc ttt att      2509
Thr Leu Phe His Tyr Val Ala Leu Glu Thr Val Gln Gly Ile Phe Ile
        800                 805                 810

act cct acc ctt gaa gag gtg gca cag cta agt ggc tct atc cac cct      2557
Thr Pro Thr Leu Glu Glu Val Ala Gln Leu Ser Gly Ser Ile His Pro
```

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    815                 820                 825

cag cta ata aag aat ttc cat cag tgt tgt ctt tcc att cgt gca gtt      2605
Gln Leu Ile Lys Asn Phe His Gln Cys Cys Leu Ser Ile Arg Ala Val
830                 835                 840                 845

ttc caa cag aca ttg gtg gaa gag aaa aag aaa gga cta aat agt gga      2653
Phe Gln Gln Thr Leu Val Glu Glu Lys Lys Lys Gly Leu Asn Ser Gly
                850                 855                 860

gac cat tca gat tct gca aag tca gtg tct tct ctt aac cct gtt aaa      2701
Asp His Ser Asp Ser Ala Lys Ser Val Ser Ser Leu Asn Pro Val Lys
            865                 870                 875

gaa cat ggt gtg ttg ttt gaa tgt tca cct gga aac tgg act gat cag      2749
Glu His Gly Val Leu Phe Glu Cys Ser Pro Gly Asn Trp Thr Asp Gln
        880                 885                 890

aaa aaa gca cca cca gtt atg gct tac tgg gta gta ggg aga ctt ttt      2797
Lys Lys Ala Pro Pro Val Met Ala Tyr Trp Val Val Gly Arg Leu Phe
    895                 900                 905

ctt cat cca aaa cct caa gaa ctt tat gtc tgt ttt cat gac tca gtc      2845
Leu His Pro Lys Pro Gln Glu Leu Tyr Val Cys Phe His Asp Ser Val
910                 915                 920                 925

aca gaa att gcc att gaa ata gct ttt aaa ttg ttc ttt ggg tta acc      2893
Thr Glu Ile Ala Ile Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr
                930                 935                 940

ttg tag ctgtgctttc ttgatgcgta gaaacacgtg catggaggat caaacactgt      2949
Leu  *


cagaattgct gaaatcaata cacaaagaga taaagtttag cttcttttta ctattcaata   3009

ttgaacataa tattgttaaa tattgagatg aaatgctgtt ggatttgata cattaaatct   3069

taatgtaata ttgtaagact tttgagaata tacttgatta aaatgtgaaa gaagggattg   3129

ttaacttatt gctattttgg tatataatgt taatttattg actagtttga aataatgtga   3189

agtgtttttt atatcagatt aatataggaa atgtttattc ttgaaaaata aaaaaaaaaa   3249



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             Met Ala Ser Val Ala Ser Cys Asp Ser Arg Pro Ser Ser
              1               5                  10

gac gag ctc cct gga gac ccc tct tca caa gaa gaa gat gag gac tat      157
Asp Glu Leu Pro Gly Asp Pro Ser Ser Gln Glu Glu Asp Glu Asp Tyr
     15                  20                  25

gat ttt gaa gat cgg gtc agc gac tcg ggt tca tat tcc tca gcg agt      205
Asp Phe Glu Asp Arg Val Ser Asp Ser Gly Ser Tyr Ser Ser Ala Ser
 30                  35                  40                  45

agc gat tat gat gat ctt gag cct gaa tgg ctg gac agt gtg cag aaa      253
Ser Asp Tyr Asp Asp Leu Glu Pro Glu Trp Leu Asp Ser Val Gln Lys
                 50                  55                  60

aat gga gag ctg ttt tat ttg gaa ttg agt gag gat gaa gaa gaa agc      301
Asn Gly Glu Leu Phe Tyr Leu Glu Leu Ser Glu Asp Glu Glu Glu Ser
             65                  70                  75

ctc ctt cct gag aca cca act gtg aac cat gtc agg ttc agt gaa aat      349
Leu Leu Pro Glu Thr Pro Thr Val Asn His Val Arg Phe Ser Glu Asn
         80                  85                  90

gag att atc att gaa gat gac tac aaa gaa aga aaa aag tat gaa ccc      397
Glu Ile Ile Ile Glu Asp Asp Tyr Lys Glu Arg Lys Lys Tyr Glu Pro
     95                 100                 105

aaa ctc aag cag ttt acc aaa att tta aga agg aaa aga ctt tta ccc      445
Lys Leu Lys Gln Phe Thr Lys Ile Leu Arg Arg Lys Arg Leu Leu Pro
110                 115                 120                 125

aag cgc tgc aat aaa aaa aat agc aat gac aat gga cca gta tcc att      493
Lys Arg Cys Asn Lys Lys Asn Ser Asn Asp Asn Gly Pro Val Ser Ile
                130                 135                 140

cta aag cat cag tcc aat cag aag aca gga gtc att gtc caa cag cgg      541
Leu Lys His Gln Ser Asn Gln Lys Thr Gly Val Ile Val Gln Gln Arg
            145                 150                 155

tac aaa gat gtg aat gtt tat gta aac ccc aaa aag cta act gtt atc      589
Tyr Lys Asp Val Asn Val Tyr Val Asn Pro Lys Lys Leu Thr Val Ile
        160                 165                 170

aaa gcc aaa gag cag ctc aag ctt ctg gaa gtg ctg gtt gga att att      637
Lys Ala Lys Glu Gln Leu Lys Leu Leu Glu Val Leu Val Gly Ile Ile
    175                 180                 185

cat cag acc aag tgg agc tgg aga aga acc gga aag cag ggt gat gga      685
His Gln Thr Lys Trp Ser Trp Arg Arg Thr Gly Lys Gln Gly Asp Gly
190                 195                 200                 205

gag agg ctt gtg gtt cat ggc ctg ctg cca ggg gga tct gct atg aag      733
Glu Arg Leu Val Val His Gly Leu Leu Pro Gly Gly Ser Ala Met Lys
                210                 215                 220
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agc ggt cag gta ctc att ggt gat gtc ctt gtt gct gtg aat gat gtc        781
Ser Gly Gln Val Leu Ile Gly Asp Val Leu Val Ala Val Asn Asp Val
            225                 230                 235

gat gtt act act gaa aac atc gag aga gtt ctg tct tgc att cct gga        829
Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly
        240                 245                 250

cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg        877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg
    255                 260                 265

gag aca tcc cat cca aga cag aaa aag aca cag tcc aac aca agt gat        925
Glu Thr Ser His Pro Arg Gln Lys Lys Thr Gln Ser Asn Thr Ser Asp
270                 275                 280                 285

tta gtc aag ctt ctc tgg gga gaa gag gtt gaa ggt atc cag cag agt        973
Leu Val Lys Leu Leu Trp Gly Glu Glu Val Glu Gly Ile Gln Gln Ser
                290                 295                 300

ggc cta aac act cct cat atc att atg tat ctc aca cta cag ctc gac       1021
Gly Leu Asn Thr Pro His Ile Ile Met Tyr Leu Thr Leu Gln Leu Asp
            305                 310                 315

tca gaa acc tca aag gaa gag cag gaa att ctt tat cat tat cca atg       1069
Ser Glu Thr Ser Lys Glu Glu Gln Glu Ile Leu Tyr His Tyr Pro Met
        320                 325                 330

tct gaa gca tct cag aaa ctt aaa agt gtg aga ggg att ttt ctc aca       1117
Ser Glu Ala Ser Gln Lys Leu Lys Ser Val Arg Gly Ile Phe Leu Thr
    335                 340                 345

ctc tgt gac atg ctg gaa aac gta act ggg aca caa gtt act agt tca       1165
Leu Cys Asp Met Leu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser
350                 355                 360                 365

tcc ctc ctt tta aat gga aaa caa att cat gtg gct tat tgg aaa gaa       1213
Ser Leu Leu Leu Asn Gly Lys Gln Ile His Val Ala Tyr Trp Lys Glu
                370                 375                 380

tct gac aag ttg ttg cta att ggc ctg cct gct gaa gaa gtt cct ctt       1261
Ser Asp Lys Leu Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu
            385                 390                 395

cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt       1309
Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe
        400                 405                 410

atg tat ggt tct tta gat agt gcc ttt tgc cag att gag aat gtt cct       1357
Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro
    415                 420                 425

cgt ttg gat cat ttt ttt aac ttg ttc ttt caa aga gca ctt cag cct       1405
Arg Leu Asp His Phe Phe Asn Leu Phe Phe Gln Arg Ala Leu Gln Pro
430                 435                 440                 445
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gcg aaa ctg cat tcc agc gcc agt ccc agt gct cag cag tac gat gct      1453
Ala Lys Leu His Ser Ser Ala Ser Pro Ser Ala Gln Gln Tyr Asp Ala
                450                 455                 460

tcc agt gca gta ctt tta gac aac ctc cct gga gtc cgg tgg ctc aca      1501
Ser Ser Ala Val Leu Leu Asp Asn Leu Pro Gly Val Arg Trp Leu Thr
            465                 470                 475

ctt cca ctg gaa atc aag atg gaa tta gac atg gca tta agt gac ttg      1549
Leu Pro Leu Glu Ile Lys Met Glu Leu Asp Met Ala Leu Ser Asp Leu
        480                 485                 490

gag gct gca gat ttt gca gaa ctg ggt tat ttg ata tgc agt cat ttg      1597
Glu Ala Ala Asp Phe Ala Glu Leu Gly Tyr Leu Ile Cys Ser His Leu
    495                 500                 505

ccc aag gat gat ctt att gat att gcc gta tac tgt cgc cac tat tgc      1645
Pro Lys Asp Asp Leu Ile Asp Ile Ala Val Tyr Cys Arg His Tyr Cys
510                 515                 520                 525

ctg ctg cct tta gca gca aaa caa aga att ggt cag ttg atc ata tgg      1693
Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly Gln Leu Ile Ile Trp
                530                 535                 540

aga gaa gtg ttt cct cag cat cac ctc cga cct ttg gca gac tca agc      1741
Arg Glu Val Phe Pro Gln His His Leu Arg Pro Leu Ala Asp Ser Ser
            545                 550                 555

act gaa gtc ttt ccg gaa cct gaa gga aga tat ttt ttg cta gtt gtt      1789
Thr Glu Val Phe Pro Glu Pro Glu Gly Arg Tyr Phe Leu Leu Val Val
        560                 565                 570

ggc ttg aaa cat tat atg cta tgt gta cta tta gaa gct gga ggt tgc      1837
Gly Leu Lys His Tyr Met Leu Cys Val Leu Leu Glu Ala Gly Gly Cys
    575                 580                 585

gca tcc aaa gct att ggg agt cct gga cca gac tgt gta tat gtg gat      1885
Ala Ser Lys Ala Ile Gly Ser Pro Gly Pro Asp Cys Val Tyr Val Asp
590                 595                 600                 605

caa gtc aaa aca act ctt cac cag ctg gat gga gta gat tct cgc ata      1933
Gln Val Lys Thr Thr Leu His Gln Leu Asp Gly Val Asp Ser Arg Ile
                610                 615                 620

gat gaa cgg cta gca tct tct cca gtc ccc tgt ttg tct tgt gct gac      1981
Asp Glu Arg Leu Ala Ser Ser Pro Val Pro Cys Leu Ser Cys Ala Asp
            625                 630                 635

tgg ttc ctt act gga tca cgt gaa aaa aca gat agc ttg acc act tcg      2029
Trp Phe Leu Thr Gly Ser Arg Glu Lys Thr Asp Ser Leu Thr Thr Ser
        640                 645                 650

cct att ctc agt agg cta caa ggt act tcc aaa gta gca act tct cca      2077
Pro Ile Leu Ser Arg Leu Gln Gly Thr Ser Lys Val Ala Thr Ser Pro
    655                 660                 665

aca tgc aga aga acg ctt ttt ggt gac tat tcc tta aag aca cgc aag      2125
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Thr Cys Arg Arg Thr Leu Phe Gly Asp Tyr Ser Leu Lys Thr Arg Lys
670                 675                 680                 685

cct agt cct tcc tgt agt agt gga gga tct gac aat ggt tgt gaa ggt      2173
Pro Ser Pro Ser Cys Ser Ser Gly Gly Ser Asp Asn Gly Cys Glu Gly
                690                 695                 700

gga gaa gat gat ggc ttt agc ccc cat act aca ccg gat gca gta cgg      2221
Gly Glu Asp Asp Gly Phe Ser Pro His Thr Thr Pro Asp Ala Val Arg
            705                 710                 715

aag caa aga gaa tct cag ggc tct gat ggt tta gaa gaa agt ggg acc      2269
Lys Gln Arg Glu Ser Gln Gly Ser Asp Gly Leu Glu Glu Ser Gly Thr
        720                 725                 730

ttg ctt aag gtc act aaa aag aag tct act ctt cca aat cca ttt cat      2317
Leu Leu Lys Val Thr Lys Lys Lys Ser Thr Leu Pro Asn Pro Phe His
    735                 740                 745

ttg gga aac ttg aaa aag gac ctt cca gaa aaa gaa tta gaa ata tat      2365
Leu Gly Asn Leu Lys Lys Asp Leu Pro Glu Lys Glu Leu Glu Ile Tyr
750                 755                 760                 765

aac aca gtg aaa ctg aca tct ggt cct gag aac aca ctt ttc cac tac      2413
Asn Thr Val Lys Leu Thr Ser Gly Pro Glu Asn Thr Leu Phe His Tyr
                770                 775                 780

gtt gcc tta gaa aca gtg caa gga atc ttt att act cct acc ctt gaa      2461
Val Ala Leu Glu Thr Val Gln Gly Ile Phe Ile Thr Pro Thr Leu Glu
            785                 790                 795

gag gtg gca cag cta agt ggc tct atc cac cct cag cta ata aag aat      2509
Glu Val Ala Gln Leu Ser Gly Ser Ile His Pro Gln Leu Ile Lys Asn
        800                 805                 810

ttc cat cag tgt tgt ctt tcc att cgt gca gtt ttc caa cag aca ttg      2557
Phe His Gln Cys Cys Leu Ser Ile Arg Ala Val Phe Gln Gln Thr Leu
    815                 820                 825

gtg gaa gag aaa aag aaa gga cta aat agt gga gac cat tca gat tct      2605
Val Glu Glu Lys Lys Lys Gly Leu Asn Ser Gly Asp His Ser Asp Ser
830                 835                 840                 845

gca aag tca gtg tct tct ctt aac cct gtt aaa gaa cat ggt gtg ttg      2653
Ala Lys Ser Val Ser Ser Leu Asn Pro Val Lys Glu His Gly Val Leu
                850                 855                 860

ttt gaa tgt tca cct gga aac tgg act gat cag aaa aaa gca cca cca      2701
Phe Glu Cys Ser Pro Gly Asn Trp Thr Asp Gln Lys Lys Ala Pro Pro
            865                 870                 875

gtt atg gct tac tgg gta gta ggg aga ctt ttt ctt cat cca aaa cct      2749
Val Met Ala Tyr Trp Val Val Gly Arg Leu Phe Leu His Pro Lys Pro
        880                 885                 890

caa gaa ctt tat gtc tgt ttt cat gac tca gtc aca gaa att gcc att      2797
Gln Glu Leu Tyr Val Cys Phe His Asp Ser Val Thr Glu Ile Ala Ile
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    895                 900                 905

gaa ata gct ttt aaa ttg ttc ttt ggg tta acc ttg tag ctgtgctttc      2846
Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr Leu  *
910                 915                 920

ttgatgcgta gaaacacgtg catggaggat caaacactgt cagaattgct gaaatcaata   2906

cacaaagaga taaagtttag cttcttttta ctattcaata ttgaacataa tattgttaaa   2966

tattgagatg aaatgctgtt ggatttgata cattaaatct taatgtaata ttgtaagact   3026

tttgagaata tacttgatta aaatgtgaaa gaagggattg ttaacttatt gctattttgg   3086

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gtggaaacat gtcttgcgac acccaccagc gactgctaca acccagcggc ggcgntgntg    120

gtcacggagc tggggccggg ggcagcccgg gagctggctg ggccccctgc aaggaccgtc    180

tcgggcctgc ccagccaaga gtgtgtgcaa cacatcggtg ctgagcagca gcctgcagtc    240

actggagtat ctcatcaacg acatccggcc gccctgcatc aaggagcaga tgctgggcaa    300

gggct    atg aga cgg tgg ccg tgc ccc ggc tac tcg acc acc agc atg    347
         Met Arg Arg Trp Pro Cys Pro Gly Tyr Ser Thr Thr Ser Met
           1               5                  10

ccc aca tcc gcc tac ccg tct aca gat aag gcc tgc ctg cgg aca tac      395
Pro Thr Ser Ala Tyr Pro Ser Thr Asp Lys Ala Cys Leu Arg Thr Tyr
 15                  20                  25                  30

gga cat gcg gac agg gcg cag agc cgg gag gca ggc cgc aga aca ggg      443
Gly His Ala Asp Arg Ala Gln Ser Arg Glu Ala Gly Arg Arg Thr Gly
                 35                  40                  45
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tgg gcg gct cgc agg ggc gct cag ccc cac cct gtg cct gct gat gcc      491
Trp Ala Ala Arg Arg Gly Ala Gln Pro His Pro Val Pro Ala Asp Ala
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cac agg gga gcc agg ctg gct gcc gcc tcg ctg tgg ccg gat gga ggg      539
His Arg Gly Ala Arg Leu Ala Ala Ala Ser Leu Trp Pro Asp Gly Gly
         65                  70                  75

tgg cag ggc aac ctc aca tac caa ggc ccc tcc cca cca tcg gtt gcc      587
Trp Gln Gly Asn Leu Thr Tyr Gln Gly Pro Ser Pro Pro Ser Val Ala
     80                  85                  90

cca gga cac agt gag ggc ctg ggg gca gcc act gac gcc cat gcc ttc      635
Pro Gly His Ser Glu Gly Leu Gly Ala Ala Thr Asp Ala His Ala Phe
 95                 100                 105                 110

ctt tat cta agc tgg cag agg cag gga gag aga aac cac tca aaa aca      683
Leu Tyr Leu Ser Trp Gln Arg Gln Gly Glu Arg Asn His Ser Lys Thr
                115                 120                 125

gga atg gtt ctt tct ggg cct cct ggg aca ggg gcc cag gcc aag gtg      731
Gly Met Val Leu Ser Gly Pro Pro Gly Thr Gly Ala Gln Ala Lys Val
            130                 135                 140

ggg tgc agg agg aaa cag gcg cac cag agt cag ggt ggg ggc agg gca      779
Gly Cys Arg Arg Lys Gln Ala His Gln Ser Gln Gly Gly Gly Arg Ala
        145                 150                 155

gcc ccc cca ggg gtc agg cag ctg tgt ctc ccc aca ctg gct ccc cag      827
Ala Pro Pro Gly Val Arg Gln Leu Cys Leu Pro Thr Leu Ala Pro Gln
    160                 165                 170

tat tct gga aaa ggg gta cag gag gcc gat agg aag tca ctg ggc cca      875
Tyr Ser Gly Lys Gly Val Gln Glu Ala Asp Arg Lys Ser Leu Gly Pro
175                 180                 185                 190

aag tgt ctc ccc acc agc cag gtg aag acc act ctg aca gag gct cca      923
Lys Cys Leu Pro Thr Ser Gln Val Lys Thr Thr Leu Thr Glu Ala Pro
                195                 200                 205

ggg act ata cca gtc ccc ctg ttc ctc ctt ccc cta ccc cca cca ttc      971
Gly Thr Ile Pro Val Pro Leu Phe Leu Leu Pro Leu Pro Pro Pro Phe
            210                 215                 220

ctt cct aac aca gag ttg cac ccc cat ccc cat tct cca aac cct gga     1019
Leu Pro Asn Thr Glu Leu His Pro His Pro His Ser Pro Asn Pro Gly
        225                 230                 235

cta cca tat tcc ccc ttc cct cca ata cat ctt ata ggg ctg ctg ggt     1067
Leu Pro Tyr Ser Pro Phe Pro Pro Ile His Leu Ile Gly Leu Leu Gly
    240                 245                 250

aca gtt gtt cag gct gtg cac tgc aca agg gca cct tgt cca agg aga     1115
Thr Val Val Gln Ala Val His Cys Thr Arg Ala Pro Cys Pro Arg Arg
255                 260                 265                 270
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cac cac ttt cac cca aac ttg tat att tat tac aat ttt ctg cat ctt      1163
His His Phe His Pro Asn Leu Tyr Ile Tyr Tyr Asn Phe Leu His Leu
                275                 280                 285

gag gaa ggg gcg tca ttt tcc tgt tcg cac aaa ggc acc aca ggg gct      1211
Glu Glu Gly Ala Ser Phe Ser Cys Ser His Lys Gly Thr Thr Gly Ala
            290                 295                 300

aac agt ggg cct gca atc tta gat ccc atc ctt gcc ttc ttc gag gga      1259
Asn Ser Gly Pro Ala Ile Leu Asp Pro Ile Leu Ala Phe Phe Glu Gly
        305                 310                 315

tct ctt ggg acc ctc ctg gtt tta act ggg agg ccc aga cca act cct      1307
Ser Leu Gly Thr Leu Leu Val Leu Thr Gly Arg Pro Arg Pro Thr Pro
    320                 325                 330

ttc ctg caa acc acc ctc caa ggc ctg tcc cac acg atc aag gca ggg      1355
Phe Leu Gln Thr Thr Leu Gln Gly Leu Ser His Thr Ile Lys Ala Gly
335                 340                 345                 350

aaa gat agg cag gag tcc cct cac gaa gtc ctc aag tcc tgg ccc ctc      1403
Lys Asp Arg Gln Glu Ser Pro His Glu Val Leu Lys Ser Trp Pro Leu
                355                 360                 365

tgg cgc tct gga agc ggt act gta tct ctc tcc aag gcc tgg tca agc      1451
Trp Arg Ser Gly Ser Gly Thr Val Ser Leu Ser Lys Ala Trp Ser Ser
            370                 375                 380

act aag tgc att tac aaa tct ctg aga atg ttt ttt tta tac taa aat      1499
Thr Lys Cys Ile Tyr Lys Ser Leu Arg Met Phe Phe Leu Tyr  *
        385                 390                 395

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gcggcggggg gaggagggag aggagggccg agccggcggc acgggaggcc cggttttgaa    120

gccgcttctc tgcccgagtt aggtttcgcc cagcgcaatt tctttctcta tgtactttgc    180

gaataagttt cggagcatcg gttaacagcc tatgggtgaa atttggcttt cattcatgaa    240
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tgagaaatta ttcttgacag aagtatttta aaagaaaaat ctttacg  atg gcc tca      296
                                                     Met Ala Ser
                                                      1

gca gta ctt agt tct gtt ccc acc acc gct tct cgt ttt gcc ctg tta       344
Ala Val Leu Ser Ser Val Pro Thr Thr Ala Ser Arg Phe Ala Leu Leu
      5                  10                  15

caa gtg gat agt ggc agt ggc tct gat tct gaa cct gga aaa ggt aaa       392
Gln Val Asp Ser Gly Ser Gly Ser Asp Ser Glu Pro Gly Lys Gly Lys
 20                  25                  30                  35

ggt cga aat act gga aag tct caa act tta gga agc aag tca act aca       440
Gly Arg Asn Thr Gly Lys Ser Gln Thr Leu Gly Ser Lys Ser Thr Thr
                 40                  45                  50

aat gag aaa aaa aga gag aaa aga aga aaa aag aag gaa cag caa cag       488
Asn Glu Lys Lys Arg Glu Lys Arg Arg Lys Lys Lys Glu Gln Gln Gln
             55                  60                  65

agt gaa gca aat gag ctc agg aat ctt gct ttt aag aaa att ccc cag       536
Ser Glu Ala Asn Glu Leu Arg Asn Leu Ala Phe Lys Lys Ile Pro Gln
         70                  75                  80

aaa tcc tcc cat gct gtt tgt aac gct caa cat gat ctt cca ttg tca       584
Lys Ser Ser His Ala Val Cys Asn Ala Gln His Asp Leu Pro Leu Ser
     85                  90                  95

aac cca gta cag aag gat tca cga gaa gaa aat tgg caa gag tgg aga       632
Asn Pro Val Gln Lys Asp Ser Arg Glu Glu Asn Trp Gln Glu Trp Arg
100                 105                 110                 115

caa aga gat gag cag ctg aca tct gaa atg ttt gaa gca gat ctt gag       680
Gln Arg Asp Glu Gln Leu Thr Ser Glu Met Phe Glu Ala Asp Leu Glu
                120                 125                 130

aag gca ttg tta cta agt aaa cta gaa tat gaa gag cac aaa aag gag       728
Lys Ala Leu Leu Leu Ser Lys Leu Glu Tyr Glu Glu His Lys Lys Glu
            135                 140                 145

tat gaa gat gct gaa aat act tca act cag tcc aaa gtt atg aat aaa       776
Tyr Glu Asp Ala Glu Asn Thr Ser Thr Gln Ser Lys Val Met Asn Lys
        150                 155                 160

aaa gat aaa aga aag aat cat cag gga aaa gac aga cct ctc aca gta       824
Lys Asp Lys Arg Lys Asn His Gln Gly Lys Asp Arg Pro Leu Thr Val
    165                 170                 175

tca cta aaa gat ttt cat tcg gaa gat cac att agt aaa aag act gag       872
Ser Leu Lys Asp Phe His Ser Glu Asp His Ile Ser Lys Lys Thr Glu
180                 185                 190                 195

gaa gtg gtt ctg aaa gat gga aga att gaa aga cta aag tta gag ctt       920
Glu Val Val Leu Lys Asp Gly Arg Ile Glu Arg Leu Lys Leu Glu Leu
                200                 205                 210

gaa agg aaa gat gct gaa atc cag aag ctg aaa aat gta atc act caa       968
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Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val Ile Thr Gln
            215                 220                 225

tgg gag gca aag tat aag gaa gta aag gca aga aat gca caa tta ttg     1016
Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala Gln Leu Leu
        230                 235                 240

aaa atg ctt cag gaa ggt gaa atg aaa gat aag gca gaa ata ctt ctg     1064
Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu Ile Leu Leu
    245                 250                 255

caa gtt gat gaa tca caa agt atc aag aat gag ctc act att cag gtg     1112
Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr Ile Gln Val
260                 265                 270                 275

act tca ctt cat gct gca tta gaa caa gaa aga tct aaa gtg aaa gta     1160
Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys Val Lys Val
                280                 285                 290

tta caa gca gag tta gcc aaa tac cag ggt ggc aga aaa ggg aaa aga     1208
Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys Gly Lys Arg
            295                 300                 305

aac tct gaa tcc gac cag tgt agg tga ttaca ttagcctttg aagtcaacac     1260
Asn Ser Glu Ser Asp Gln Cys Arg  *
        310                 315

aaagtttaaa acttccagga ttttgcaaag ttgtatatat ttaatgctgt gcaactgcta   1320

aactatgcag tttttgttga aggaactaaa agcaactagc tccctaatgg tctataattt   1380

tatttctttt ggcttaaagt gaaaaagaag aatagagatt ccagcagatt cagtggtggt   1440

cactatccaa cttctatcac ttg                                           1463




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     <212> DNA
     <213> Homo sapiens

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tctacagtta tgccccaata gtagccaaag gaaaaagggg gaagatgata gtttgactaa    120

acaaatacca gttcatacat tcttgttcca ataggagtt  atg gga gga aaa att      174
                                            Met Gly Gly Lys Ile
                                             1               5

att cca agc aat cac aca gga tca act ttt tct cct tgt aga ata tgt      222
```

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Ile Pro Ser Asn His Thr Gly Ser Thr Phe Ser Pro Cys Arg Ile Cys
                 10                  15                  20

gtc atc aca ttg gca gaa tct cat cca gtt ctt caa agt gga aaa aca        270
Val Ile Thr Leu Ala Glu Ser His Pro Val Leu Gln Ser Gly Lys Thr
             25                  30                  35

att aaa agc att tcc tat cag atc agt acc aac tgt agc aga ctt cag        318
Ile Lys Ser Ile Ser Tyr Gln Ile Ser Thr Asn Cys Ser Arg Leu Gln
         40                  45                  50

aac aag gtc tct ggg aaa ttt aag cgg gta tgt tcc tgt aat tct gtg        366
Asn Lys Val Ser Gly Lys Phe Lys Arg Val Cys Ser Cys Asn Ser Val
     55                  60                  65

att atc tac tta cat cct cta tat tca tgg taa tgacagat ccaatgaacc        417
Ile Ile Tyr Leu His Pro Leu Tyr Ser Trp  *
 70                  75                  80

ttagaatcca gtagcatatg cttagcatac ttctctagca gtttgaggtg ctaattttag      477

gtatactttc acctaaagaa attctcagct cccccaaatt aggtatctca ggaggtgtag      537

tatctgttat attaggttct gtgctactat ccctataatg cccaggatgg aggaggggga      597

aggcaggcct ttgaaaggag aactctaata gcaatataac aagatatttt gtcccttcta      657

gttgtattaa actagtatgt cgagttctgt aaaatttagg tgactaactc ttctttacca      717

tatatttcca catgtaaatt aaacagaaaa aaaa                                  751



     <210> 210
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     <213> Homo sapiens

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gctgtgtgac atcaatgggg atctcttccc ccgtccgggc cctaagtctg gggccaggaa      120

aaagaagggt ctgcattttt gctttgcaac tctaaaagca gcagaatcct ttttttaaaa      180

aggtacttat gggcacctca ccatataaaa ccgataaaag catacctctt ctggttaagg      240

tggggaggat cctcgagctc cctgaattgt ccttttaccc tgtctccccc tccccccttgt      300

ccctcatggc accttaaaga tctctgagtc cctccagttc tcaagtttaa ggactctact      360

accatggtaa gagctggtcc agcctcagtt tccacaatgc ttttggccac tcgaatccag      420
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cctaacaagc acgcagttcc tgatgattgg cctcaggtcc cagagagctc cagcaggtgt    480

aggagtccat gggcctgaca cctttgctgg tctctgctgg atcccgacga agtcaggtcc    540

tttctggaaa ggggttcgaa gtccacatac tctccgcact acccccagga agtacgtcct    600

tgggtgtgtg tttgggggag tgagaggaat gaagaaccac tccccctata gcctggccat    660

actccccaag atgagggcag taaggtgctg aggaccctgg aagtaacttg cttttctcaa    720

cttctcagga gaaggccatc agcatttggg agtcaaagaa tttctttttt gaacttgagc    780

ctctgccagg ggccgtggaa gctgtcaagg ag  atg gcc agc cta caa aac act     833
                                     Met Ala Ser Leu Gln Asn Thr
                                       1               5

gac gtc ttc atc tgc aca agc ccc atc aag atg ttc aag tac tgt ccc      881
Asp Val Phe Ile Cys Thr Ser Pro Ile Lys Met Phe Lys Tyr Cys Pro
          10                 15                  20

tat gag aag tat gcc tgg gtg gag aag tac ttt ggc cct gac ttt ctg      929
Tyr Glu Lys Tyr Ala Trp Val Glu Lys Tyr Phe Gly Pro Asp Phe Leu
     25                  30                  35

gag cag att gtg ctg acc aga gac aag acc gtg gtc tct gct gac ctt      977
Glu Gln Ile Val Leu Thr Arg Asp Lys Thr Val Val Ser Ala Asp Leu
 40                  45                  50                  55

ctc ata gac gac cgg ccg gac atc aca ggg gcc gag cca acc ccc agc     1025
Leu Ile Asp Asp Arg Pro Asp Ile Thr Gly Ala Glu Pro Thr Pro Ser
                 60                  65                  70

tgg gag cat gtc ctc ttc acc gcc tgc cac aac cag cac ctg cag ctg     1073
Trp Glu His Val Leu Phe Thr Ala Cys His Asn Gln His Leu Gln Leu
             75                  80                  85

cag ccc ccc cgc cgc agg ctg cac tcg tgg gcg gac gac tgg aag gcc     1121
Gln Pro Pro Arg Arg Arg Leu His Ser Trp Ala Asp Asp Trp Lys Ala
         90                  95                 100

att ctg gac agc aag cgg ccc tgc tga gctgg actgtgcttc gggctcctct     1173
Ile Leu Asp Ser Lys Arg Pro Cys  *
    105                 110

gtggggctct gacctcaggg ctcccagctc ggggcctgtg gggccagtat gctggtctgg   1233

gagtccctcc tagactcctg ggccccatga cctcctgctg catgtccctt cccttcccca   1293

gcccctgcca ggccttaacc tgatcacggg gcagggctgg gccctctggg cgcttggaca   1353

taacaacgtg gtcccaggcc gttcagcctg acctcaggca gcaggcacca agctgccaga   1413

agcccagggg ctcaggacaa ggaggagttt aggccactgt tcagggggct ggtggccgtc   1473

ttcactccct aaggcaagtt ttttaggca aaagggggtt ccctgttccc aaagtttgca    1533
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gccatcagca aggaggacca ggaacccggc gattgaggtg cttccaggtg gggacaagcc   1593

ccttttggtt tcagccacag cacccсttat tccaggtgcc ctgcccaacc tgctcacccc   1653

acatgacctt ttgtgtattc agcaaaccct cattaggtga cagcggcccc caggctttgt   1713

gctgggggac gatactggcc ctggcctcga ccagcttaaa ggtttttcac acctttgttc   1773

ccagggcccc gctcagggcc cagcaaaaag tccgtaggct tgaacatgtg ttgagggcat   1833

gaaaaataaa tgctgttcat gtgtgtagct caaaaaaaaa aaa                      1876



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     <211> 3051
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (527)..(2308)

     <400> 211
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caagcactgg catgtggccc tcccagaccg ggtcacaaga cgccagtgca agtgctggtt    120

aaccaggggt gctaaaaata accaggccca aatggaccag aagcaactcc catggacttt    180

ggcttgcagt catggtcaga agagatacag gcacagatcc cactattacg aaggagccaa    240

aatatctgcc aagataaaaa tggaagtaac tcctctggat ttatgtgtcc aggggtggat    300

atggaaagac ttgtgaagta ttaatcaaaa atcacccgag gctttttcag actattattc    360

aaatgacaca gaatgaagac ctccgagaaa acatgtacgg caagttctgg agcatttgtc    420

tcagcacagt gaaagccagt acctaaagat tctaacaagc cttgctgaag ttgctacaac    480

aaatggtcat aaactgctta gcctctctag caattatgat gctcaa   atg aag agc      535
                                                     Met Lys Ser
                                                       1

ctt tta agg att gtg aga atg ttt tgt cac gtc ttt cga att ggt cca      583
Leu Leu Arg Ile Val Arg Met Phe Cys His Val Phe Arg Ile Gly Pro
      5                  10                  15

tcc tcc ccc agt aat gga att gat atg ggc tac aat ggg aat aaa act      631
Ser Ser Pro Ser Asn Gly Ile Asp Met Gly Tyr Asn Gly Asn Lys Thr
 20                  25                  30                  35

cca aaa agc cag gtg ttc aag cct ctg gaa ttg ctt tgg cac tcg tta      679
Pro Lys Ser Gln Val Phe Lys Pro Leu Glu Leu Leu Trp His Ser Leu
                 40                  45                  50
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gat gaa tgg cta gtt tta ata gcc cca gaa ttg atg aaa aac aaa aga      727
Asp Glu Trp Leu Val Leu Ile Ala Pro Glu Leu Met Lys Asn Lys Arg
            55                  60                  65

gac tca aca gag atc act tct att tta ctg aaa caa aaa ggc caa gat      775
Asp Ser Thr Glu Ile Thr Ser Ile Leu Leu Lys Gln Lys Gly Gln Asp
        70                  75                  80

caa gat gct gct tcc att cct cca ttt gaa cct cca gga cct ggg agc      823
Gln Asp Ala Ala Ser Ile Pro Pro Phe Glu Pro Pro Gly Pro Gly Ser
    85                  90                  95

tat gaa aat ctg tcc act ggc aca agg gaa tct aaa cca gat gct ctt      871
Tyr Glu Asn Leu Ser Thr Gly Thr Arg Glu Ser Lys Pro Asp Ala Leu
100                 105                 110                 115

gca ggg aga cag gaa gcc agt gca gat tgt cag gat gtt att tct atg      919
Ala Gly Arg Gln Glu Ala Ser Ala Asp Cys Gln Asp Val Ile Ser Met
                120                 125                 130

aca gct aac cgg cta agt gct gtc att caa gct ttt tac atg tgc tgt      967
Thr Ala Asn Arg Leu Ser Ala Val Ile Gln Ala Phe Tyr Met Cys Cys
            135                 140                 145

tct tgt cag atg cct ccg gga atg act tca cct cgt ttc att gaa ttt     1015
Ser Cys Gln Met Pro Pro Gly Met Thr Ser Pro Arg Phe Ile Glu Phe
        150                 155                 160

gtc tgc aaa cat gat gaa gtt tta aaa tgc ttt gtt aat aga aat ccc     1063
Val Cys Lys His Asp Glu Val Leu Lys Cys Phe Val Asn Arg Asn Pro
    165                 170                 175

aaa att ata ttt gac cac ttt cac ttt ctc ctt gaa tgt cct gag ttg     1111
Lys Ile Ile Phe Asp His Phe His Phe Leu Leu Glu Cys Pro Glu Leu
180                 185                 190                 195

atg tca aga ttc atg cat atc ata aaa gca cag cct ttt aaa gat cgc     1159
Met Ser Arg Phe Met His Ile Ile Lys Ala Gln Pro Phe Lys Asp Arg
                200                 205                 210

tgt gaa tgg ttc tat gaa cat ttg cat tca gga cag cca gat tca gat     1207
Cys Glu Trp Phe Tyr Glu His Leu His Ser Gly Gln Pro Asp Ser Asp
            215                 220                 225

atg gtg cac agg cca gtg aat gaa aat gat atc ctg ctg gtt cac aga     1255
Met Val His Arg Pro Val Asn Glu Asn Asp Ile Leu Leu Val His Arg
        230                 235                 240

gat tct att ttt agg agt agc tgt gaa gtt gtg tca aaa gca aat tgt     1303
Asp Ser Ile Phe Arg Ser Ser Cys Glu Val Val Ser Lys Ala Asn Cys
    245                 250                 255

gca aag cta aag caa ggg att gct gta cgg ttc cat gga gaa gaa ggc     1351
Ala Lys Leu Lys Gln Gly Ile Ala Val Arg Phe His Gly Glu Glu Gly
260                 265                 270                 275

atg ggt caa ggt gtt gtg cgt gag tgg ttt gat att ctg tcc aat gag     1399
```

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Met Gly Gln Gly Val Val Arg Glu Trp Phe Asp Ile Leu Ser Asn Glu
                280                 285                 290

ata gtc aat cct gat tat gca ttg ttt acc cag tca gct gat gga aca      1447
Ile Val Asn Pro Asp Tyr Ala Leu Phe Thr Gln Ser Ala Asp Gly Thr
            295                 300                 305

act ttt cag cct aat agc aac tct tat gta aat cct gat cac ttg aac      1495
Thr Phe Gln Pro Asn Ser Asn Ser Tyr Val Asn Pro Asp His Leu Asn
        310                 315                 320

tat ttt cgg ttt gct ggg cag atc ttg gga tta gcg ttg aac cac agg      1543
Tyr Phe Arg Phe Ala Gly Gln Ile Leu Gly Leu Ala Leu Asn His Arg
    325                 330                 335

cag ctg gtc aat att tac ttc aca cga tcc ttc tac aag cac att ctt      1591
Gln Leu Val Asn Ile Tyr Phe Thr Arg Ser Phe Tyr Lys His Ile Leu
340                 345                 350                 355

ggt att cct gta aat tac caa gat gtg gca tcc att gat cca gaa tat      1639
Gly Ile Pro Val Asn Tyr Gln Asp Val Ala Ser Ile Asp Pro Glu Tyr
                360                 365                 370

gcg aaa aat ttg caa tgg att tta gat aat gat ata agt gat ctg ggt      1687
Ala Lys Asn Leu Gln Trp Ile Leu Asp Asn Asp Ile Ser Asp Leu Gly
            375                 380                 385

cta gaa cta act ttt tct gtt gag act gat gtg ttt gga gca atg gaa      1735
Leu Glu Leu Thr Phe Ser Val Glu Thr Asp Val Phe Gly Ala Met Glu
        390                 395                 400

gag gtg cct ttg aaa cct ggg ggt ggg agt att ctt gtg aca caa aat      1783
Glu Val Pro Leu Lys Pro Gly Gly Gly Ser Ile Leu Val Thr Gln Asn
    405                 410                 415

aat aaa gcg gag tac gtc cag ctt gtt act gaa ctt cga atg aca aga      1831
Asn Lys Ala Glu Tyr Val Gln Leu Val Thr Glu Leu Arg Met Thr Arg
420                 425                 430                 435

gcc att cag cct cag atc aat gct ttt tta cag ggc ttt cat atg ttc      1879
Ala Ile Gln Pro Gln Ile Asn Ala Phe Leu Gln Gly Phe His Met Phe
                440                 445                 450

att cca ccc tcc ctc ata cag ctt ttt gat gaa tat gaa ttg gag cta      1927
Ile Pro Pro Ser Leu Ile Gln Leu Phe Asp Glu Tyr Glu Leu Glu Leu
            455                 460                 465

ctg ctt tct ggc atg cca gaa att gat gtg agt gat tgg ata aaa aat      1975
Leu Leu Ser Gly Met Pro Glu Ile Asp Val Ser Asp Trp Ile Lys Asn
        470                 475                 480

aca gaa tac aca agt ggc tat gaa aga gaa gat cca gtt att cag tgg      2023
Thr Glu Tyr Thr Ser Gly Tyr Glu Arg Glu Asp Pro Val Ile Gln Trp
    485                 490                 495

ttc tgg gaa gtt gta gaa gac att act caa gag gag aga gtt ctt ctc      2071
Phe Trp Glu Val Val Glu Asp Ile Thr Gln Glu Glu Arg Val Leu Leu
```

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500                 505                 510                 515

tta cag ttt gtt acg ggc agt tcc agg gtc cca cat ggt ggg ttt gct      2119
Leu Gln Phe Val Thr Gly Ser Ser Arg Val Pro His Gly Gly Phe Ala
                520                 525                 530

aat atc atg ggt gga agt gga ttg caa aac ttt aca atc gct gct gtg      2167
Asn Ile Met Gly Gly Ser Gly Leu Gln Asn Phe Thr Ile Ala Ala Val
            535                 540                 545

cca tat act cca aat ctt tta cca act tca agc aca tgc atc aac atg      2215
Pro Tyr Thr Pro Asn Leu Leu Pro Thr Ser Ser Thr Cys Ile Asn Met
        550                 555                 560

ctc aag tta cct gaa tac cca agt aaa gaa ata ctc aag gac aga ctt      2263
Leu Lys Leu Pro Glu Tyr Pro Ser Lys Glu Ile Leu Lys Asp Arg Leu
    565                 570                 575

ctt gtg gca cta cat tgt ggc agc tat ggt tac aca atg gca taa tga      2311
Leu Val Ala Leu His Cys Gly Ser Tyr Gly Tyr Thr Met Ala  *
580                 585                 590

agtctggaaa actcctctga ctactgatgc acaattcaga atggcagaag taatttggga   2371

aaatgtcaac aaaaaagcag cctaaatgca acccataggc agggctgatg cttccaattt   2431

ataaaggatc atcaggtttt ctgtttctct cttttccctt ttatgttttc tctgtttgta   2491

tacaattaga aaatataaaa tcacagtaga ttttattttt taaaatgcta actgaaagta   2551

atagagactg tcctttttca taattaattt tatccaagat tgtattaagg caaaatctga   2611

ttctacattc cacctctgct atgtaactgt cttgttaaaa gggtgttttc tcctaatttc   2671

tgatatatta tatgaggtca tccagctggt gtgttctttt gcatgtaaac tgccatttat   2731

attttagaaa actattgtat agaatggatt tagattgtct ataaagccac aaatacgtat   2791

tttgccacag tgtattctat attgcaatga ttttttagc attttaatat tttaatatat    2851

attgtaaaat ttagactgat gatactaaca gttgatgaaa tgacatataa tttatatatg   2911

aaagcttacg ctatattgta tgaattattt gcatctttca gtggccagtt ttccatatgt   2971

atatattatg gtctcaatgt ttttcttacg cctcatttta atttataatg aaggtaaaat   3031

taaaatgtaa aaaaaaaaaa                                                3051


      <210> 212
      <211> 1435
      <212> DNA
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      <220>
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     <222> (1)...(1435)
     <223> n = a,t,c or g

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ccccaagtgt agatatactc ggggcatcat atgcttcctg tgccatcgag cccncgtctg      60

ggtgtacacg agtggagaac tgacacaggc gcctgcaaat cagccgggag ttcctggcct     120

tggctcctcc tccagcccct tggctctctg ctgctccccc cggggcagga gaaagaagga     180

aagagggcca ggggtcccct gccccaccac tttccatgat gacaagagat gggaaggtag     240

ccaggcagca acagtgtacg gcgacattgg agcggacctc acggcgacct caatttccac     300

tgcgcctcct cccagagctt aagaagctgc aggcctgtgg tgcccagcac caagtgcaga     360

tggacacggg tcttcatccc cttccttggc accttccatt taagccaaac attagaaatg     420

taaagaaggg cttgtttctg gagtttccag tttgttccat tcatctactc agagcatctt     480

ctttggacaa cactgtctgc agctgtgggc ccactccaag gggaggcgat ggactgtagg     540

tctgtggagc tcagcacagg gctgtgccac ggacgcgggt gtcagtgaag tcacgcgcat     600

tttcagatgg aattctcctc cccgatgtga aca atg aac gac ggt gtc act ttc      654
                                     Met Asn Asp Gly Val Thr Phe
                                      1               5

ata gga ttg tcc tgg agc cca cgg aga cgc ggg ctt ggg att caa cgt       702
Ile Gly Leu Ser Trp Ser Pro Arg Arg Arg Gly Leu Gly Ile Gln Arg
        10                  15                  20

gat gct gag cgg atc ttc tct gct tca gac cag gcc tca tgt ggc ttc       750
Asp Ala Glu Arg Ile Phe Ser Ala Ser Asp Gln Ala Ser Cys Gly Phe
    25                  30                  35

act att cat cca cac ata gat gct gca gag aca ctg agg gga ctc aca       798
Thr Ile His Pro His Ile Asp Ala Ala Glu Thr Leu Arg Gly Leu Thr
40                  45                  50                  55

aat gca cct gtg cag aag gtg tca acg tgg aca aac aca ggc agg gaa       846
Asn Ala Pro Val Gln Lys Val Ser Thr Trp Thr Asn Thr Gly Arg Glu
                60                  65                  70

act ccc atg agc ccg tgt gcc aca tgc agt gag gga act ttg gtg gct       894
Thr Pro Met Ser Pro Cys Ala Thr Cys Ser Glu Gly Thr Leu Val Ala
            75                  80                  85

gag tct ggg cgg ggg tgg gct ggg ggc tca atc gat ttc cac cga gtg       942
Glu Ser Gly Arg Gly Trp Ala Gly Gly Ser Ile Asp Phe His Arg Val
        90                  95                  100
```

```
tgt ctc caa atc ttt gct gga agt gca ggc aag ggg caa ggc ttg gac        990
Cys Leu Gln Ile Phe Ala Gly Ser Ala Gly Lys Gly Gln Gly Leu Asp
    105                 110                 115

acc agc gtc gct gtt cct cca ggc tgg gct gat ccc ttt tta ttt cca       1038
Thr Ser Val Ala Val Pro Pro Gly Trp Ala Asp Pro Phe Leu Phe Pro
120                 125                 130                 135

agt cac agg agc ctg ttc cct gaa atc ctg ggg aag tgt ggt gag gtg       1086
Ser His Arg Ser Leu Phe Pro Glu Ile Leu Gly Lys Cys Gly Glu Val
                140                 145                 150

gcc ccg tgc cgt cga atc ccc atc ctg gtt tac tga agtg cagaagtgac       1136
Ala Pro Cys Arg Arg Ile Pro Ile Leu Val Tyr  *
            155                 160

ataagtgctt gtgaatcagc agggagctct tggctttgac tccctgtgca gatgagccca     1196

gggcgccagc tccttgctgg agaactcctt tgtccatttg cacgtatgga tctttcctca     1256

ctgcttgatg ttttgaactc tcttctttgc ggttattaat gagatactca aaggtggtca     1316

tcttcttggc ctctatttca gccacgagct tccatggagg ggccaaactc tccatgcttc     1376

tttccctaaa caccaacacc gtgagagccg atgtcttgtg actatttctg gagactggg      1435



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      <213> Homo sapiens

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      <222> (469)..(1380)

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ccatagatgc ctgtcgcctg caggttcggg tccggtattc ccgggtcgac ccacgcgtcc       60

gaaaaaaaaa gaaaaaatat atattatata ttaaatggcg aaaatggtaa attttatgtt      120

atgtgtattt caccacaatt taagaaatat gtaatttgag gcttggagaa tttaattaag      180

tgatttatct gatgttaact tacagctgat acatggtaga gctgcatttt aatctcagtc      240

atctggctct ttttaaaaca attacagaga aaactttatt ttgggccatt taggaggttt      300

agatcatttt gatcatcttc agctgtcttc tcttcacata caggaaaggc cttggaaagc      360

agtcgttgcg ccagacagcc cagggaagag cggcagcctg aggacctagg gccacctgct      420

gttccctggg attcatgtcc ttctggggag gagggaggac ccaggaca atg gct gct       477
                                                     Met Ala Ala
                                                      1
```

```
gtt cat gat ctg gag atg gag agc atg aat ctg aat atg ggg aga gag        525
Val His Asp Leu Glu Met Glu Ser Met Asn Leu Asn Met Gly Arg Glu
      5                  10                  15

atg aaa gaa gag ctg gag gaa gag gag aaa atg aga gag gat ggg gga        573
Met Lys Glu Glu Leu Glu Glu Glu Glu Lys Met Arg Glu Asp Gly Gly
 20                  25                  30                  35

ggt aaa gat cgg gcc aag agt aaa aag gtc cac agg att gtc tca aaa        621
Gly Lys Asp Arg Ala Lys Ser Lys Lys Val His Arg Ile Val Ser Lys
                 40                  45                  50

tgg atg ctg ccc gaa aag tcc cga gga aca tac ttg gag aga gct aac        669
Trp Met Leu Pro Glu Lys Ser Arg Gly Thr Tyr Leu Glu Arg Ala Asn
             55                  60                  65

tgc ttc ccg cct ccc gtg ttc atc atc tcc atc agc ctg gcc gag ctg        717
Cys Phe Pro Pro Pro Val Phe Ile Ile Ser Ile Ser Leu Ala Glu Leu
         70                  75                  80

gca gtg ttt att tac tat gct gtg tgg aag cct cag aaa cag tgg atc        765
Ala Val Phe Ile Tyr Tyr Ala Val Trp Lys Pro Gln Lys Gln Trp Ile
     85                  90                  95

acg ttg gac aca ggc atc ttg gag agt ccc ttt atc tac agt cct gag        813
Thr Leu Asp Thr Gly Ile Leu Glu Ser Pro Phe Ile Tyr Ser Pro Glu
100                 105                 110                 115

aag agg gag gaa gcc tgg agg ttt atc tca tac atg ctg gta cat gct        861
Lys Arg Glu Glu Ala Trp Arg Phe Ile Ser Tyr Met Leu Val His Ala
                120                 125                 130

gga gtt cag cac atc ttg ggg aat ctt tgt atg cag ctt gtt ttg ggt        909
Gly Val Gln His Ile Leu Gly Asn Leu Cys Met Gln Leu Val Leu Gly
            135                 140                 145

att ccc ttg gaa atg gtc cac aaa ggc ctc cgt gtg ggg ctg gtg tac        957
Ile Pro Leu Glu Met Val His Lys Gly Leu Arg Val Gly Leu Val Tyr
        150                 155                 160

ctg gca gga gtg att gca ggg tcc ctt gcc agc tcc atc ttt gac cca       1005
Leu Ala Gly Val Ile Ala Gly Ser Leu Ala Ser Ser Ile Phe Asp Pro
    165                 170                 175

ctc aga tat ctt gtg gga gct tca gga gga gtc tat gct ctg atg gga       1053
Leu Arg Tyr Leu Val Gly Ala Ser Gly Gly Val Tyr Ala Leu Met Gly
180                 185                 190                 195

ggc tat ttt atg aat gtt ctg gtg aat ttt caa gaa atg att cct gcc       1101
Gly Tyr Phe Met Asn Val Leu Val Asn Phe Gln Glu Met Ile Pro Ala
                200                 205                 210

ttt gga att ttc aga ctg ctg atc atc atc ctg ata att gtg ttg gac       1149
Phe Gly Ile Phe Arg Leu Leu Ile Ile Ile Leu Ile Ile Val Leu Asp
            215                 220                 225

atg gga ttt gct ctc tat aga agg ttc ttt gtt cct gaa gat ggg tct       1197
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Met Gly Phe Ala Leu Tyr Arg Arg Phe Phe Val Pro Glu Asp Gly Ser
        230                 235                 240

ccg gtg tct ttt gca gct cac att gca ggt gga ttt gct gga atg tcc      1245
Pro Val Ser Phe Ala Ala His Ile Ala Gly Gly Phe Ala Gly Met Ser
    245                 250                 255

att ggc tac acg gtg ttt agc tgc ttt gat aaa gca ctg atg aaa gat      1293
Ile Gly Tyr Thr Val Phe Ser Cys Phe Asp Lys Ala Leu Met Lys Asp
260                 265                 270                 275

cca agg ttt tgg ata gca att gct gca tat tta gct tgt gtc tta ttt      1341
Pro Arg Phe Trp Ile Ala Ile Ala Ala Tyr Leu Ala Cys Val Leu Phe
                280                 285                 290

gct gtg ttt ttc aac att ttc cta tct cca gca aac tga cctgccccta       1390
Ala Val Phe Phe Asn Ile Phe Leu Ser Pro Ala Asn  *
            295                 300

ttgtaagtca attaataaaa agagccatct ggaggaaata ataaaaaaaa ggaagactct    1450

atgaagaaac agagaagtct cagcaaaggc taacaatttt atatagagga caaaacagca    1510

ttaaactcat cagttgcaaa gattgcctat aaaaggacct taggatttaa ggaaggggct    1570

tcttaatgta gaaagggaaa aaaaaaaaaa                                      1600




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ttgaaaaagc tgcatgcagt tggaagggat cttcagatgg tgctggtgac tttctgttcc     120

ttttggagtt gacatgcatg tggattggag gaaaaataat caacatatat tctcctttcg     180

tactgtttaa atcacaggaa gaagcggctt taagacaaag atcaaaccaa a atg aca      237
                                                         Met Thr
                                                         1

act gct cac ttt tac tgt caa tac tgc aca gca tca ctt ctt ggg aag      285
Thr Ala His Phe Tyr Cys Gln Tyr Cys Thr Ala Ser Leu Leu Gly Lys
        5                   10                  15

aaa tat gta cta aag gat gac agt cca tac tgt gtt aca tgt tat gat      333
Lys Tyr Val Leu Lys Asp Asp Ser Pro Tyr Cys Val Thr Cys Tyr Asp
    20                  25                  30
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cgt gta ttt tct aac tat tgc gag gaa tgc aaa aaa cca att gaa tct       381
Arg Val Phe Ser Asn Tyr Cys Glu Glu Cys Lys Lys Pro Ile Glu Ser
 35                  40                  45                  50

gat tct aag gat ctt tgt tac aaa gac cgg cac tgg cat gaa gga tgc       429
Asp Ser Lys Asp Leu Cys Tyr Lys Asp Arg His Trp His Glu Gly Cys
                 55                  60                  65

ttc aag tgc acc aaa tgc aat cac tct ttg gtg gaa aag cct ttt gct       477
Phe Lys Cys Thr Lys Cys Asn His Ser Leu Val Glu Lys Pro Phe Ala
             70                  75                  80

gcc aag gat gag cgc ctg ctg tgc acg gag tgc tat tct aac gag tgc       525
Ala Lys Asp Glu Arg Leu Leu Cys Thr Glu Cys Tyr Ser Asn Glu Cys
         85                  90                  95

tcc tcc aag tgc ttc cac tgc aag agg acc atc atg cct ggt tcc cgc       573
Ser Ser Lys Cys Phe His Cys Lys Arg Thr Ile Met Pro Gly Ser Arg
    100                 105                 110

aaa atg gaa ttt aag gga aac tac tgg cat gaa acc tgt ttt gtg tgt       621
Lys Met Glu Phe Lys Gly Asn Tyr Trp His Glu Thr Cys Phe Val Cys
115                 120                 125                 130

gag aat tgc cga caa cct ata ggg aca aag cct ttg atc tcc aaa gag       669
Glu Asn Cys Arg Gln Pro Ile Gly Thr Lys Pro Leu Ile Ser Lys Glu
                135                 140                 145

agt ggc aat tat tgt gtg cca tgt ttt gag aag gag ttt gct cac tac       717
Ser Gly Asn Tyr Cys Val Pro Cys Phe Glu Lys Glu Phe Ala His Tyr
            150                 155                 160

tgc aac ttt tgt aag aag gtg ata act tca ggt ggg ata aca ttt tgt       765
Cys Asn Phe Cys Lys Lys Val Ile Thr Ser Gly Gly Ile Thr Phe Cys
        165                 170                 175

gac cag cta tgg cat aaa gag tgt ttt ctg tgt agt ggc tgt agg aaa       813
Asp Gln Leu Trp His Lys Glu Cys Phe Leu Cys Ser Gly Cys Arg Lys
    180                 185                 190

gat ctc tgt gaa gaa cag ttc atg tcc aga gac gac tat cca ttc tgc       861
Asp Leu Cys Glu Glu Gln Phe Met Ser Arg Asp Asp Tyr Pro Phe Cys
195                 200                 205                 210

atg gac tgc tac aac cat ctt tat gcc aac aag tgt gta gcc tgt tcc       909
Met Asp Cys Tyr Asn His Leu Tyr Ala Asn Lys Cys Val Ala Cys Ser
                215                 220                 225

aaa ccc att agt ggt ctc aca ggt gcc aag ttt atc tgc ttt caa gac       957
Lys Pro Ile Ser Gly Leu Thr Gly Ala Lys Phe Ile Cys Phe Gln Asp
            230                 235                 240

agc cag tgg cat agc gaa tgc ttt aac tgc ggg aaa tgc tct gtc tcc      1005
Ser Gln Trp His Ser Glu Cys Phe Asn Cys Gly Lys Cys Ser Val Ser
        245                 250                 255
```

ttg gtg ggt aaa ggc ttc ctg acc cag aac aag gaa atc ttc tgc caa 1053
Leu Val Gly Lys Gly Phe Leu Thr Gln Asn Lys Glu Ile Phe Cys Gln
260 265 270

aaa tgt ggc tcc gga atg gac act gac atc tag gagacagt ccttgcccac 1104
Lys Cys Gly Ser Gly Met Asp Thr Asp Ile *
275 280 285

ctaaaatcca ttttgccttc gttgtcacta aagccagaac tcaaaaaaaa aaaa 1158

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<220>
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<222> (1)..(1920)

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Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln Phe
1 5 10 15

ctc ctg ctg ctc ctg atg ctg gga tgc gtc ctg atg atg gtg gcg atg 96
Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val Ala Met
20 25 30

ttg cac cct ccc cac cac acc ctg cac cag act gtc aca gcc caa gcc 144
Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr Ala Gln Ala
35 40 45

agc aag cac agc cct gaa gcc agg tac cgc ctg gac ttt ggg gaa tcc 192
Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp Phe Gly Glu Ser
50 55 60

cag gat tgg gta ctg gaa gct gag gat gag ggt gaa gag tac agc cct 240
Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly Glu Glu Tyr Ser Pro
65 70 75 80

ctg gag ggc ctg cca ccc ttt atc tca ctg cgg gag gat cag ctg ctg 288
Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu Arg Glu Asp Gln Leu Leu
85 90 95

gtg gcc gtg gcc tta ccc cag gcc aga agg aac cag agc cag ggc agg 336
Val Ala Val Ala Leu Pro Gln Ala Arg Arg Asn Gln Ser Gln Gly Arg
100 105 110

aga ggt ggg agc tac cgc ctc atc aag cag cca agg agg cag gat aag 384
Arg Gly Gly Ser Tyr Arg Leu Ile Lys Gln Pro Arg Arg Gln Asp Lys
115 120 125

gaa gcc cca aag agg gac tgg ggg gct gat gag gac ggg gag gtg tct 432
Glu Ala Pro Lys Arg Asp Trp Gly Ala Asp Glu Asp Gly Glu Val Ser

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    130                 135                 140

gaa gaa gag gag ttg acc ccg ttc agc ctg gac cca cgt ggc ctc cag         480
Glu Glu Glu Glu Leu Thr Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln
145                 150                 155                 160

gag gca ctc agt gcc cgc atc ccc ctc cag agg gct ctg ccc gag gtg         528
Glu Ala Leu Ser Ala Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val
                165                 170                 175

cgg cac cca ctg tgt ctg cag cag cac cct cag gac agc ctg ccc aca         576
Arg His Pro Leu Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr
            180                 185                 190

gcc agc gtc atc ctc tgt ttc cat gat gag gcc tgg tcc act ctc ctg         624
Ala Ser Val Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu
        195                 200                 205

cgg act gta cac agc atc ctc gac aca gtg ccc agg gcc ttc ctg aag         672
Arg Thr Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys
    210                 215                 220

gag atc atc ctc gtg gac gac ctc agc cag caa gga caa ctc aag tct         720
Glu Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
225                 230                 235                 240

gct ctc agc gaa tat gtg gcc agg ctg gag ggg gtg aag tta ctc agg         768
Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu Arg
                245                 250                 255

agc aac aag agg ctg ggt gcc atc agg gcc cgg atg ctg ggg gcc acc         816
Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly Ala Thr
            260                 265                 270

aga gcc acc ggg gat gtg ctc gtc ttc atg gat gcc cac tgc gag tgc         864
Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His Cys Glu Cys
        275                 280                 285

cac cca ggc tgg ctg gag ccc ctc ctc agc aga ata gct ggt gac agg         912
His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile Ala Gly Asp Arg
    290                 295                 300

agc cga gtg gta tct ccg gtg ata gat gtg att gac tgg aag act ttc         960
Ser Arg Val Val Ser Pro Val Ile Asp Val Ile Asp Trp Lys Thr Phe
305                 310                 315                 320

cag tat tac ccc tca aag gac ctg cag cgt ggg gtg ttg gac tgg aag        1008
Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg Gly Val Leu Asp Trp Lys
                325                 330                 335

ctg gat ttc cac tgg gaa cct ttg cca gag cat gtg agg aag gcc ctc        1056
Leu Asp Phe His Trp Glu Pro Leu Pro Glu His Val Arg Lys Ala Leu
            340                 345                 350

cag tcc ccc ata agc ccc atc agg agc cct gtg gtg ccc gga gag gtg        1104
Gln Ser Pro Ile Ser Pro Ile Arg Ser Pro Val Val Pro Gly Glu Val
        355                 360                 365
```

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gtg gcc atg gac aga cat tac ttc caa aac act gga gcg tat gac tct      1152
Val Ala Met Asp Arg His Tyr Phe Gln Asn Thr Gly Ala Tyr Asp Ser
    370                 375                 380

ctt atg tcg ctg cga ggt ggt gaa aac ctc gaa ctg tct ttc aag gcc      1200
Leu Met Ser Leu Arg Gly Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala
385                 390                 395                 400

tgg ctc tgt ggt ggc tct gtt gaa atc ctt ccc tgc tct cgg gta gga      1248
Trp Leu Cys Gly Gly Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly
                405                 410                 415

cac atc tac caa aat cag gat tcc cat tcc ccc ctc gac cag gag gcc      1296
His Ile Tyr Gln Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala
            420                 425                 430

acc ctg agg aac agg gtt cgc att gct gag acc tgg ctg ggg tca ttc      1344
Thr Leu Arg Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe
        435                 440                 445

aaa gaa acc ttc tac aag cat agc cca gag gcc ttc tcc ttg agc aag      1392
Lys Glu Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys
    450                 455                 460

gct gag aag cca gac tgc atg gaa cgc ttg cag ctg caa agg aga ctg      1440
Ala Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu
465                 470                 475                 480

ggt tgt cgg aca ttc cac tgg ttt ctg gct aat gtc tac cct gag ctg      1488
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu Leu
                485                 490                 495

tac cca tct gaa ccc agg ccc agt ttc tct gga aag ctc cac aac act      1536
Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His Asn Thr
            500                 505                 510

gga ctt ggg ctc tgt gca gac tgc cag gca gaa ggg gac atc ctg ggc      1584
Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp Ile Leu Gly
        515                 520                 525

tgt ccc atg gtg ttg gct cct tgc agt gac agc cgg cag caa cag tac      1632
Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg Gln Gln Gln Tyr
    530                 535                 540

ctg cag cac acc agc agg aag gag att cac ttt ggc agc cca cag cac      1680
Leu Gln His Thr Ser Arg Lys Glu Ile His Phe Gly Ser Pro Gln His
545                 550                 555                 560

ctg tgc ttt gct gtc agg cag gag cag gtg att ctt cag aac tgc acg      1728
Leu Cys Phe Ala Val Arg Gln Glu Gln Val Ile Leu Gln Asn Cys Thr
                565                 570                 575

gag gaa ggc ctg gcc atc cac cag cag cac tgg gac ttc cag gag aat      1776
Glu Glu Gly Leu Ala Ile His Gln Gln His Trp Asp Phe Gln Glu Asn
            580                 585                 590
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ggg atg att gtc cac att ctt tct ggg aaa tgc atg gaa gct gtg gtg      1824
Gly Met Ile Val His Ile Leu Ser Gly Lys Cys Met Glu Ala Val Val
        595                 600                 605

caa gaa aac aat aaa gat ttg tac ctg cgt ccg tgt gat gga aaa gcc      1872
Gln Glu Asn Asn Lys Asp Leu Tyr Leu Arg Pro Cys Asp Gly Lys Ala
    610                 615                 620

cgc cag cag tgg cgt ttt gac cag atc aat gct gtg gat gaa cga tga      1920
Arg Gln Gln Trp Arg Phe Asp Gln Ile Asn Ala Val Asp Glu Arg  *
625                 630                 635                 640

atgtcaatgt cagaaggaaa agagaatttt ggccatcaaa atccagctcc aagtgaactt    1980

aaagagctta tatatttcat gaagctgatc cttttgtgtg tgtgctcctg gtgttaggag    2040

agaaaaaagc tctatgaaag aatataggaa gtttctcctt ttcacacctt aaaaaaaaaa    2100

aa                                                                   2102




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gcccctcctc ctaccacctg cattgcctca acccgccgct gcccgagatc ccaaacgtgc     120

cccccactga agggcaaagt ccagcggatt ctacactgga ggtggacgga gccccctgcc     180

cccttc   atg gtg ggg ctg ccg ggg cct gac gtg gag ccc agc ctc cct      228
         Met Val Gly Leu Pro Gly Pro Asp Val Glu Pro Ser Leu Pro
           1               5                  10

cca cct aag ccc ctg gag ggc atc cct gag aga gag ttc ttt gtc aag      276
Pro Pro Lys Pro Leu Glu Gly Ile Pro Glu Arg Glu Phe Phe Val Lys
 15                  20                  25                  30

tgg gca ggg ctg tcc tac tgg cat tgc tcc tgg gtg aag gag cta cag      324
Trp Ala Gly Leu Ser Tyr Trp His Cys Ser Trp Val Lys Glu Leu Gln
                35                  40                  45

ctg gag ctg tac cac acg gtg atg tat cgc aac tac caa aga aag aac      372
Leu Glu Leu Tyr His Thr Val Met Tyr Arg Asn Tyr Gln Arg Lys Asn
            50                  55                  60

gac atg gat gag ccg ccc ccc ttt gac tac ggc tct ggg gat gaa gac      420
Asp Met Asp Glu Pro Pro Pro Phe Asp Tyr Gly Ser Gly Asp Glu Asp
```

```
         65                  70                  75

ggc aag agc gag aag agg aag aac aag gac ccc ctc tat gcc aag atg       468
Gly Lys Ser Glu Lys Arg Lys Asn Lys Asp Pro Leu Tyr Ala Lys Met
     80                  85                  90

gag gag cgc ttc tac cgc tat ggc atc aag cca gag tgg atg atg att       516
Glu Glu Arg Phe Tyr Arg Tyr Gly Ile Lys Pro Glu Trp Met Met Ile
 95                 100                 105                 110

cac cga atc ctg aac cat agc ttt gac aag aag ggg gat gtg cac tac       564
His Arg Ile Leu Asn His Ser Phe Asp Lys Lys Gly Asp Val His Tyr
                115                 120                 125

ctg atc aag tgg aaa gac ctg ccc tat gac cag tgc acc tgg gag atc       612
Leu Ile Lys Trp Lys Asp Leu Pro Tyr Asp Gln Cys Thr Trp Glu Ile
            130                 135                 140

gat gac atc gac atc ccc tac tac gac aac ctc aag cag gcc tac tgg       660
Asp Asp Ile Asp Ile Pro Tyr Tyr Asp Asn Leu Lys Gln Ala Tyr Trp
        145                 150                 155

ggc cac agg gag ctg atg ctg gga gaa gac acc agg ctg ccc aag agg       708
Gly His Arg Glu Leu Met Leu Gly Glu Asp Thr Arg Leu Pro Lys Arg
    160                 165                 170

ctg ctc aag aag ggc aag aag ctg agg gac gac aag cag gag aag ccg       756
Leu Leu Lys Lys Gly Lys Lys Leu Arg Asp Asp Lys Gln Glu Lys Pro
175                 180                 185                 190

ccg gac acg ccc att gtg gac ccc acg gtc aag ttc gac aag cag cca       804
Pro Asp Thr Pro Ile Val Asp Pro Thr Val Lys Phe Asp Lys Gln Pro
                195                 200                 205

tgg tac atc gac tcc aca ggc ggc aca ctg cac ccg tac cag ctg gag       852
Trp Tyr Ile Asp Ser Thr Gly Gly Thr Leu His Pro Tyr Gln Leu Glu
            210                 215                 220

ggc ctc aac tgg ctg cgc ttc tct tgg gcc cag ggc act gac acc atc       900
Gly Leu Asn Trp Leu Arg Phe Ser Trp Ala Gln Gly Thr Asp Thr Ile
        225                 230                 235

ctg gcc gat gag atg ggt ctg ggc aag acg gtg cag acc atc gtg ttc       948
Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Val Gln Thr Ile Val Phe
    240                 245                 250

ctt tac tcc ctc tac aag gag ggc cac tcc aaa ggg ccc tac ctg gtt       996
Leu Tyr Ser Leu Tyr Lys Glu Gly His Ser Lys Gly Pro Tyr Leu Val
255                 260                 265                 270

agc gcg ccc ctc tcc acc atc atc aac tgg gaa cgc gag ttt gag atg      1044
Ser Ala Pro Leu Ser Thr Ile Ile Asn Trp Glu Arg Glu Phe Glu Met
                275                 280                 285

tgg gcg ccc gac ttc tac gtg gtc acc tac acg ggg gac aag gag agc      1092
Trp Ala Pro Asp Phe Tyr Val Val Thr Tyr Thr Gly Asp Lys Glu Ser
            290                 295                 300
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cgc tcg gtg att cgg gag aac gag ttt tcc ttt gag gac aac gcc att      1140
Arg Ser Val Ile Arg Glu Asn Glu Phe Ser Phe Glu Asp Asn Ala Ile
        305                 310                 315

cgg agt ggg aag aag gta ttc cgt atg aag aaa gaa gtg cag atc aaa      1188
Arg Ser Gly Lys Lys Val Phe Arg Met Lys Lys Glu Val Gln Ile Lys
    320                 325                 330

ttc cac gtg ctg ctc acc tcc tat gag ctc atc acc atc gac cag gcc      1236
Phe His Val Leu Leu Thr Ser Tyr Glu Leu Ile Thr Ile Asp Gln Ala
335                 340                 345                 350

atc ctg ggc tcc atc gag tgg gcc tgc ctg gtg gta gat gag gcc cac      1284
Ile Leu Gly Ser Ile Glu Trp Ala Cys Leu Val Val Asp Glu Ala His
                355                 360                 365

cgc ctc aag aac aac cag tcc aag ttt ttt agg gtc tta aac agc tac      1332
Arg Leu Lys Asn Asn Gln Ser Lys Phe Phe Arg Val Leu Asn Ser Tyr
            370                 375                 380

aag att gat tac aag ctg ctg ctg aca ggg acc ccc ctt cag aac aac      1380
Lys Ile Asp Tyr Lys Leu Leu Leu Thr Gly Thr Pro Leu Gln Asn Asn
        385                 390                 395

ctg gag gag ctg ttc cat ctc ctc aac ttc ctg act cca gag agg ttc      1428
Leu Glu Glu Leu Phe His Leu Leu Asn Phe Leu Thr Pro Glu Arg Phe
    400                 405                 410

aac aac ctg gag ggc ttc ctg gag gag ttt gct gac atc tcc aag gaa      1476
Asn Asn Leu Glu Gly Phe Leu Glu Glu Phe Ala Asp Ile Ser Lys Glu
415                 420                 425                 430

gac cag atc aag aag ctg cat gac ctg ctg ggg ccg cac atg ctc agg      1524
Asp Gln Ile Lys Lys Leu His Asp Leu Leu Gly Pro His Met Leu Arg
                435                 440                 445

cgg ctc aag gct gac gtg ttc aag aac atg ccg gcc aag acc gag ctc      1572
Arg Leu Lys Ala Asp Val Phe Lys Asn Met Pro Ala Lys Thr Glu Leu
            450                 455                 460

att gtc cgg gtg gag ctg agc cag atg cag aag aag tac tac aag ttc      1620
Ile Val Arg Val Glu Leu Ser Gln Met Gln Lys Lys Tyr Tyr Lys Phe
        465                 470                 475

atc ctc aca cgg aac ttt gag gca ctg aac tcc aag ggg ggc ggg aac      1668
Ile Leu Thr Arg Asn Phe Glu Ala Leu Asn Ser Lys Gly Gly Gly Asn
    480                 485                 490

caa gta tcg ctg ctc aac atc atg atg gac ctg aaa aag tgc tgc aac      1716
Gln Val Ser Leu Leu Asn Ile Met Met Asp Leu Lys Lys Cys Cys Asn
495                 500                 505                 510

cac ccc tac ctc ttc cct gtg gct gcc gtg gag gcc cct gtc ttg ccc      1764
His Pro Tyr Leu Phe Pro Val Ala Ala Val Glu Ala Pro Val Leu Pro
                515                 520                 525
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aat ggc tcc tac gat gga agc tcc ctg gtc aag tct tca ggg aag ctc       1812
Asn Gly Ser Tyr Asp Gly Ser Ser Leu Val Lys Ser Ser Gly Lys Leu
            530                 535                 540

atg ctg cta cag aag atg ctg aag aaa ctg cgg gat gag ggg cac cgt       1860
Met Leu Leu Gln Lys Met Leu Lys Lys Leu Arg Asp Glu Gly His Arg
        545                 550                 555

gtg ctc atc ttc tcc cag atg acc aag atg ctg gac ctc ctg gag gac       1908
Val Leu Ile Phe Ser Gln Met Thr Lys Met Leu Asp Leu Leu Glu Asp
    560                 565                 570

ttc ctg gag tac gaa ggc tac aag tat gag cgg att gat ggt ggc atc       1956
Phe Leu Glu Tyr Glu Gly Tyr Lys Tyr Glu Arg Ile Asp Gly Gly Ile
575                 580                 585                 590

acc ggg ggc ctc cgg cag gag gca atc gac aga ttc aat gcc ccc ggg       2004
Thr Gly Gly Leu Arg Gln Glu Ala Ile Asp Arg Phe Asn Ala Pro Gly
                595                 600                 605

gcc cag cag ttc tgc ttc ctc ctc tca acc cgg gca ggt ggt ctg ggc       2052
Ala Gln Gln Phe Cys Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly
            610                 615                 620

atc aac ctg gcc acg gcg gac act gtc atc atc tac gac tcg gac tgg       2100
Ile Asn Leu Ala Thr Ala Asp Thr Val Ile Ile Tyr Asp Ser Asp Trp
        625                 630                 635

aac ccg cac aat gac atc cag gcc ttc agc cgc gcc cac cgc atc ggc       2148
Asn Pro His Asn Asp Ile Gln Ala Phe Ser Arg Ala His Arg Ile Gly
    640                 645                 650

cag aac aag aag gtg atg atc tac cgc ttc gtg act cgg gcc tcg gtg       2196
Gln Asn Lys Lys Val Met Ile Tyr Arg Phe Val Thr Arg Ala Ser Val
655                 660                 665                 670

gag gag cgc atc acg cag gtg gcc aag cgc aag atg atg ctc acc cac       2244
Glu Glu Arg Ile Thr Gln Val Ala Lys Arg Lys Met Met Leu Thr His
                675                 680                 685

ctg gtg gtg cgg ccc ggc ctc ggc tcc aag tcg ggg tcc atg acc aag       2292
Leu Val Val Arg Pro Gly Leu Gly Ser Lys Ser Gly Ser Met Thr Lys
            690                 695                 700

cag gag ctg gac gac atc ctc aag ttc ggc acg gag gaa ctc ttc aag       2340
Gln Glu Leu Asp Asp Ile Leu Lys Phe Gly Thr Glu Glu Leu Phe Lys
        705                 710                 715

gac gac gtg gag ggc atg atg tct cag ggc cag agg ccg gtc aca ccc       2388
Asp Asp Val Glu Gly Met Met Ser Gln Gly Gln Arg Pro Val Thr Pro
    720                 725                 730

atc cct gat gtc cag tcc tcc aaa ggg ggg aac ttg gcc gcc agt gca       2436
Ile Pro Asp Val Gln Ser Ser Lys Gly Gly Asn Leu Ala Ala Ser Ala
735                 740                 745                 750

aag aag aag cac ggt agc acc ccg cca ggt gac aac aag gac gtg gag       2484
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Lys Lys Lys His Gly Ser Thr Pro Pro Gly Asp Asn Lys Asp Val Glu
                755                 760                 765

gac agc agt gtg atc cac tat gac gat gcg gcc atc tcc aag ctg ctg      2532
Asp Ser Ser Val Ile His Tyr Asp Asp Ala Ala Ile Ser Lys Leu Leu
            770                 775                 780

gac cgg aac cag gac gct aca gat gac acg gag cta cag aac atg aac      2580
Asp Arg Asn Gln Asp Ala Thr Asp Asp Thr Glu Leu Gln Asn Met Asn
        785                 790                 795

gag tac ctg agc tcc ttc aag gtg gcg cag tac gtg gtg cgc gag gag      2628
Glu Tyr Leu Ser Ser Phe Lys Val Ala Gln Tyr Val Val Arg Glu Glu
    800                 805                 810

gac ggc gtg gag gag gtg gag cgg gaa atc atc aag cag gag gag aac      2676
Asp Gly Val Glu Glu Val Glu Arg Glu Ile Ile Lys Gln Glu Glu Asn
815                 820                 825                 830

gtg gac ccc gac tac tgg gag aag ctg ctg cgg cac cac tat gag cag      2724
Val Asp Pro Asp Tyr Trp Glu Lys Leu Leu Arg His His Tyr Glu Gln
                835                 840                 845

cag cag gag gac ctg gcc cgc aac ctg ggc aag ggc aag cgc atc cgc      2772
Gln Gln Glu Asp Leu Ala Arg Asn Leu Gly Lys Gly Lys Arg Ile Arg
            850                 855                 860

aag cag gtc aac tac aac gat gcc tcc cag gag gac cag gag tgg cag      2820
Lys Gln Val Asn Tyr Asn Asp Ala Ser Gln Glu Asp Gln Glu Trp Gln
        865                 870                 875

gat gag ctc tct gat aac cag tca gaa tat tcc att ggc tct gag gat      2868
Asp Glu Leu Ser Asp Asn Gln Ser Glu Tyr Ser Ile Gly Ser Glu Asp
    880                 885                 890

gag gat gag gac ttt gaa gag agg ccg gaa ggg cag agt gga cga cga      2916
Glu Asp Glu Asp Phe Glu Glu Arg Pro Glu Gly Gln Ser Gly Arg Arg
895                 900                 905                 910

caa tcc cgg agg cag ctg aag agt gac agg gac aag ccc ctg ccc ccg      2964
Gln Ser Arg Arg Gln Leu Lys Ser Asp Arg Asp Lys Pro Leu Pro Pro
                915                 920                 925

ctt ctc gcc cga gtt ggt ggc aac atc gag gtg ctg ggc ttc aat gcc      3012
Leu Leu Ala Arg Val Gly Gly Asn Ile Glu Val Leu Gly Phe Asn Ala
            930                 935                 940

cga cag cgg aag gcc ttt ctg aac gcc atc atg cgc tgg ggc atg ccc      3060
Arg Gln Arg Lys Ala Phe Leu Asn Ala Ile Met Arg Trp Gly Met Pro
        945                 950                 955

ccg cag gac gcc ttc aac tcc cac tgg ctg gtg cgg gac ctt cga ggg      3108
Pro Gln Asp Ala Phe Asn Ser His Trp Leu Val Arg Asp Leu Arg Gly
    960                 965                 970

aag agc gag aag gag ttt aga gcc tat gtg tcc ctc ttc atg cgg cac      3156
Lys Ser Glu Lys Glu Phe Arg Ala Tyr Val Ser Leu Phe Met Arg His
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 975                 980                 985                 990

 ctg tgt gag ccg ggg gcg gat ggt gca gag acc ttc gca gac ggc gtg      3204
 Leu Cys Glu Pro Gly Ala Asp Gly Ala Glu Thr Phe Ala Asp Gly Val
                 995                1000                1005

 ccc cgg gag ggc ctc tcc agg cag cac gtg ctg acc cgc atc ggg gtc      3252
 Pro Arg Glu Gly Leu Ser Arg Gln His Val Leu Thr Arg Ile Gly Val
            1010                1015                1020

 atg tca cta gtt agg aag aag gtt cag gag ttt gag cat gtc aac ggg      3300
 Met Ser Leu Val Arg Lys Lys Val Gln Glu Phe Glu His Val Asn Gly
        1025                1030                1035

 aag tac agc acc cca gac ttg atc cct gag ggg ccc gag ggg aag aag      3348
 Lys Tyr Ser Thr Pro Asp Leu Ile Pro Glu Gly Pro Glu Gly Lys Lys
    1040                1045                1050

 ccg ggc gag gtg atc tcc tcg gac ccc aac aca cca gtg ccc gcc agc      3396
 Pro Gly Glu Val Ile Ser Ser Asp Pro Asn Thr Pro Val Pro Ala Ser
1055                1060                1065                1070

 cct gcc cac ctc ctg cca gcc ccg ctg ggc ctg cca gac aaa atg gaa      3444
 Pro Ala His Leu Leu Pro Ala Pro Leu Gly Leu Pro Asp Lys Met Glu
                1075                1080                1085

 gcc cag ctg ggc tac atg gat gag aaa gac ccc ggg gca cag aag cca      3492
 Ala Gln Leu Gly Tyr Met Asp Glu Lys Asp Pro Gly Ala Gln Lys Pro
            1090                1095                1100

 agg cag ccc ctg gaa gtc cag gcc ctt cca gcc gcc ttg gat aga gtg      3540
 Arg Gln Pro Leu Glu Val Gln Ala Leu Pro Ala Ala Leu Asp Arg Val
        1105                1110                1115

 gag agt gag gac aag cac gag agc cca gcc agc aag gag aga gcc cga      3588
 Glu Ser Glu Asp Lys His Glu Ser Pro Ala Ser Lys Glu Arg Ala Arg
    1120                1125                1130

 gag gag cgg cca gag gag acg gag aag gcc ccg ccc tcc ccg gag cag      3636
 Glu Glu Arg Pro Glu Glu Thr Glu Lys Ala Pro Pro Ser Pro Glu Gln
1135                1140                1145                1150

 ctg ccg aga gag gag gtg ctt cct gag aag gag aag atc ctg gac aag      3684
 Leu Pro Arg Glu Glu Val Leu Pro Glu Lys Glu Lys Ile Leu Asp Lys
                1155                1160                1165

 ctg gag ctg agc ttg atc cac agc aga ggg gac agt tcc gaa ctc agg      3732
 Leu Glu Leu Ser Leu Ile His Ser Arg Gly Asp Ser Ser Glu Leu Arg
            1170                1175                1180

 cca gat gac acc aag gct gag gag aag gag ccc att gaa aca cag caa      3780
 Pro Asp Asp Thr Lys Ala Glu Glu Lys Glu Pro Ile Glu Thr Gln Gln
        1185                1190                1195

 aat ggt gac aaa gag gaa gat gac gag ggg aag aag gag gac aag aag      3828
 Asn Gly Asp Lys Glu Glu Asp Asp Glu Gly Lys Lys Glu Asp Lys Lys
    1200                1205                1210
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 ggg aaa ttc aag ttc atg ttc aac atc gcg gac ggg ggc ttc acg gag     3876
 Gly Lys Phe Lys Phe Met Phe Asn Ile Ala Asp Gly Gly Phe Thr Glu
1215                1220                1225                1230

 ttg cac acg ctg tgg cag aac gag gag cgg gct gct gta tcc tct ggg     3924
 Leu His Thr Leu Trp Gln Asn Glu Glu Arg Ala Ala Val Ser Ser Gly
                1235                1240                1245

 aaa atc tac gac atc tgg cac cgg cgc cat gac tac tgg ctg ctg gcg     3972
 Lys Ile Tyr Asp Ile Trp His Arg Arg His Asp Tyr Trp Leu Leu Ala
            1250                1255                1260

 ggc atc gtg acg cac ggc tac gcc cgc tgg cag gac atc cag aat gac     4020
 Gly Ile Val Thr His Gly Tyr Ala Arg Trp Gln Asp Ile Gln Asn Asp
        1265                1270                1275

 cca cgg tac atg atc ctc aac gag ccc ttc aag tct gag gtc cac aag     4068
 Pro Arg Tyr Met Ile Leu Asn Glu Pro Phe Lys Ser Glu Val His Lys
    1280                1285                1290

 ggc aac tac ctg gag atg aag aac aag ttc ctg gcc cgc agg ttt aag     4116
 Gly Asn Tyr Leu Glu Met Lys Asn Lys Phe Leu Ala Arg Arg Phe Lys
1295                1300                1305                1310

 ctg ctg gag cag gcg ttg gtc att gag gag cag ctc cgg agg gcc gcg     4164
 Leu Leu Glu Gln Ala Leu Val Ile Glu Glu Gln Leu Arg Arg Ala Ala
                1315                1320                1325

 tac ctg aac atg acg cag gac ccc aac cac ccc gcc atg gcc ctc aac     4212
 Tyr Leu Asn Met Thr Gln Asp Pro Asn His Pro Ala Met Ala Leu Asn
            1330                1335                1340

 gcc cgc ctg gct gaa gtg gag tgc ctc gcc gag agc cac cag cac ctg     4260
 Ala Arg Leu Ala Glu Val Glu Cys Leu Ala Glu Ser His Gln His Leu
        1345                1350                1355

 tcc aag gag tcc ctt gct ggg aac aag cct gcc aat gcc gtc ctg cac     4308
 Ser Lys Glu Ser Leu Ala Gly Asn Lys Pro Ala Asn Ala Val Leu His
    1360                1365                1370

 aag gtc ctg aac cag ctg gag gag ctg ctg agc gac atg aag gcc gac     4356
 Lys Val Leu Asn Gln Leu Glu Glu Leu Leu Ser Asp Met Lys Ala Asp
1375                1380                1385                1390

 gtg acc cgg ctg cca tcc atg ctg tcc cgc atc ccc ccg gtg gcc gcc     4404
 Val Thr Arg Leu Pro Ser Met Leu Ser Arg Ile Pro Pro Val Ala Ala
                1395                1400                1405

 cgg ctg cag atg tcg gag cgc agc atc ctg agc cgc ctg acc aac cgc     4452
 Arg Leu Gln Met Ser Glu Arg Ser Ile Leu Ser Arg Leu Thr Asn Arg
            1410                1415                1420

 gcc ggg gac ccc acc atc cag cag ggc gct ttc ggc tcc tcc cag atg     4500
 Ala Gly Asp Pro Thr Ile Gln Gln Gly Ala Phe Gly Ser Ser Gln Met
        1425                1430                1435
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tac agc aac aac ttt ggg ccc aac ttc cgg ggc cct gga ccg gga ggg     4548
Tyr Ser Asn Asn Phe Gly Pro Asn Phe Arg Gly Pro Gly Pro Gly Gly
   1440                1445                1450

att gtc aac tac aac cag atg ccc ctg ggg ccc tat gtg acc gat atc     4596
Ile Val Asn Tyr Asn Gln Met Pro Leu Gly Pro Tyr Val Thr Asp Ile
1455                1460                1465                1470

tag cgtc ctcaattcct gtgtgcaggt cattcagctg acagctgcgg gcactgcgac     4653
 *


caatggagag aagtgcactt tt                                            4675




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     <222> (63)..(524)

     <400> 217
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gc   atg gcc tcg ccc gac ccg ccc gcc acc agc tac gcc ccg tcc gac      107
     Met Ala Ser Pro Asp Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp
       1               5                  10                  15

gtg ccc tcg ggg gtc gcg ctg ttc ctc acc atc cct ttc gcc ttc ttc      155
Val Pro Ser Gly Val Ala Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe
                20                  25                  30

ctg ccc gag ctg ata ttt ggg ttc ttg gtc tgg acc atg gta gcc gcc      203
Leu Pro Glu Leu Ile Phe Gly Phe Leu Val Trp Thr Met Val Ala Ala
            35                  40                  45

acc cac ata gta tac ccc ttg ctg caa gga tgg gtg atg tat gtc tcg      251
Thr His Ile Val Tyr Pro Leu Leu Gln Gly Trp Val Met Tyr Val Ser
        50                  55                  60

ctc acc tcg ttt ctc atc tcc ttg atg ttc ctg ttg tct tac ttg ttt      299
Leu Thr Ser Phe Leu Ile Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe
    65                  70                  75

gga ttt tac aaa aga ttt gaa tcc tgg aga gtt ctg gac agc ctg tac      347
Gly Phe Tyr Lys Arg Phe Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr
80                  85                  90                  95

cac ggg acc act ggc atc ctg tac atg agc gct gcc gtc cta caa gta      395
His Gly Thr Thr Gly Ile Leu Tyr Met Ser Ala Ala Val Leu Gln Val
                100                 105                 110
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cat gcc acg att gtt tct gag aaa ctg ctg gac cca aga att tac tac      443
His Ala Thr Ile Val Ser Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr
            115                 120                 125

att aat tcg gca gcc tcg ttc ttc gcc ttc atc gcc acg ctg ctc tac      491
Ile Asn Ser Ala Ala Ser Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr
        130                 135                 140

att ctc cat gcc ttc agc atc tat tac cac tga tgcacagg cgccaggcca      542
Ile Leu His Ala Phe Ser Ile Tyr Tyr His  *
    145                 150

agggggaaat gctctttgaa agctccaatt attggtcccc aaaagcagct tccaacgttt    602

gccatctgga tgacaaacgg aagatccact aaaacgtcca cgggattaac agaacgtcct    662

tgcagactga gcgatgacac cacactttgt ttggacattt aaattcactc tgctgaatag    722

gaggaagctt ttctttttcc tgggaaaaca actgtctctt ggaattatct gaccatgaac    782

ttgctcttct agacaactca catcaaagcc ctcactccac taatggagaa tcctagcccc    842

actaatgcca agtctgtttg gggattttgc ctcagctatg ggcttcccta gagtaggtct    902

aggggaatac tcagtctgat ctttttttg tttgttttat tttgtttttt ttgagacgga    962

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gcctccgggg ttcccgccat                                               1042




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     <213> Homo sapiens

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     <222> (166)..(831)

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gggctggaga ggtcctgccg tggtaccagc ctccagcctg cccccaggac tgcccctgac    120

ccaggcgcgc ccgctgctcg gtggcaggag ggccggcgga gcgcc    atg gcc tgc      174
                                                     Met Ala Cys
                                                       1

atc ctg aag aga aag tct gtg att gct gtg agc ttc ata gca gcg ttc      222
Ile Leu Lys Arg Lys Ser Val Ile Ala Val Ser Phe Ile Ala Ala Phe
      5                  10                  15

ctt ttc ctg ctg gtt gtg cgt ctt gta aat gaa gtg aat ttc cca ttg      270
Leu Phe Leu Leu Val Val Arg Leu Val Asn Glu Val Asn Phe Pro Leu
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 20                  25                  30                  35

cta cta aac tgc ttt gga caa cct ggt aca aag tgg ata cca ttc tcc       318
Leu Leu Asn Cys Phe Gly Gln Pro Gly Thr Lys Trp Ile Pro Phe Ser
                 40                  45                  50

tac aca tac agg cgg ccc ctt cga act cac tat gga tac ata aat gtg       366
Tyr Thr Tyr Arg Arg Pro Leu Arg Thr His Tyr Gly Tyr Ile Asn Val
             55                  60                  65

aag aca caa gag cct ttg caa ctg gac tgt gac ctt tgt gcc ata gtg       414
Lys Thr Gln Glu Pro Leu Gln Leu Asp Cys Asp Leu Cys Ala Ile Val
         70                  75                  80

tca aac tca ggt cag atg gtt ggc cag aag gtg gga aat gag ata gat       462
Ser Asn Ser Gly Gln Met Val Gly Gln Lys Val Gly Asn Glu Ile Asp
     85                  90                  95

cga tcc tcc tgc att tgg aga atg aac aat gcc ccc acc aaa ggt tat       510
Arg Ser Ser Cys Ile Trp Arg Met Asn Asn Ala Pro Thr Lys Gly Tyr
100                 105                 110                 115

gaa gaa gat gtc ggc cgc atg acc atg att cga gtt gtg tcc cat acc       558
Glu Glu Asp Val Gly Arg Met Thr Met Ile Arg Val Val Ser His Thr
                120                 125                 130

agc gtt cct ctt ttg cta aaa aac cct gat tat ttt ttc aag gaa gcg       606
Ser Val Pro Leu Leu Leu Lys Asn Pro Asp Tyr Phe Phe Lys Glu Ala
            135                 140                 145

aat act act att tgt gtt att tgg gga cct ttc cgc aat atg agg aaa       654
Asn Thr Thr Ile Cys Val Ile Trp Gly Pro Phe Arg Asn Met Arg Lys
        150                 155                 160

gat ggc aat ggc atc gtt tac aac atg ttg aaa aag aca gtt ggt atc       702
Asp Gly Asn Gly Ile Val Tyr Asn Met Leu Lys Lys Thr Val Gly Ile
    165                 170                 175

tat ccg aat gcc caa ata tac gtg acc aca gag aag cgc atg agt tac       750
Tyr Pro Asn Ala Gln Ile Tyr Val Thr Thr Glu Lys Arg Met Ser Tyr
180                 185                 190                 195

tgt gat gga gtt ttt aag aag gaa act ggg aag gac agg ggg cat gca       798
Cys Asp Gly Val Phe Lys Lys Glu Thr Gly Lys Asp Arg Gly His Ala
                200                 205                 210

agg cga ctg ctg att tct aca gac act ttt taa gcgattac cagtgctggc       849
Arg Arg Leu Leu Ile Ser Thr Asp Thr Phe  *
            215                 220

aagtggaact acctttccgg tcctcttaca agcatccagt cacttgctga aatgtcataa     909

gcgatataaa cctgctgaca ggccaggatc attgcatctc ctgcctcctc cttccacgta     969

acaaatctca ttgttgattg gcatatggca gcaagcatcc caacacccag agtggtgttc    1029

ttatttctga gggagcaggg tctgtgtgtg aattgcacac acagggagca atcccctgcc    1089
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ctgatacagg caacctgagt gcttagttcc ttctctgctc agaacttagt gtgactatgt   1149

ggcctacctc acattgtttg tgttacacct acacaggaaa aaggaaaaat gtccttttga   1209

ttccatgctt gtagagatgt tcatccaatt tgaatgaaca tgtagccaag gtagtgtctt   1269

cccccttttct tctccttttt ttttg                                         1294
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tcggccatga acttacccgg gacagcggcg gcggcggacc ttttggccat cttctcgcag     120

agtgctccct gctaacgggg acagatttta acatt  atg gca ggg agg cat cag     173
                                         Met Ala Gly Arg His Gln
                                         1               5

aat cgt agt ttt cct ctt cca gga gtt cag tca agt ggt caa gta cat     221
Asn Arg Ser Phe Pro Leu Pro Gly Val Gln Ser Ser Gly Gln Val His
            10                  15                  20

gca ttt gga aat tgt tca gac agt gat att ttg gag gag gat gct gaa     269
Ala Phe Gly Asn Cys Ser Asp Ser Asp Ile Leu Glu Glu Asp Ala Glu
        25                  30                  35

gtg tat gaa ctt cga tcc aga gga aaa gag aaa gtc cga aga agt aca     317
Val Tyr Glu Leu Arg Ser Arg Gly Lys Glu Lys Val Arg Arg Ser Thr
    40                  45                  50

tca aga gat aga ctt gac gac att ata gta tta aca aaa gat ata caa     365
Ser Arg Asp Arg Leu Asp Asp Ile Ile Val Leu Thr Lys Asp Ile Gln
55                  60                  65                  70

gaa gga gat aca tta aat gca ata gcc ctt cag tac tgt tgt acg gta     413
Glu Gly Asp Thr Leu Asn Ala Ile Ala Leu Gln Tyr Cys Cys Thr Val
                75                  80                  85

gca gat atc aag aga gtt aac aat ctc atc agt gat caa gac ttt ttt     461
Ala Asp Ile Lys Arg Val Asn Asn Leu Ile Ser Asp Gln Asp Phe Phe
            90                  95                  100

gcc ctt agg tct atc aaa att cca gta aaa aag ttc agt tcc ttg acc     509
Ala Leu Arg Ser Ile Lys Ile Pro Val Lys Lys Phe Ser Ser Leu Thr
        105                 110                 115
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gaa aca ctt tgt cct cca aaa gga aga cag act tca cgt cat tca tct        557
Glu Thr Leu Cys Pro Pro Lys Gly Arg Gln Thr Ser Arg His Ser Ser
    120                 125                 130

gtt caa tac tct tcc gaa caa cag gaa att ttg cca gct aat gat tct        605
Val Gln Tyr Ser Ser Glu Gln Gln Glu Ile Leu Pro Ala Asn Asp Ser
135                 140                 145                 150

ctt gct tac agt gac tca gct ggt agc ttt tta aaa gaa gta gac cga        653
Leu Ala Tyr Ser Asp Ser Ala Gly Ser Phe Leu Lys Glu Val Asp Arg
                155                 160                 165

gac ata gaa caa ata gta aag tgt aca gac aat aag aga gag aac ctc        701
Asp Ile Glu Gln Ile Val Lys Cys Thr Asp Asn Lys Arg Glu Asn Leu
            170                 175                 180

aat gag gta gta tcg gcc tta aca gca caa caa atg cgt ttt gaa cct        749
Asn Glu Val Val Ser Ala Leu Thr Ala Gln Gln Met Arg Phe Glu Pro
        185                 190                 195

gat aac aaa aac act caa cgt aaa gac ccc tat tat gga gca gac tgg        797
Asp Asn Lys Asn Thr Gln Arg Lys Asp Pro Tyr Tyr Gly Ala Asp Trp
    200                 205                 210

gga ata ggg tgg tgg aca gct gta gtg ata atg ttg ata gta ggt ata        845
Gly Ile Gly Trp Trp Thr Ala Val Val Ile Met Leu Ile Val Gly Ile
215                 220                 225                 230

ata aca cca gtg ttt tat ttg ttg tat tat gaa att tta gct aag gtg        893
Ile Thr Pro Val Phe Tyr Leu Leu Tyr Tyr Glu Ile Leu Ala Lys Val
                235                 240                 245

gat gtt agt cat cat tca aca gtg gac tct tca cat tta cat tca aaa        941
Asp Val Ser His His Ser Thr Val Asp Ser Ser His Leu His Ser Lys
            250                 255                 260

atc aca ccc cca tca cag cag aga gaa atg gaa aat gga att gtg cca        989
Ile Thr Pro Pro Ser Gln Gln Arg Glu Met Glu Asn Gly Ile Val Pro
        265                 270                 275

act aaa gga ata cat ttc agc caa caa gat gat cat aaa ctg tat agt       1037
Thr Lys Gly Ile His Phe Ser Gln Gln Asp Asp His Lys Leu Tyr Ser
    280                 285                 290

caa gat tct cag tca cct gct gct caa cag gaa aca tag caattagctc        1086
Gln Asp Ser Gln Ser Pro Ala Ala Gln Gln Glu Thr  *
295                 300                 305

ataatcaaat gttagtggtc aggtcacatg tgcatctgga atgtggtgaa tcagttatat     1146

ccaataatag cttcaaaggc agaatttaga gagattgagg atgcttttgt ttttaacaaa     1206

agggtttcac actttgaaaa ttttttgagc aactagttgt tgatgttgag agcagttgat     1266

ccataaatct ggtgtgtgaa tgtttcaagc agaaattaat ttaaatgtgt gtttaggaag     1326
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tacttaactt ggaagatgta tcatttttct taaaatgcat gtttaaattt tattttttta   1386

agtaattttt aaaaagttta ttaatgttaa atttatgatg cagaatgata gcatcagatg   1446

tctgcagctg aaaaaaattt actactatga acccccaaaa tattcagttg caagaaaatt   1506

tgattctaaa attattcatg gtaggatacg taacacaccc cttcaaaact tttaaaaaat   1566

acatttagca catgtgctat gaaagcatac gtacaaagag aaaggggaaa gtgatttata   1626

attcctacaa cagaggccaa gaaatagatt aaaatatttt caagacccca aaataatgta   1686

ttatggttgg gaagtcagta gaacactgga ataggtgaag acctgacagt aatttttgtc   1746

ttaagaatgc tttctttagg acagaccctt taacctcacc tctgtgcatc tgtttttaaa   1806

atgattatat ttgcctctga tatttgaaag cacttttgta gttttgatga tgaaaaatat   1866

attaaacgtg catattacca ttatttagga aataattcct tatatactgt gataaatcat   1926

tgctgttaca tacagtaaca tgccttaatt acatttaatg ccttactgct ttatgtaagt   1986

aaatccaagt ttcagaatta aaaataagca ttatttcata tggtccaatc agattcgtta   2046

cataggctat ataaatttgt ctccattttc accatcaagc acaaataatt gggtcaaaac   2106

tgcctttgag gtctgttgaa gaaaatggtt cattaagcaa aaaagagtag aggtatttta   2166

tattagcagt aacagacaaa ttatttagta atcccttaac ctctgttttt caaagagaaa   2226

atatccaatt tagacttttt tcctgatctc tatatatagc atcaagttgg gaaacaaagg   2286

ccaaaggtgt atagattgct tgaaaggggg tggtagtgcc tctttttaag atctgttgag   2346

tcggctacag tctggctaag taagaagcat ttgcatactg attccatcat ttaatcttta   2406

aaagtatgtg ttttaaaaat gtaaccagaa tgattcttca atagaaatga gatttggtgg   2466

agtctggatt gcctgttttg tatataatat atacttaaga tatataatac cacctcattt   2526

tctgggcatt atttcctaat tgttgatgtt tcaggctttt gataagtcat tttatatatt   2586

tcaaatttaa ctcagaataa gtaaatattt atggcaaatg cagttttatg tactttcagg   2646

agaagaccat caggaaaaga caggacaaag aagtcaaaca ttaaagccct tgcaaatatt   2706

agaggacctt agacaattac caaaaagtgt ttaataggga agttgcaaat gattctctta   2766

gtaaattaaa catttaaaaa gtagttttaa tgtgccttgg gcatcttgaa aagaagagtg   2826

tgatataatt tatgcttagt gttaactggt cattttacat tgtatttatt aagtctgctg   2886

aaaaatgagg ttttaaggaa gaaaatgcag attattttag ggtaaacagg ccaggtgtcc   2946

tttgaagaac tttgtttaca tcaaattgat gaaattacag tgattcctta cttttttttgc   3006

tagttgtact ttgaaattgt tatgggttcg atttccaaaa tatgtaactt atttttttaaa   3066
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ggaataaggt gtgctgtgta tttgttgatt aaaaatcatt tgtcttgcag agtatccttt   3126

tttgaaggaa atatacatcc ttataacaca tcaggtagtt ttcttttttc tgtatttaaa   3186

ttatatattt gaattaattg aatataattt gagttacata taattctata taaaggttac   3246

atattgaatt atggttctaa tctgtttagg aaagaaatga attttctaag catttaatac   3306

atttggaata attttagttt ctaaaaagta ctaatgtaag ttaagtttat atcaaatgca   3366

aattaccttg tataactaac aagcacagtt attgtttaac attatggatt ttaattgtgt   3426

tgacaccctt ctttgaattt gttgcttt                                      3454
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<210> 220
<211> 1873
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (179)..(1480)

<400> 220
ctccccctcc aggacctccc tgggtcagct tattgaactg accgtagaaa ggcagaaaac      60

cactggcagc agccctcccc atctgcccag caaacggctg cccccatggg acagggccag     120

gccgagggat ccctccgagg acaccccagc agtggacggc agcacagaca cggacagg       178
atg ccc ttg aag ctc tac ttg cct ggt ggt aat tcc agg atg acc cag       226
Met Pro Leu Lys Leu Tyr Leu Pro Gly Gly Asn Ser Arg Met Thr Gln
 1               5                  10                  15

gag agg ctg gaa aga gcg ttc aaa cgg cag ggc agc cag ccc gca cct       274
Glu Arg Leu Glu Arg Ala Phe Lys Arg Gln Gly Ser Gln Pro Ala Pro
            20                  25                  30

gtc agg aaa aat cag ttg ctg ccg tct gac aag gtg gat ggt gag ctg       322
Val Arg Lys Asn Gln Leu Leu Pro Ser Asp Lys Val Asp Gly Glu Leu
        35                  40                  45

ggt gcc ctg cgg ctc gag gat gtg gag gat gag ttg ata agg gaa gag       370
Gly Ala Leu Arg Leu Glu Asp Val Glu Asp Glu Leu Ile Arg Glu Glu
    50                  55                  60

gtc atc ctg tcg cca gtc cca tca gtg ctc aag ttg cag aca gca tca       418
Val Ile Leu Ser Pro Val Pro Ser Val Leu Lys Leu Gln Thr Ala Ser
65                  70                  75                  80

aaa cca att gac ctc tca gta gca aag gaa ata aag acc ctt ctg ttt       466
Lys Pro Ile Asp Leu Ser Val Ala Lys Glu Ile Lys Thr Leu Leu Phe
                85                  90                  95
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ggt tcc agc ttt tgc tgt ttc aat gaa gaa tgg aaa ctt cag agt ttt        514
Gly Ser Ser Phe Cys Cys Phe Asn Glu Glu Trp Lys Leu Gln Ser Phe
            100                 105                 110

tcc ttt agt aac aca gcc tca tta aaa tac ggc ata gtg cag aac aag        562
Ser Phe Ser Asn Thr Ala Ser Leu Lys Tyr Gly Ile Val Gln Asn Lys
        115                 120                 125

ggt ggt cct tgc gga gtc ctg gca gct gtc caa ggc tgt gtc cta cag        610
Gly Gly Pro Cys Gly Val Leu Ala Ala Val Gln Gly Cys Val Leu Gln
    130                 135                 140

aaa ctc ctg ttt gaa gga gat agc aaa gcc gac tgt gct cag gga ctg        658
Lys Leu Leu Phe Glu Gly Asp Ser Lys Ala Asp Cys Ala Gln Gly Leu
145                 150                 155                 160

cag cct tca gat gcc cac cgg acc cgc tgc ctc gtc ctg gcc ctc gca        706
Gln Pro Ser Asp Ala His Arg Thr Arg Cys Leu Val Leu Ala Leu Ala
                165                 170                 175

gac att gtg tgg cgg gca ggg ggc cga gag aga gcc gtt gtt gca ctg        754
Asp Ile Val Trp Arg Ala Gly Gly Arg Glu Arg Ala Val Val Ala Leu
            180                 185                 190

gct tcg aga aca cag cag ttc agt cca aca ggg aaa tac aaa gca gat        802
Ala Ser Arg Thr Gln Gln Phe Ser Pro Thr Gly Lys Tyr Lys Ala Asp
        195                 200                 205

gga gtc tta gaa aca ctt acg ctt cac agt ttg acc tgc tat gag gac        850
Gly Val Leu Glu Thr Leu Thr Leu His Ser Leu Thr Cys Tyr Glu Asp
    210                 215                 220

ctg gtg act ttt ctt caa caa agc att cat cag ttt gaa gtg ggc ccc        898
Leu Val Thr Phe Leu Gln Gln Ser Ile His Gln Phe Glu Val Gly Pro
225                 230                 235                 240

tat ggc tgc atc ctg ctc acc ctt tct gcc atc ctg tcc agg tct aca        946
Tyr Gly Cys Ile Leu Leu Thr Leu Ser Ala Ile Leu Ser Arg Ser Thr
                245                 250                 255

gag ctc atc cgc cag gac ttt gat gtc ccc acc agc cac ctg att gga        994
Glu Leu Ile Arg Gln Asp Phe Asp Val Pro Thr Ser His Leu Ile Gly
            260                 265                 270

gca cat ggc tac tgt aca cag gaa ctt gtc aat ctg ctc ctg act ggg       1042
Ala His Gly Tyr Cys Thr Gln Glu Leu Val Asn Leu Leu Leu Thr Gly
        275                 280                 285

aaa gct gtg tcc aac gtt ttc aac gat gtg gtt gag ctg gat tct ggg       1090
Lys Ala Val Ser Asn Val Phe Asn Asp Val Val Glu Leu Asp Ser Gly
    290                 295                 300

gat ggg aac atc aca ctt ctc aga ggc att gct gca cgc agt gat att       1138
Asp Gly Asn Ile Thr Leu Leu Arg Gly Ile Ala Ala Arg Ser Asp Ile
305                 310                 315                 320

ggc ttc tta tct ctc ttt gag cat tac aac atg tgc cag gtt ggc tgc       1186
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Gly Phe Leu Ser Leu Phe Glu His Tyr Asn Met Cys Gln Val Gly Cys
                325                 330                 335

ttc ctg aag acc ccg agg ttc ccc atc tgg gtg gtt tgc agt gag agc      1234
Phe Leu Lys Thr Pro Arg Phe Pro Ile Trp Val Val Cys Ser Glu Ser
            340                 345                 350

cac ttc agc atc ctc ttt agc ctg cag ccg ggg ctc ctg cgt gac tgg      1282
His Phe Ser Ile Leu Phe Ser Leu Gln Pro Gly Leu Leu Arg Asp Trp
        355                 360                 365

agg act gag agg ctc ttt gac ttg tac tac tac gat ggc ctg gcc aac      1330
Arg Thr Glu Arg Leu Phe Asp Leu Tyr Tyr Tyr Asp Gly Leu Ala Asn
    370                 375                 380

cag cag gag cag atc cgg ctg acc att gac acc acc caa acc atc tct      1378
Gln Gln Glu Gln Ile Arg Leu Thr Ile Asp Thr Thr Gln Thr Ile Ser
385                 390                 395                 400

gag gac aca gac aac gac ctt gtc cca ccc ctc gag ctc tgc atc aga      1426
Glu Asp Thr Asp Asn Asp Leu Val Pro Pro Leu Glu Leu Cys Ile Arg
                405                 410                 415

acc aag tgg aag ggg gca tca gtg aac tgg aac ggc tca gac ccc atc      1474
Thr Lys Trp Lys Gly Ala Ser Val Asn Trp Asn Gly Ser Asp Pro Ile
            420                 425                 430

ctg tga ccgttggatg tgggtaaacc ctgtggtcca ccactcatca cctcatcacc      1530
Leu  *

gaggatgaca gctgaacccc aagcctctgg ggcaggtctc atgtacccca acctgggtca   1590

gcatgactgc agaagcatcc agagcctccc tgccccttcc atgaagggcc cacccaagac   1650

tgtgctgggg acccagtgtg ttgctgggtc ccctcccagc tgagctgtga ctgctgagta   1710

ctggaaggag gttgccaggg tctctgctac ctttgtctgc atccctccct tgctccctgc   1770

tgggtggtcc ctcacccagg cctccaatgt ggttggccct ggggactcat tacttctggt   1830

agctggcttt ctataaaaat gggtcaaacc caaaaaaaaa aaa                      1873
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<211> 787
<212> DNA
<213> Homo sapiens

<220>
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<222> (371)..(595)

<400> 221

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ccccacacct ttgccccaga gccacaggtc ccacggagtg tcacgtaatt ccccacatcc     120

agaacagcta cccatctcaa accccaggag tcaccagccc ttgggccctc acatccctgg     180

agcctcagcc ccctccacac acgtgctgtg aatcataggg ggatcaggat actcctgctc     240

acagacaccc atctccccct accaaaaata acgctgggct cctccttcca ccctgactct     300

gcctctctgt ctgcaggagc ctggtcgggg tgctccacag aagctgtgcc tgggcttggg     360

agccaaggcc   atg tcc ctc tcc cgg cca ggg gag acg gag ccc atc cac       409
             Met Ser Leu Ser Arg Pro Gly Glu Thr Glu Pro Ile His
               1               5                  10

agt gtc agc tat ggc cat gtg gcc gcc tgc cag cta atg ggc ccc cac       457
Ser Val Ser Tyr Gly His Val Ala Ala Cys Gln Leu Met Gly Pro His
    15                  20                  25

acc ctg gcc ttg agg gtg gga gag agc cag ctc ctc ctg cag agc ccc       505
Thr Leu Ala Leu Arg Val Gly Glu Ser Gln Leu Leu Leu Gln Ser Pro
 30                  35                  40                  45

cag gtg agt gag aag agg agt tgt ggg agg agg aga gaa ggg aag cga       553
Gln Val Ser Glu Lys Arg Ser Cys Gly Arg Arg Arg Glu Gly Lys Arg
                50                  55                  60

tgt cag gaa gca ttt aca gaa cac caa acc tgg gcc agg tag agctcta       602
Cys Gln Glu Ala Phe Thr Glu His Gln Thr Trp Ala Arg  *
            65                  70                  75

agcactgggg atccagcagt gatcacagac aagctgaagg agcttacact agagtggagt     662

cagacaataa acaaggaatc ccaggctatg aagacagtga gaaatgctac aaaggaaaga     722

gtgatgtgac aggaagccag ggaagggttc tcaaaaaggg tgccatttaa gctagccagg     782

gaaga                                                                 787



     <210> 222
     <211> 1184
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (66)..(425)

     <400> 222
gatgccctgc tgtgccatgc ttgctagtca tgttcttttc ctcctagatc tccatttgcc      60

aggag    atg ccc agc ctg gag gtg atc acg ctc agg tac ctc gct cct       107
         Met Pro Ser Leu Glu Val Ile Thr Leu Arg Tyr Leu Ala Pro
           1               5                  10
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gct gtc atg ctc agc ctg ggg cct gga agc cgg ggc aga gcc tca cgt       155
Ala Val Met Leu Ser Leu Gly Pro Gly Ser Arg Gly Arg Ala Ser Arg
 15                  20                  25                  30

ccc tcc agt ggg acc cag cac tgt gac ata acc tgg aaa cct cca aca       203
Pro Ser Ser Gly Thr Gln His Cys Asp Ile Thr Trp Lys Pro Pro Thr
                 35                  40                  45

cag act gag ggc ggc ttc cag aag ggg agg ggc cgg gac agc gag agc       251
Gln Thr Glu Gly Gly Phe Gln Lys Gly Arg Gly Arg Asp Ser Glu Ser
             50                  55                  60

tgg gcc tac cct gtg gcc ccc atg ttc agc cct cct tcc tca gag cct       299
Trp Ala Tyr Pro Val Ala Pro Met Phe Ser Pro Pro Ser Ser Glu Pro
         65                  70                  75

cac ctg ggc ctc ctg atg gct cct gtc ccc tgc ctg ccc tgc tgt acg       347
His Leu Gly Leu Leu Met Ala Pro Val Pro Cys Leu Pro Cys Cys Thr
     80                  85                  90

cct gcc cac cct tgg cct gtg tgc tcc gat aag cca ttg ctg tgt tca       395
Pro Ala His Pro Trp Pro Val Cys Ser Asp Lys Pro Leu Leu Cys Ser
 95                 100                 105                 110

ctg ggc cag tcg gtg gtg gag ccc tcc taa g gattcacggt ggcccgccct       446
Leu Gly Gln Ser Val Val Glu Pro Ser  *
                115                 120

ggccgccccc acggtggcca catctgccct gggacccccca gagtcctggc ctcttctgcc    506

ccccagtgcc accactgcct accagtttct ctgcacccca tgacctgtgc ccgtcttctg     566

gggtcactgc cctcccagca gactaaggga agcttgaatg aacaaatgtt actggacttt     626

caggcagttg gggtgtattt gggggctctg gggaagagaa gagctccctt tatccctgaa     686

ttccctcctg cctactgtgg gacccacgga gggagcagac gctcatggct caccactgcc     746

caccagacgc tggatgggcg ccttctgtgg gtttccgcat ttaaaagctt cacaagggtt     806

taaacctgtg gggaagccca cccctctggc agctcagaag tctctagggc ttgccctctg     866

agagtgggta ttgcaggccc ctggtccctg actgtgacct accttcttga tctcacaggc     926

agccacgggg taggccagcc cctgcccatc ctccgtaatg ccctctgagg ttggcattgc     986

catgttgatg cccgtgccca gcctgctgcc cgccatgggc tgaggccagt ccatctggtg    1046

ttcaggcatc cccagcgcgg gcaccagcct gtcctgcccg agccttgctg aatgaatgaa    1106

atgggcttgg aggcatgctc atgggtcaaa tctcagccct cccatctatt ggctggctaa    1166

ccttgggcga ggcatggc                                                  1184
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     <210> 223
     <211> 4716
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (74)..(1732)

     <400> 223
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agagccttgg gag   atg acg agt gag atg aca aga agc cca ttc tca gat      109
                 Met Thr Ser Glu Met Thr Arg Ser Pro Phe Ser Asp
                   1               5                  10

tgg gaa tct ata tat gtg aca cag gaa tta cct ctg aag cag ttc atg      157
Trp Glu Ser Ile Tyr Val Thr Gln Glu Leu Pro Leu Lys Gln Phe Met
         15                  20                  25

tat gat gat gca tgc atg gag gga att act agc tat gga ctt gag tgt      205
Tyr Asp Asp Ala Cys Met Glu Gly Ile Thr Ser Tyr Gly Leu Glu Cys
     30                  35                  40

tcc act ttt gaa gaa aat tgg aaa tgg gaa gac ctt ttt gag aag cag      253
Ser Thr Phe Glu Glu Asn Trp Lys Trp Glu Asp Leu Phe Glu Lys Gln
 45                  50                  55                  60

atg gga agt cat gag atg ttt agc aag aaa gaa ata atc act cat aaa      301
Met Gly Ser His Glu Met Phe Ser Lys Lys Glu Ile Ile Thr His Lys
                 65                  70                  75

gaa acc atc act aag gaa aca gaa ttc aaa tat act aaa ttt ggg aaa      349
Glu Thr Ile Thr Lys Glu Thr Glu Phe Lys Tyr Thr Lys Phe Gly Lys
             80                  85                  90

tgt atc cat ctg gaa aac ata gaa gag agt att tat aat cac aca tca      397
Cys Ile His Leu Glu Asn Ile Glu Glu Ser Ile Tyr Asn His Thr Ser
         95                 100                 105

gat aaa aaa agc ttc tcc aaa aat tct att gta ata aaa cac aag aaa      445
Asp Lys Lys Ser Phe Ser Lys Asn Ser Ile Val Ile Lys His Lys Lys
    110                 115                 120

gtc tat gta gga aag aag ctt ttt aaa tgt aat gaa tgt gac aaa acc      493
Val Tyr Val Gly Lys Lys Leu Phe Lys Cys Asn Glu Cys Asp Lys Thr
125                 130                 135                 140

ttc acc cat agc tca tcc ctt act gtt cat ttt aga att cat act ggt      541
Phe Thr His Ser Ser Ser Leu Thr Val His Phe Arg Ile His Thr Gly
                145                 150                 155

gaa aaa cca tat gca tgt gag gaa tgt gga aaa gcc ttc aag caa agg      589
Glu Lys Pro Tyr Ala Cys Glu Glu Cys Gly Lys Ala Phe Lys Gln Arg
            160                 165                 170
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caa cac ctt gct caa cat cac aga aca cat act gga gag aaa ctc ttt       637
Gln His Leu Ala Gln His His Arg Thr His Thr Gly Glu Lys Leu Phe
        175                 180                 185

gaa tgt aaa gaa tgt agg aaa gcc ttc aaa caa agt gaa cac ctt att       685
Glu Cys Lys Glu Cys Arg Lys Ala Phe Lys Gln Ser Glu His Leu Ile
    190                 195                 200

cag cat caa aga att cat act gga gaa aaa cca tat aaa tgt aag gaa       733
Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu
205                 210                 215                 220

tgc aga aaa gcc ttc aga cag cct gca cac ctt gct cag cat cag aga       781
Cys Arg Lys Ala Phe Arg Gln Pro Ala His Leu Ala Gln His Gln Arg
                225                 230                 235

att cat act gga gag aaa ccc tat gaa tgt aaa gaa tgt ggc aaa gcc       829
Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala
            240                 245                 250

ttc agt gat ggc tcg tct ttt gct cga cat cag aga tgt cac act ggc       877
Phe Ser Asp Gly Ser Ser Phe Ala Arg His Gln Arg Cys His Thr Gly
        255                 260                 265

aaa aga ccc tat gaa tgt att gag tgt ggg aag gct ttt agg tat aac       925
Lys Arg Pro Tyr Glu Cys Ile Glu Cys Gly Lys Ala Phe Arg Tyr Asn
    270                 275                 280

aca tct ttt att cgt cac tgg agg agt tat cat act gga gag aag cct       973
Thr Ser Phe Ile Arg His Trp Arg Ser Tyr His Thr Gly Glu Lys Pro
285                 290                 295                 300

ttt aat tgc att gat tgt ggg aaa gcc ttc agt gtt cac ata gga ctt      1021
Phe Asn Cys Ile Asp Cys Gly Lys Ala Phe Ser Val His Ile Gly Leu
                305                 310                 315

att ctg cat agg aga att cat aca gga gag aaa cct tac aaa tgt gat      1069
Ile Leu His Arg Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asp
            320                 325                 330

gtg tgt gga aaa acc ttc agc tcg ggt tca tcc cgt act gta cat cag      1117
Val Cys Gly Lys Thr Phe Ser Ser Gly Ser Ser Arg Thr Val His Gln
        335                 340                 345

aga att cat aca gga gag aaa cct tat gaa tgt gat ata tgt ggg aaa      1165
Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asp Ile Cys Gly Lys
    350                 355                 360

gat ttt agc cat cat gca tca ctc act cag cat caa aga gta cat tct      1213
Asp Phe Ser His His Ala Ser Leu Thr Gln His Gln Arg Val His Ser
365                 370                 375                 380

gga gag aaa ccg tat gaa tgc aag gaa tgt ggg aaa gcc ttt agg cag      1261
Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Gln
                385                 390                 395

aat gta cac ctt gtt agt cat ttg aga att cat act ggt gaa aaa ccc      1309
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Asn Val His Leu Val Ser His Leu Arg Ile His Thr Gly Glu Lys Pro
            400                 405                 410

tat gaa tgt aaa gaa tgt gga aaa gct ttt aga atc agt tca cag ctg      1357
Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Ile Ser Ser Gln Leu
        415                 420                 425

gct act cat cag aga att cat act gga gag aag cct tat gaa tgt att      1405
Ala Thr His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Ile
    430                 435                 440

gaa tgt gga aat gct ttc aaa cag aga tca cac ctt gcc caa cat cag      1453
Glu Cys Gly Asn Ala Phe Lys Gln Arg Ser His Leu Ala Gln His Gln
445                 450                 455                 460

aaa act cat aca gga gag aaa cct tat gag tgt aat gaa tgc ggg aaa      1501
Lys Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys
                465                 470                 475

gcc ttc agc caa act tgc aat ctt act caa cat caa aga att cat act      1549
Ala Phe Ser Gln Thr Cys Asn Leu Thr Gln His Gln Arg Ile His Thr
            480                 485                 490

gga gag aaa ccc tat aaa tgt act gaa tgt gga aag gct ttt agt gat      1597
Gly Glu Lys Pro Tyr Lys Cys Thr Glu Cys Gly Lys Ala Phe Ser Asp
        495                 500                 505

agc tca tcc tgt gct cag cat caa aga ctc cac act ggc caa agg ccc      1645
Ser Ser Ser Cys Ala Gln His Gln Arg Leu His Thr Gly Gln Arg Pro
    510                 515                 520

tat cag tgt ttt gaa tgt ggg aag gcg ttc aga aga aag tta tcc tta      1693
Tyr Gln Cys Phe Glu Cys Gly Lys Ala Phe Arg Arg Lys Leu Ser Leu
525                 530                 535                 540

att tgt cat caa aga agt cat act gga gaa gaa cct taa gaatgtagtg       1742
Ile Cys His Gln Arg Ser His Thr Gly Glu Glu Pro  *
                545                 550

catgtggcca agcctttagt tatcaccaat cccctactgt taatcagaga tgtcccactg    1802

gataaaaaac atataaatgt aagaaatgta gaaaaacctt cagccaggag gctggcaaga    1862

tggccgaata ggaacagctc tgatctgcag ttcccagtga gatcaacgca gaaggtgggt    1922

gctttctgta tttccagctg aggtacctgg ctcatctcat tgggactggt tagacagtgg    1982

gtgcagccca cggagggtga gctgaagcag ggtggggtgt aacctcacct gggaagtgca    2042

aggagtcggg gatctccctc ccctagccaa gggaagccat gagggactgt gccatgagga    2102

atggtgcact ccggcacaga tactacgctt ttcccatggt cttcgcaacc cacagaccag    2162

gagatcccct tgggtgccta tgccaccaag gccctgggtt tcaagcacaa aactgggcgg    2222

ccattcgggc agacaccgag ctagctgtag gagttttttt gatagcccag tggcacctgg    2282
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aatgccagtg aaacagaacc gcttactccc ttgttaaggg ggctgaagcc ggggagccaa 2342

gtggttccca tgcccactga gcccagcaag ctaagatcca ctggcttgga attctccctg 2402

ccagcacagc agtctgaagt caacctggga tgatcaagct tggtgggggg aggggcgcca 2462

accattacca aagcttgaat aggtggtttt cccctcacag cgtaaacaaa gccatgggga 2522

agttccagct gagcagagcc ctccacagct cagcaaagcc tctgtagcca gactgcctct 2582

ctagattcct cctctctggg cagcgcatct ttgaaaaaag tgcagataaa accctcatct 2642

ccctgggaca aagcacgtgg gggaaagggg tgcctgtggg cacagcttca gcagacttaa 2702

acattcctgc ctgccagctc tgaagagagc agcagttctt ccagcacagc gcttgagctc 2762

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tgggtgcccc tctgggacaa agcttccaga ggaaggaaca ggcagcaatc tttgctgttc 2942

tgcagcctcc actggtgata cccaggcaga cagggtctgg agtggacctc cagcaaactc 3002

cagcagacct gcagccgagg ggcctcactg ttagaaggaa aactaacagg aatataatca 3062

acatcaacaa aggacatcca cacagaaacc ccatctgaag gttaccagca tcaaagacca 3122

aaggtagata aattcacgaa gatgaggaga aaccagtgca aaaagcctga aaattccaaa 3182

aaccagaatg cctcttctcc tccaaaggat cacaactcct tgccggcaag ggaacaaaac 3242

tggatagaga atgagtttga caaattgaca gaagtaggct tcagaaggtg ggaaataaca 3302

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gccagctctt cctcacccac tacatcacca agtcctgtgg atatatctgc taaatatttt 3662

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aaaaaaaaag tctgtgcata gttttagtga tacaccacct ccaataagca aaaaagtcct 3902

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ttagtaaatg ttagataagt attctccaga gttgatgtaa attattttta aacagtgcat 4142

tcttgaaagc agtatggcag tcataaaaat tttggaacca aaacagtatc tttttttaag 4202

ctaaaaaaaa gttttaaatg gtgtctttct atgttgccca gggtggtctc aaactcctgt 4262

gctcaagtga ccctcccacc tcattctcaa gtggctgcaa ttacaggcaa ccagcctgac 4322

ttaaaacagt atcttaaggt agatggtgat tagcacatgt agtatgctta acatttaata 4382

ttataataag acatcacagc ggctgtctca tgattaaggc tgtgttccct tgttggtgag 4442

gaaattaatt atgacttgat aaatagaaca tgttttaaga agtggctata tagctctgga 4502

taaaacgaac aaaagaatta gaattcctgc ggggaatata tacaagactt tatttagtca 4562

agtaaaaaaa aatcactaat gtttaactga agaaagagaa attgaataat atagttctat 4622

ttcaacatgt gggttcacag atttattcta accttccaag taaagttgtt ccactagtaa 4682

agttgttctg gagtatattt ttaaaaaaaa aaaa 4716

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<213> Homo sapiens

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<222> (578)..(916)

<400> 224
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gactctcagg gccactgctg cacagggtga caaccgggca tggcacgcag tgtggctggt 120

gcagaggagg cttaaggctg gcctgggaga gattcttggt ctagctccca gcacggagcc 180

ttgcttgtgt cccagggcgg cactaaccag aaccagaaaa ggaaatcttt ggccctcggg 240

gagaattatg ccaattatct gtctggttcc tgtctttgaa aatgcccaga tgttggttta 300

caaatcagga agctgtcttg gggcaatctc tgttccctct ttgatgcaga gagcctttct 360

ctgtaaacac tggagagcag ggcttcactg tctggctccc ctcccgcctc ttgcaggaag 420

gactagatgc tgctgatcag ctgatcatgg ctgagccggg tagagcttgg ggctctccta 480

agaggtcacc cactgggagg gagcttcaca gctgttcttt tgacccagga aggagctctt 540

tcaggactgt ggcacccaga gccgtggccc tcctgcc atg cca ttg ttc cca ctt 595

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                                            Met Pro Leu Phe Pro Leu
                                             1               5

ccc tgc cct tgg gag tct tgg aga cag ctg act agc tgc cct gag ggg       643
Pro Cys Pro Trp Glu Ser Trp Arg Gln Leu Thr Ser Cys Pro Glu Gly
            10                  15                  20

tcc acc gct ctc acc ttc tca ctg gtg gct gct gcc att ctc ctg ggc       691
Ser Thr Ala Leu Thr Phe Ser Leu Val Ala Ala Ala Ile Leu Leu Gly
        25                  30                  35

tct gca cag aaa gct ttg gtc ctt ctg aaa gcc act ctg ccc ctt cct       739
Ser Ala Gln Lys Ala Leu Val Leu Leu Lys Ala Thr Leu Pro Leu Pro
    40                  45                  50

gca gca cca gat ccc cct gag ccg gta ctg ctg cct cca cct ggg cca       787
Ala Ala Pro Asp Pro Pro Glu Pro Val Leu Leu Pro Pro Pro Gly Pro
 55                  60                  65                  70

aga cta gtc ttg gtg ttc acc ctt ctt cgt gct tca gaa agt agg gat       835
Arg Leu Val Leu Val Phe Thr Leu Leu Arg Ala Ser Glu Ser Arg Asp
                75                  80                  85

atc tgg gga cat gac tgt gtt tcc ctg ggg tcc ttt cag aag aga ctt       883
Ile Trp Gly His Asp Cys Val Ser Leu Gly Ser Phe Gln Lys Arg Leu
            90                  95                  100

agg aag ctc ctg ctc agg aat ctg gcc ctc tga aagagccc cttcaaagca       934
Arg Lys Leu Leu Leu Arg Asn Leu Ala Leu  *
        105                 110

gcctgggcag caggtaacgt ggtttccctt gcggccccct cctcccagct gcatagactc     994

gtggtttgaa gtgaacagat cttgtccgga ac                                  1026


     <210> 225
     <211> 1267
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (70)..(609)

     <400> 225
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accgccaag    atg gtg gtg ggc gcg ttc cct atg gcg aag ctg cta tac      108
             Met Val Val Gly Ala Phe Pro Met Ala Lys Leu Leu Tyr
              1               5                  10

ttg ggc atc cgg cag gtc agc aag ccg ctt gcc aac cgt att aag gag      156
Leu Gly Ile Arg Gln Val Ser Lys Pro Leu Ala Asn Arg Ile Lys Glu
    15                  20                  25
```

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gcc gcc cgc cga agc gag ttc ttc aag acc tat atc tgc ctc ccg ccg      204
Ala Ala Arg Arg Ser Glu Phe Phe Lys Thr Tyr Ile Cys Leu Pro Pro
 30                  35                  40                  45

gct caa ctg tat cac tgg gtg gag atg cgg acc aag atg cgc atc atg      252
Ala Gln Leu Tyr His Trp Val Glu Met Arg Thr Lys Met Arg Ile Met
                 50                  55                  60

ggc ttc cgg ggc acg gtc atc aag ccg ctg aac gag gag gcg gca gct      300
Gly Phe Arg Gly Thr Val Ile Lys Pro Leu Asn Glu Glu Ala Ala Ala
             65                  70                  75

gag ctg ggc gca gag ctg ctg ggc gaa gcc acc atc ttc atc gtg ggc      348
Glu Leu Gly Ala Glu Leu Leu Gly Glu Ala Thr Ile Phe Ile Val Gly
         80                  85                  90

ggc ggc tgc cta gtg ctg gag tac tgg cgc cac cag gcg cag cag cgc      396
Gly Gly Cys Leu Val Leu Glu Tyr Trp Arg His Gln Ala Gln Gln Arg
     95                  100                 105

cac aag gag gag gag cag cgt gct gcc tgg aac gcg ctg cgg gac gag      444
His Lys Glu Glu Glu Gln Arg Ala Ala Trp Asn Ala Leu Arg Asp Glu
110                 115                 120                 125

gtg ggc cac ctg gcg ctg gcg ctg gaa gcg ctg cag gcg cag gtg cag      492
Val Gly His Leu Ala Leu Ala Leu Glu Ala Leu Gln Ala Gln Val Gln
                130                 135                 140

gcg gcg ccg cca cag ggc gcc ctg gag gaa ctg cgc aca gag ctg caa      540
Ala Ala Pro Pro Gln Gly Ala Leu Glu Glu Leu Arg Thr Glu Leu Gln
            145                 150                 155

gag gtg cgc gcc cag ctc tgc aat ccc ggc cgg tcc gct tcc cac gca      588
Glu Val Arg Ala Gln Leu Cys Asn Pro Gly Arg Ser Ala Ser His Ala
        160                 165                 170

gtg cct gcg tcc aag aaa tag ga gcttgctgga tggaacctga atttggacat      641
Val Pro Ala Ser Lys Lys  *
    175                 180

ggcctatgta cctaacgtgg ccttcttccc gcaccaccct tgcctgcgct ggcccagtgg    701

aaaccaccag gatcttgatg caacttggca tttggttacc cctgctgata agagcagcca    761

ttacctgcca ctgggaccag caggtgaagc gttgcaacat agccccctcc atcatccttc    821

acctcctatc cccactcca aaccaggacg acctgcaagg tcccagccag caggacaccg     881

tgggcactct ggcaaatgaa aaaatggaac ctggtcttga gctgaatcaa tgtgttattg    941

ttacccccac ccccggttta cctgatcagt gttaaccttt actgggacac tcatctgtta   1001

cactggaaca ccttcttctt tttgtcaatc ggcacagacc actgtaagga aatgcagtgt   1061

gttgcagtgg ccttttctcc ccctcacctt ctaaggtcag ctctagctga gcatcagtgc   1121
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tctcttaagg aggaaaaaaa cggtgcggct gggagcggtg gctcacgcct gtaatcctag   1181

caccttggga ggccgaggcg ggcggatcac ttgaggtcag gagttccaga ccagcctggc   1241

caacatggtg aaactccgtc tttcta                                        1267




      <210> 226
      <211> 1813
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (494)..(1126)

      <400> 226
ccggaattcc cgggtcgacc cacgcgtccg aaagaacccg gccaggtgca gggtttcatg     60

cctataatcc cagcactttg ggaggcctag acgggaggat tgcttgagct cagaagtttg    120

agatcagcct caacaagatg atgagacccc ttctctacaa aagaaattat aaaaaattag    180

tcaggtgtgg tagtacacac ctatagcccc agctactcag gaggctgaag cgggaggatc    240

acttgaggcc aggagtttga ggccatagtg agcaaggatc atgccactgc cctccagcct    300

gggcaacaac gagaccctgt ctctaaaaaa taaataaaaa ctagttcctc gcccgctggg    360

tgctgaagtt gggcggatgg cagcaaaccg gctccgctag aggaccgagc cgcccagccc    420

cgctcccccg gacccatcgg cgcgctgccc acacctccag gcgaccggcc aactgggtcc    480

tgaagtagct gaa   atg cga aaa agg cag cag tcc caa aat gaa gga aca     529
                 Met Arg Lys Arg Gln Gln Ser Gln Asn Glu Gly Thr
                 1               5                   10

cct gcc gtg tct caa gct cct gga aac cag agg ccc aac aac acc tgt      577
Pro Ala Val Ser Gln Ala Pro Gly Asn Gln Arg Pro Asn Asn Thr Cys
        15                  20                  25

tgc ttt tgt tgg tgc tgt tgt tgc agc tgc tcc tgc ctc act gtg agg      625
Cys Phe Cys Trp Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg
    30                  35                  40

aat gaa gaa aga ggg gaa aat gcg gga aga ccc aca cac act aca aaa      673
Asn Glu Glu Arg Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys
45                  50                  55                  60

atg gag agt atc cag gtc cta gag gaa tgc caa aac ccc act gca gag      721
Met Glu Ser Ile Gln Val Leu Glu Glu Cys Gln Asn Pro Thr Ala Glu
                65                  70                  75

gaa gtc ttg tcc tgg tct caa aat ttt gac aag atg atg aag gcc cca      769
Glu Val Leu Ser Trp Ser Gln Asn Phe Asp Lys Met Met Lys Ala Pro
```

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             80                  85                  90

gca gga aga aac ctt ttc aga gag ttc ctc cga aca gaa tac agt gaa      817
Ala Gly Arg Asn Leu Phe Arg Glu Phe Leu Arg Thr Glu Tyr Ser Glu
         95                 100                 105

gag aac cta ctt ttc tgg ctt gct tgt gaa gac tta aag aag gag cag      865
Glu Asn Leu Leu Phe Trp Leu Ala Cys Glu Asp Leu Lys Lys Glu Gln
    110                 115                 120

aac aaa aaa gta att gaa gaa aag gct agg atg ata tat gaa gat tac      913
Asn Lys Lys Val Ile Glu Glu Lys Ala Arg Met Ile Tyr Glu Asp Tyr
125                 130                 135                 140

att tct ata cta tca cca aaa gag gtc agt ctt gat tct cga gtt aga      961
Ile Ser Ile Leu Ser Pro Lys Glu Val Ser Leu Asp Ser Arg Val Arg
                145                 150                 155

gag gtg atc aat aga aat ctg ttg gat ccc aat cct cac atg tat gaa     1009
Glu Val Ile Asn Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu
            160                 165                 170

gat gcc caa ctt cag ata tat act tta atg cac aga gat tct ttt cca     1057
Asp Ala Gln Leu Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro
        175                 180                 185

agg ttt ttg aac tct caa att tat aag tca ttt gtt gaa agt act gct     1105
Arg Phe Leu Asn Ser Gln Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala
    190                 195                 200

ggc tct tct tct gaa tct taa tg ttcatttaaa aacaatcatt ttggagggct     1158
Gly Ser Ser Ser Glu Ser  *
205                 210

gagatgggaa ataaaagtag ttaaataaca tcagaaactg agttcctgga gaactacagt   1218

ttagcattcc tcaggctact gtgaaaacac aaccgttatg gtctttgtct ccatttttat   1278

caaggttttc catggttaag tttggagaaa ataccacaca aaacaatgaa ttgccaaatt   1338

gtttgtttta ttcaagactc attctacttg caagcaaagt gtatttgtag tcctatgaac   1398

agtctcctcg tgtatctcca gagactgcat gtgcaaagta aaatgcttca tttgccacat   1458

agttgttgta atatttaatc cagtagcata acttatatct gtatttaagg acttttgtgc   1518

aatatggtct taagaaataa ttgccaaaaa aatcggccat gggttgcatt ttttaacata   1578

atctaagacc caaaaaaaag catttttact atggaacaat ggtattcaac aatctatata   1638

ctgtgtttag taccctaatt tttgagccaa tatttctgta ccttaaaaaa aactatttat   1698

ctttgtttgt tggaaaaacc taatggggaa tcctctggtg gtccttgcca aaactgtgga   1758

tttttctttc cgggaaagtt tcctttgcct aaagccccaa acccaaaaaa aaaaa        1813
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<210> 227
<211> 3404
<212> DNA
<213> Homo sapiens

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<222> (170)..(2119)

<400> 227
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atccggcggc tcagcccggg gcggcgaggc tcggcacgga gatggcggcg cgctcggcgc     120

agacagagct gtgaaccaac cccgctcacg gctaacaagc ccacccacc  atg gcg        175
                                                       Met Ala
                                                        1

agc ccc act ctg agc ccc gac tcc tca tcc cag gag gcc ctg tcg gcc       223
Ser Pro Thr Leu Ser Pro Asp Ser Ser Ser Gln Glu Ala Leu Ser Ala
        5                  10                  15

ccc acc tgc tcc cca acc tct gac tcc gag aac ctc agc ccc gat gag       271
Pro Thr Cys Ser Pro Thr Ser Asp Ser Glu Asn Leu Ser Pro Asp Glu
    20                  25                  30

ctg gag ctg ctg gcc aag ctc gaa gag cag aac cgg ctc ctg gag gcc       319
Leu Glu Leu Leu Ala Lys Leu Glu Glu Gln Asn Arg Leu Leu Glu Ala
35                  40                  45                  50

gac tcc aag tcc atg cgc tcc atg aat ggc tcg cgg cgg aac agt ggc       367
Asp Ser Lys Ser Met Arg Ser Met Asn Gly Ser Arg Arg Asn Ser Gly
                55                  60                  65

tcc tcg cta gtg tcc agc tcc tcg gcc tcc tcc aac ctg agc cac ctg       415
Ser Ser Leu Val Ser Ser Ser Ser Ala Ser Ser Asn Leu Ser His Leu
            70                  75                  80

gag gag gac acg tgg atc ctg tgg ggc cgg atc gcc aac gag tgg gag       463
Glu Glu Asp Thr Trp Ile Leu Trp Gly Arg Ile Ala Asn Glu Trp Glu
        85                  90                  95

gag tgg cgg cgc agg aag gag aag ctg ctc aag gag ctg atc cgc aag       511
Glu Trp Arg Arg Arg Lys Glu Lys Leu Leu Lys Glu Leu Ile Arg Lys
    100                 105                 110

ggc atc ccc cac cac ttc cgg gcc atc gtg tgg cag ctt ctg tgc agc       559
Gly Ile Pro His His Phe Arg Ala Ile Val Trp Gln Leu Leu Cys Ser
115                 120                 125                 130

gcc acg gac atg ccc gtc aag aac cag tac tcc gag ctg ctc aag atg       607
Ala Thr Asp Met Pro Val Lys Asn Gln Tyr Ser Glu Leu Leu Lys Met
                135                 140                 145

tcc tcg ccg tgc gag aag ctg atc cgc agg gac atc gcc cgc acc tac       655
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Ser Ser Pro Cys Glu Lys Leu Ile Arg Arg Asp Ile Ala Arg Thr Tyr
            150                 155                 160

ccg gaa cac gag ttc ttc aag ggc cag gac agc ctg ggc cag gag gtc      703
Pro Glu His Glu Phe Phe Lys Gly Gln Asp Ser Leu Gly Gln Glu Val
        165                 170                 175

ctc ttc aac gtc atg aag gca tac tcg ctg gta gac cgg gag gtg ggc      751
Leu Phe Asn Val Met Lys Ala Tyr Ser Leu Val Asp Arg Glu Val Gly
    180                 185                 190

tac tgc cag gga agc gcc ttc atc gtg ggc ctg ctc ctc atg cag atg      799
Tyr Cys Gln Gly Ser Ala Phe Ile Val Gly Leu Leu Leu Met Gln Met
195                 200                 205                 210

cct gag gag gag gcc ttc tgt gtg ttc gtg cgg ctg atg cag gag tac      847
Pro Glu Glu Glu Ala Phe Cys Val Phe Val Arg Leu Met Gln Glu Tyr
                215                 220                 225

cgg ctg cgg gag ctc ttc aaa ccc agc atg gcc gag ctc ggg ctc tgc      895
Arg Leu Arg Glu Leu Phe Lys Pro Ser Met Ala Glu Leu Gly Leu Cys
            230                 235                 240

atc tat cag ttc gag tac atg ctg cag gag cag ctc cca gac ctc aac      943
Ile Tyr Gln Phe Glu Tyr Met Leu Gln Glu Gln Leu Pro Asp Leu Asn
        245                 250                 255

acc cac ttc cgt tcc caa agc ttc cac aca tcc atg tat gcc tcg tcc      991
Thr His Phe Arg Ser Gln Ser Phe His Thr Ser Met Tyr Ala Ser Ser
    260                 265                 270

tgg ttc ctc aca ctg ttc ctg acc acc ttc cca ctc ccc gtc gcc acc     1039
Trp Phe Leu Thr Leu Phe Leu Thr Thr Phe Pro Leu Pro Val Ala Thr
275                 280                 285                 290

cgg gtc ttt gac atc ttc atg tat gag ggg ctg gag atc gtg ttc cga     1087
Arg Val Phe Asp Ile Phe Met Tyr Glu Gly Leu Glu Ile Val Phe Arg
                295                 300                 305

gtg ggc ctc gcc ctg ctg cag gtg aac cag gcg gag ctg atg cag ctg     1135
Val Gly Leu Ala Leu Leu Gln Val Asn Gln Ala Glu Leu Met Gln Leu
            310                 315                 320

gac atg gag ggg atg tcc cag tac ttc cag aga gtg atc ccc cac cag     1183
Asp Met Glu Gly Met Ser Gln Tyr Phe Gln Arg Val Ile Pro His Gln
        325                 330                 335

ttc gac agc tgc ccg gac aag ctg gtc ctc aaa gcc tac cag gtc aag     1231
Phe Asp Ser Cys Pro Asp Lys Leu Val Leu Lys Ala Tyr Gln Val Lys
    340                 345                 350

tac aac ccc aag aag atg aag agg ctg gag aag gag tac gca gcc atg     1279
Tyr Asn Pro Lys Lys Met Lys Arg Leu Glu Lys Glu Tyr Ala Ala Met
355                 360                 365                 370

aag agc aag gag atg gag gag cag atc gag atc aaa aga ctt cgg acg     1327
Lys Ser Lys Glu Met Glu Glu Gln Ile Glu Ile Lys Arg Leu Arg Thr
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                375                 380                 385

gag aac cgg ctc ctg aaa cag cgg att gaa acc cta gag aag gag agc      1375
Glu Asn Arg Leu Leu Lys Gln Arg Ile Glu Thr Leu Glu Lys Glu Ser
            390                 395                 400

gct gct ctg gct gat agg tta atc cag ggg caa gtg aca cgg gcg cag      1423
Ala Ala Leu Ala Asp Arg Leu Ile Gln Gly Gln Val Thr Arg Ala Gln
        405                 410                 415

gag gcg gag gag aac tac gtc atc aag cgg gag ctg gcg gtg gtg cgg      1471
Glu Ala Glu Glu Asn Tyr Val Ile Lys Arg Glu Leu Ala Val Val Arg
    420                 425                 430

cag cag tgc agc tcg gcg gcc gag gac ctg cag aag gca cag agc acc      1519
Gln Gln Cys Ser Ser Ala Ala Glu Asp Leu Gln Lys Ala Gln Ser Thr
435                 440                 445                 450

atc cgg cag cta cag gag cag cag gag aac ccc cgc ctc aca gaa gac      1567
Ile Arg Gln Leu Gln Glu Gln Gln Glu Asn Pro Arg Leu Thr Glu Asp
                455                 460                 465

ttc gtg tcc cac ctg gag acc gag ctg gag cag tcg agg ctg cgg gag      1615
Phe Val Ser His Leu Glu Thr Glu Leu Glu Gln Ser Arg Leu Arg Glu
            470                 475                 480

acg gag aca ctg ggg gcc ctt cgg gag atg cag gac aag gtt ctc gac      1663
Thr Glu Thr Leu Gly Ala Leu Arg Glu Met Gln Asp Lys Val Leu Asp
        485                 490                 495

atg gaa aag agg aac agc tcg ctg ccc gac gag aac aat gtg gcg cag      1711
Met Glu Lys Arg Asn Ser Ser Leu Pro Asp Glu Asn Asn Val Ala Gln
    500                 505                 510

ctg cag gag gag ctg aag gcg ctc aag gtg cgg gaa ggc cag gcg gtg      1759
Leu Gln Glu Glu Leu Lys Ala Leu Lys Val Arg Glu Gly Gln Ala Val
515                 520                 525                 530

gcc tcg acg cga gag ctt aaa ctg cag ctg cag gag ctc tcg gac acc      1807
Ala Ser Thr Arg Glu Leu Lys Leu Gln Leu Gln Glu Leu Ser Asp Thr
                535                 540                 545

tgg cag gac cag atc gag gag ctg aag acc gag gtg cgg ctg ctg aag      1855
Trp Gln Asp Gln Ile Glu Glu Leu Lys Thr Glu Val Arg Leu Leu Lys
            550                 555                 560

ggc ccg ccg ccc ttc gag gac ccg ctg gct ttc gat ggg ctg agc ctg      1903
Gly Pro Pro Pro Phe Glu Asp Pro Leu Ala Phe Asp Gly Leu Ser Leu
        565                 570                 575

gcg cgg cac ttg gac gag gac tcg ctg ccg tcg tcg gac gag gag cta      1951
Ala Arg His Leu Asp Glu Asp Ser Leu Pro Ser Ser Asp Glu Glu Leu
    580                 585                 590

ctt ggc gta ggc gtg ggc gct gcc ctg cag gac gca ttg tac cct ctg      1999
Leu Gly Val Gly Val Gly Ala Ala Leu Gln Asp Ala Leu Tyr Pro Leu
595                 600                 605                 610
```

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tcc ccg cgc gat gcg cgc ttc ttc cgc cgt ctg gag cgg ccg gcc aag      2047
Ser Pro Arg Asp Ala Arg Phe Phe Arg Arg Leu Glu Arg Pro Ala Lys
                615                 620                 625

gac agc gag ggc agc tca gac agc gac gcc gat gag ctg gcc gcg ccc      2095
Asp Ser Glu Gly Ser Ser Asp Ser Asp Ala Asp Glu Leu Ala Ala Pro
            630                 635                 640

tac agc cag ggt ctg gac aac tga ggccatgccc agcgcgcccg gagtcaggag     2149
Tyr Ser Gln Gly Leu Asp Asn  *
        645                 650

gccgcagccg cgggggcgc ccgggcagtc cgcgttctgc tccccacctg ccgcacttga     2209

caaactacgc gccctctgtg gctcggccac ccctaaagcg aggcccggcg aggcagcgca     2269

gagggtaggg tccgacctgg gctcctcagg gccccggggc aggctctctc tccccagcag     2329

tgtttaccca tcttggtctg taccccctccg ggccctctgg cgttccaggg gtgcctggag   2389

gggctgactg ctctcttaac aggagggcag agggcagggg acagacgacc cagaggtccc     2449

agcactgaat gagcaggcag ctcccacctc ctggcaggct tccttctggg acaggggcga     2509

cattgctggg aagtgctcag gaggtagccg aggcctgagg aaggagagcg ccagctctgg     2569

gctggacatc agcaccccac aacactcctc gggatgaagt gacccttgac tagcccctgg     2629

ccatctctag gggagtcagg ccgctgggga cagatggcca ggccggcctc tcctgcctgg     2689

cgcaggcacc gtggcccctg cagcggaaac caaagtcccc ctactatgtg cggggcgcct     2749

ggggactgag tggctaacgg gaagcctccc tgcttctctg gggccagagc agcttccagg     2809

aagtgaagag acccctctcc ccagtgcccc acatctttct ctgggagaca ctcgcgcccc     2869

ctatcctggc cagtgatgga ggggtatctc tacaggggtc ctcggtctcc atctacttcc     2929

ctttcttcat gtgtttccag ccccaccctc agccagagcc aggcccccag gcaggagctt     2989

cccagcgagc ggcctcccct cacttcctcc tggtggtccc gttgtctctg ctgaatcaga     3049

gctgagaacg gtgccaaaat ccaacgatgc cccccaggcc ccttcctccc ttcccccggc     3109

cccccgggcc tcatgaccct gggggctgcc cccctcggtg ctcccggagc ctccagtaga     3169

gtagcgtcac aagcaatctc cctggcgctt cctgggtggg gacccctgct ccgtccccgc     3229

ttcctagctg cccacttttc agtgttacga agcctgggga ccggggcagg cacccacggg     3289

gctctccaca cgccccctac actgcccgcc accattttgc acactgcctg ttcacatgtc     3349

gcccaggcgg gaaaaatgga aaataaagtg tatttacaca gtcaaaaaaa aaaaa          3404
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agcagcgagg acacctgcag aaatacattc ccaaagcaag gctgggcggc cgtgtgaagt     180

aagcaatggc ctcagttttg cttctgtttt ggatgaacac caccacatag ggcctgaatg     240

tgaaagaaga ccctctattt gtctgttccg gggcagcctg gtagtaaaac actgttgaat     300

gggccacagt ttcagcagac catcaggtga     atg gga cca gtc tct ctt ctt      351
                                     Met Gly Pro Val Ser Leu Leu
                                     1               5

cca aaa tat cag aag tta aac act tgg aac gga gat ttg gcc aag atg      399
Pro Lys Tyr Gln Lys Leu Asn Thr Trp Asn Gly Asp Leu Ala Lys Met
        10                  15                  20

acc cat tta cag gct gga ctc agt cca gag act ata gag aaa gct cgc      447
Thr His Leu Gln Ala Gly Leu Ser Pro Glu Thr Ile Glu Lys Ala Arg
    25                  30                  35

ctg gaa ctg aat gaa aac ccc gat gtt tta cat cag gat att cag caa      495
Leu Glu Leu Asn Glu Asn Pro Asp Val Leu His Gln Asp Ile Gln Gln
40                  45                  50                  55

gtc agg gac atg atc atc acc agg cct gac att gga ttt tta cgt aca      543
Val Arg Asp Met Ile Ile Thr Arg Pro Asp Ile Gly Phe Leu Arg Thr
                60                  65                  70

gat gat gcc ttc atc ctg aga ttt ctc cga gcc agg aag ttt cac caa      591
Asp Asp Ala Phe Ile Leu Arg Phe Leu Arg Ala Arg Lys Phe His Gln
            75                  80                  85

gcg gat gcc ttt aga ctc ctg gct cag tat ttc cag tac cgc cag cta      639
Ala Asp Ala Phe Arg Leu Leu Ala Gln Tyr Phe Gln Tyr Arg Gln Leu
        90                  95                  100

aac ctg gac atg ttc aaa aac ttc aag gca gat gat ccc ggc att aag      687
Asn Leu Asp Met Phe Lys Asn Phe Lys Ala Asp Asp Pro Gly Ile Lys
    105                 110                 115

agg gct ctg atc gat ggg ttc ccc ggg gtg ctg gaa aac cga gac cat      735
Arg Ala Leu Ile Asp Gly Phe Pro Gly Val Leu Glu Asn Arg Asp His
120                 125                 130                 135
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```
tac ggc agg aag att ctt ttg ctg ttt gca gcc aat tgg gat cag agt       783
Tyr Gly Arg Lys Ile Leu Leu Leu Phe Ala Ala Asn Trp Asp Gln Ser
                140                 145                 150

agg aac tcc ttc aca gac atc ctt cgt gcc atc ctg ctg tca ttg gaa       831
Arg Asn Ser Phe Thr Asp Ile Leu Arg Ala Ile Leu Leu Ser Leu Glu
            155                 160                 165

gtc cta atc gaa gat ccg gag ctt cag ata aat ggc ttc att tta att       879
Val Leu Ile Glu Asp Pro Glu Leu Gln Ile Asn Gly Phe Ile Leu Ile
        170                 175                 180

ata gac tgg agt aat ttt tcc ttc aaa caa gcc tcc aaa ctg aca cct       927
Ile Asp Trp Ser Asn Phe Ser Phe Lys Gln Ala Ser Lys Leu Thr Pro
    185                 190                 195

tca atc ctt aaa ctg gcc att gaa ggg ttg cag gac agc ttt cct gcc       975
Ser Ile Leu Lys Leu Ala Ile Glu Gly Leu Gln Asp Ser Phe Pro Ala
200                 205                 210                 215

cgc ttt gga gga gtc cac ttt gtc aac cag ccc tgg tac att cat gcc      1023
Arg Phe Gly Gly Val His Phe Val Asn Gln Pro Trp Tyr Ile His Ala
                220                 225                 230

ctc tac aca ctc atc aag cca ttt ctt aaa gac aag acc agg aaa cgg      1071
Leu Tyr Thr Leu Ile Lys Pro Phe Leu Lys Asp Lys Thr Arg Lys Arg
            235                 240                 245

att ttc ctg cat gga aac aat tta aac agc ctt cac cag cta ata cac      1119
Ile Phe Leu His Gly Asn Asn Leu Asn Ser Leu His Gln Leu Ile His
        250                 255                 260

cct gaa ttt ttg ccc tct gaa ttt gga gga act ctt cct ccc tta tga      1167
Pro Glu Phe Leu Pro Ser Glu Phe Gly Gly Thr Leu Pro Pro Leu  *
    265                 270                 275

catgggaact tgggcccgga cgttactcgg tcccgactac agcgatgaaa atgactatac    1227

tcacacatcc tataatgcaa tgcacgtgaa gcatacgtcc tcgaatctgg agagagaatg    1287

ctcacccaag ctgatgaaaa gatctcagtc tgtggtagaa gctgggaccc tgaaacatga    1347

ggagaaggga gagaatgaga acacccagcc actcctggct ctggactgaa ccctgagtca    1407

ccccaatgct cctgcacact ggccttcagt ggtatcagcc acccaggaag cacatgcaca    1467

actgacccat gcagacacgt gtgttctgct tgacacaagg tcctccactc ctgaacccct    1527

gcagtgactg tcaccagcca tcggtctgag cagccaaagt tggacaaaga cttgagagat    1587

gctttttttt tcccccagtg aggggactgg aggatgatgc aaggcattta tgtaaaaaag    1647

attctccctc ctttcatatt tattgtagta aattgaaaaa ataaagacta aatttgatgg    1707

aaaaaaaaaa aa                                                        1719
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<213> Homo sapiens

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tggtttcctt actcccacaa ttacttacct acagtctgtt ctcgatacaa gactgacaga     120

agtcagattc tgactctgca tacccctcca     atg gct ttc gcc acc ccc aaa      171
                                     Met Ala Phe Ala Thr Pro Lys
                                      1               5

tca ctt gga gta aaa gcc gaa gtc ctt cca gca gct tac cag gtg ctg      219
Ser Leu Gly Val Lys Ala Glu Val Leu Pro Ala Ala Tyr Gln Val Leu
        10                  15                  20

cat gat cca gac tcc ttc tta gcc ctc tgg ctc tcc tgc tgc tct cct      267
His Asp Pro Asp Ser Phe Leu Ala Leu Trp Leu Ser Cys Cys Ser Pro
    25                  30                  35

tct tca ttt ctc tct agc cac acc agc ttt ctt gct gag agc act ggg      315
Ser Ser Phe Leu Ser Ser His Thr Ser Phe Leu Ala Glu Ser Thr Gly
40                  45                  50                  55

tgc tct gtc tac act att ctc caa aat atc cat atg gtt tgt cct cct      363
Cys Ser Val Tyr Thr Ile Leu Gln Asn Ile His Met Val Cys Pro Pro
                60                  65                  70

tca ttt act ttc ttg aat tcc acg gtc tca gtg aga tta cct tgg cat      411
Ser Phe Thr Phe Leu Asn Ser Thr Val Ser Val Arg Leu Pro Trp His
            75                  80                  85

cct agt taa agctgct gcctgtcctc tcaccctgcg tcctgcagtc ccctttctag      467
Pro Ser  *
        90

cgtcccctcc ctttttctat agcactcttc aacttctaac atacttttaa aacataattt     527

ccttgtatgt tttgctgag                                                  546



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<213> Homo sapiens

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tccgcgggcg cttcggatcc tcgcgggacc ccaccctctc ccagcctgcc cagcccgctg     120

cagccgccag cgcgccccgt cggcagctct ccatctgcac gtctctccgt gaaccccgtg     180

agcggtgtgc agccacc atg ttc agc tgg ctg aag cgg ggc ggg gca cgg        230
                   Met Phe Ser Trp Leu Lys Arg Gly Gly Ala Arg
                   1               5                   10

ggc cag cag ccc gag gcc atc cgc acg gtg acc tcg gcc ctc aag gag       278
Gly Gln Gln Pro Glu Ala Ile Arg Thr Val Thr Ser Ala Leu Lys Glu
            15                  20                  25

ctg tac cgc acg aag ctg ctg ccg ctg gag gag cac tac cgc ttt ggg       326
Leu Tyr Arg Thr Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe Gly
        30                  35                  40

gcc ttc cac tcg ccg gcc ctg gag gac gca gac ttc gac ggc aag ccc       374
Ala Phe His Ser Pro Ala Leu Glu Asp Ala Asp Phe Asp Gly Lys Pro
    45                  50                  55

atg gtg ctg gtg gcc ggc cag tac agc acg ggc aag acc agc ttc atc       422
Met Val Leu Val Ala Gly Gln Tyr Ser Thr Gly Lys Thr Ser Phe Ile
60                  65                  70                  75

cag tac ctg ctg gag cag gag gtg ccc ggc tcc cgc gtg ggg cct gag       470
Gln Tyr Leu Leu Glu Gln Glu Val Pro Gly Ser Arg Val Gly Pro Glu
                80                  85                  90

ccc acc acc gac ttc ttt gtg gcc gtc atg cac ggg gac act gag ggc       518
Pro Thr Thr Asp Phe Phe Val Ala Val Met His Gly Asp Thr Glu Gly
            95                  100                 105

acc gtg ccc ggc aac gcc ctc gtc gtg gac ccg gac aag ccc ttc cgc       566
Thr Val Pro Gly Asn Ala Leu Val Val Asp Pro Asp Lys Pro Phe Arg
        110                 115                 120

aaa ctc aac cct ttc gga aac acc ttc ctc aac agg ttc atg tgt gcc       614
Lys Leu Asn Pro Phe Gly Asn Thr Phe Leu Asn Arg Phe Met Cys Ala
    125                 130                 135

cag ctc cct aat cag gtc ctg gag agc atc agc atc atc gac acc ccg       662
Gln Leu Pro Asn Gln Val Leu Glu Ser Ile Ser Ile Ile Asp Thr Pro
140                 145                 150                 155

ggt atc ctg tcg ggt gcc aag cag aga gtg agc cgc ggc tac gac ttc       710
Gly Ile Leu Ser Gly Ala Lys Gln Arg Val Ser Arg Gly Tyr Asp Phe
                160                 165                 170

ccg gcc gtg ctg cgc tgg ttc gcg gag cgc gtg gac ctc atc atc ctg       758
Pro Ala Val Leu Arg Trp Phe Ala Glu Arg Val Asp Leu Ile Ile Leu
            175                 180                 185
```

```
ctc ttt gat gcg cac aag ctg gag atc tcg gac gag ttc tca gag gcc        806
Leu Phe Asp Ala His Lys Leu Glu Ile Ser Asp Glu Phe Ser Glu Ala
        190                 195                 200

atc ggc gcg ttg cgg ggc cat gag gac aag atc cgc gtg gtg ctc aac        854
Ile Gly Ala Leu Arg Gly His Glu Asp Lys Ile Arg Val Val Leu Asn
    205                 210                 215

aag gcc gac atg gtg gag acg cag cag ctg atg cgc gtc tac ggc gcg        902
Lys Ala Asp Met Val Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala
220                 225                 230                 235

ctc atg tgg gcg ctg ggc aag gtg gtg ggc acg ccc gag gtg ctg cgc        950
Leu Met Trp Ala Leu Gly Lys Val Val Gly Thr Pro Glu Val Leu Arg
                240                 245                 250

gtc tac atc ggc tcc ttc tgg tcc cag ccc ctc ctc gtg ccc gac aac        998
Val Tyr Ile Gly Ser Phe Trp Ser Gln Pro Leu Leu Val Pro Asp Asn
            255                 260                 265

cgg cgc ctc ttc gag ctg gag gag cag gac ctc ttc cgc gac atc cag       1046
Arg Arg Leu Phe Glu Leu Glu Glu Gln Asp Leu Phe Arg Asp Ile Gln
        270                 275                 280

ggc ctg ccc cgg cac gca gcc ttg cgc aag ctc aac gac ctg gtg aag       1094
Gly Leu Pro Arg His Ala Ala Leu Arg Lys Leu Asn Asp Leu Val Lys
    285                 290                 295

agg gcc cgg ctg gtg cga gtt cac gct tac atc atc agc tac ctg aag       1142
Arg Ala Arg Leu Val Arg Val His Ala Tyr Ile Ile Ser Tyr Leu Lys
300                 305                 310                 315

aag gag atg ccc tct gtg ttt ggg aag gag aac aag aag aag cag ctg       1190
Lys Glu Met Pro Ser Val Phe Gly Lys Glu Asn Lys Lys Lys Gln Leu
                320                 325                 330

atc ctc aaa ctg ccc gtc atc ttt gcg aag att cag ctg gaa cat cac       1238
Ile Leu Lys Leu Pro Val Ile Phe Ala Lys Ile Gln Leu Glu His His
            335                 340                 345

atc tcc cct ggg gac ttt cct gat tgc cag aaa atg cag gag ctg ctg       1286
Ile Ser Pro Gly Asp Phe Pro Asp Cys Gln Lys Met Gln Glu Leu Leu
        350                 355                 360

atg gcg cac gac ttc acc aag ttt cac tcg ctg aag ccg aag ctg cta       1334
Met Ala His Asp Phe Thr Lys Phe His Ser Leu Lys Pro Lys Leu Leu
    365                 370                 375

gag gca ctg gac gag atg ctg acg cac gac atc gcc aag ctc atg ccc       1382
Glu Ala Leu Asp Glu Met Leu Thr His Asp Ile Ala Lys Leu Met Pro
380                 385                 390                 395

ctg ctg cgg cag gag gag ctg gag agc acc gag gtg ggc gtg cag ggg       1430
Leu Leu Arg Gln Glu Glu Leu Glu Ser Thr Glu Val Gly Val Gln Gly
                400                 405                 410
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ggc gct ttt gag ggc acc cac atg ggc ccg ttt gtg gag cgg gga cct      1478
Gly Ala Phe Glu Gly Thr His Met Gly Pro Phe Val Glu Arg Gly Pro
            415                 420                 425

gac gag gcc atg gag gac ggc gag gag ggc tcg gac gac gag gcc gag      1526
Asp Glu Ala Met Glu Asp Gly Glu Glu Gly Ser Asp Asp Glu Ala Glu
        430                 435                 440

tgg gtg gtg acc aaa gac aag tcc aaa tac gac gag atc ttc tac aac      1574
Trp Val Val Thr Lys Asp Lys Ser Lys Tyr Asp Glu Ile Phe Tyr Asn
    445                 450                 455

ctg gcg cct gcc gac ggc aag ctg agc ggc tcc aag gcc aag acc tgg      1622
Leu Ala Pro Ala Asp Gly Lys Leu Ser Gly Ser Lys Ala Lys Thr Trp
460                 465                 470                 475

atg gtg ggg acc aag ctc ccc aac tca gtg ctg ggg cgc atc tgg aag      1670
Met Val Gly Thr Lys Leu Pro Asn Ser Val Leu Gly Arg Ile Trp Lys
                480                 485                 490

ctc agc gat gtg gac cgc gac ggc atg ctg gat gat gaa gag ttc gcg      1718
Leu Ser Asp Val Asp Arg Asp Gly Met Leu Asp Asp Glu Glu Phe Ala
            495                 500                 505

ctg gcc agc cac ctc atc gag gcc aag ctg gaa ggc cac ggg ctg ccc      1766
Leu Ala Ser His Leu Ile Glu Ala Lys Leu Glu Gly His Gly Leu Pro
        510                 515                 520

gcc aac ctg ccc cgt cgc ctg gtg cca ccc tcc aag cga cgc cac aag      1814
Ala Asn Leu Pro Arg Arg Leu Val Pro Pro Ser Lys Arg Arg His Lys
    525                 530                 535

ggc tcc gcc gag tga gccgggcccc cctcccatgg ccctgctgtg gctccccagc      1869
Gly Ser Ala Glu  *
540

tccagtcggc tgcacgcaca cccctgctcc ggctcacaca cgccctgcct gccctccctg    1929

cccagctgta aggaccgggg gtctccctcc tcactaccgc cagacacccc ggtggaagca    1989

tttagagggg accacgggag ggacaaggct tctctgtccg cccttcacac ctccagcctc    2049

acgttcactt aggcacatca cacacacact ggcacacgca ggcatccatc catccgtcat    2109

tcattcaaat atttattgag cacctactat gtgcccagcc ctgttctagg cactgggcat    2169

taccatagag aacaaaatag acaaatacat ctgccctcat ggaaggtgac gttcccagga    2229

gagggcacct acacagtcac gcaaacacac actaattcct ggcagggccc ccagcccctc    2289

ccctggctga gcagccctgt ggctgaaatg actagcagat aaacagaccc ccttctgctc    2349

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gggaccatgg ggggctcaga ggggagacac acctactgct tcctcagatg ggcccctccg    2469

cagccccttc ccttgctcgg ggaaagcccc caattctgcc cacacccatt tatttccttc    2529
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cttccttcct tcttttcttt ccttccttcc ttcttttttg tttttgcccc caattctgcc 2589

catacccatt tctttctttc cttccttcct tcttttttgt ttttgccccc agttctgtcc 2649

acaccccttc cctttcctgt cctgtccttt ctttcttttt tgatagaatc ttgctctgtc 2709

gcccaggctg gagtgcagtg gtgagatctc agctcactgc aacctccacc tcctgggttg 2769

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aaagcccctt ccatcctgct cctctgatac tgtgcccccт tggagatatt tccgtcctcc 3069

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cagctggtaa tctggactta aggattgctg ggccaccgcc tctctgccta ccaccattcc 3189

atatttaagt ggagccccta cgtagaaagg ccccggggct ttattttagt ctccttttca 3249

gggatgtcgt gggcggggga gggggttctt ggtgctacag ccctctcccc acccctaaag 3309

ggacgccgac gctgtttgct gccttcacca catattagtg cttgaccctg gcaggggacc 3369

ccatggaaaa gatggggaag agcaaaatac atggagacga cgcaccctcc aggatgctcg 3429

ctgggattcc cacgcccacc actgtccccc accccatggc tgggaggggc ctctgaacgg 3489

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ctgtccgctg ccaagggaag tgacagccgc agccgggctc tcagccagcg gccgggcgcc 180

```
ccgcggacc    atg ctc tcc agt acg cag aac gcg ggc ggc tcc tat cag     228
             Met Leu Ser Ser Thr Gln Asn Ala Gly Gly Ser Tyr Gln
              1               5                  10
```

```
cgg gtc cgc ggg gcg ctt gat aca cag aaa tgc agt cca gag aaa agt         276
Arg Val Arg Gly Ala Leu Asp Thr Gln Lys Cys Ser Pro Glu Lys Ser
     15                  20                  25

gcc tca ttt ttc agt aaa gtg aca tat tcc tgg ttt agc aga gta att         324
Ala Ser Phe Phe Ser Lys Val Thr Tyr Ser Trp Phe Ser Arg Val Ile
 30                  35                  40                  45

act tta ggc tat aag aga cct ttg gaa aga gag gat ctt ttt gaa cta         372
Thr Leu Gly Tyr Lys Arg Pro Leu Glu Arg Glu Asp Leu Phe Glu Leu
                 50                  55                  60

aag gaa agt gat tcc ttc tgc act gcg tgt ccc atc ttt gaa aaa caa         420
Lys Glu Ser Asp Ser Phe Cys Thr Ala Cys Pro Ile Phe Glu Lys Gln
             65                  70                  75

tgg aga aag gaa gtt tta agg aat caa gag agg caa aaa gta aag gta         468
Trp Arg Lys Glu Val Leu Arg Asn Gln Glu Arg Gln Lys Val Lys Val
         80                  85                  90

tct tgt tat aaa gag gca cat atc aag aaa cca tct cta ctc tat gca         516
Ser Cys Tyr Lys Glu Ala His Ile Lys Lys Pro Ser Leu Leu Tyr Ala
     95                 100                 105

ttg tgg aac acc ttt aaa tcc atc ctg att caa gtt gcc tta ttc aaa         564
Leu Trp Asn Thr Phe Lys Ser Ile Leu Ile Gln Val Ala Leu Phe Lys
110                 115                 120                 125

gtg ttt gct gat att ttg tcc ttc act agc cca ctc ata atg aag caa         612
Val Phe Ala Asp Ile Leu Ser Phe Thr Ser Pro Leu Ile Met Lys Gln
                130                 135                 140

att atc att ttc tgt gaa cac agc tca gat ttt ggc tgg aat ggc tat         660
Ile Ile Ile Phe Cys Glu His Ser Ser Asp Phe Gly Trp Asn Gly Tyr
            145                 150                 155

ggc tat gca gtg gca ctt ctt gtt gta gtc ttt ttg caa act ctg att         708
Gly Tyr Ala Val Ala Leu Leu Val Val Val Phe Leu Gln Thr Leu Ile
        160                 165                 170

ctt cag caa tat caa cgt ttt aac atg ctc acc tca gca aaa gtt aag         756
Leu Gln Gln Tyr Gln Arg Phe Asn Met Leu Thr Ser Ala Lys Val Lys
    175                 180                 185

aca gct gta aat gga ctg atc tac aaa aag gcc tta ctt tta tca aat         804
Thr Ala Val Asn Gly Leu Ile Tyr Lys Lys Ala Leu Leu Leu Ser Asn
190                 195                 200                 205

gtt tct cga caa aag ttt tcc act ggg gaa att att aac ttg atg tca         852
Val Ser Arg Gln Lys Phe Ser Thr Gly Glu Ile Ile Asn Leu Met Ser
                210                 215                 220

gca act cat gga ctt gac agc aaa cct caa tct cct ctg gtc tgc ccc         900
Ala Thr His Gly Leu Asp Ser Lys Pro Gln Ser Pro Leu Val Cys Pro
            225                 230                 235
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```
ttt tca aat cct aat ggc cgt ata tct cct ttg gca aga gct ggg tcc      948
Phe Ser Asn Pro Asn Gly Arg Ile Ser Pro Leu Ala Arg Ala Gly Ser
        240                 245                 250

agc agt gtt agc agg ggt ggc agt cct tgt gtt tgt tat acc aat aaa      996
Ser Ser Val Ser Arg Gly Gly Ser Pro Cys Val Cys Tyr Thr Asn Lys
    255                 260                 265

tgc ttt agc tgc aac taa aataaa aaagttaaag gtaaaaaaat gactgcctca     1050
Cys Phe Ser Cys Asn  *
270                 275

tgttacatgt gtcaaacagg agctgagttt tctgacttga gttaacaatc accatctcgc   1110

taattatata gagagagtta caaatggaag tcatcgaatt ttatcattta cttattcact   1170

caaccagtat tgaacaagca tgtatcttat gtcagccagt gtttcaggca caggaagtac   1230

agcagtgagg ggaaatgaca agtccagctc tcatgagggg tagtggagga gacaggcatt   1290

aagcaagtac ataaatagag agaaaacatt tgtatatgaa aaagatttag taaaatacag   1350

tgatgaagag acaaaggatg ccattttaca tttaagatc                          1389



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     <211> 707
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (56)..(439)

     <400> 232
ctactactac tactactaaa ttcgcggccg cgtcgaccat agcgctcacg caagc atg      58
                                                             Met
                                                               1

gtt aac gtc cct aaa acc cgc cgg act ttc tgt aag aag tgt ggc aag      106
Val Asn Val Pro Lys Thr Arg Arg Thr Phe Cys Lys Lys Cys Gly Lys
              5                  10                  15

cac caa ccc cat aaa gtg aca cag tac aag aag ggc aag gat tct ctg      154
His Gln Pro His Lys Val Thr Gln Tyr Lys Lys Gly Lys Asp Ser Leu
         20                  25                  30

tac gcc cag gga aag cgg cgt tat gac agg aag cag agt ggc tat ggt      202
Tyr Ala Gln Gly Lys Arg Arg Tyr Asp Arg Lys Gln Ser Gly Tyr Gly
     35                  40                  45

ggg caa act aag ccg att ttc cgg aaa aag gct aaa act aca aag aag      250
Gly Gln Thr Lys Pro Ile Phe Arg Lys Lys Ala Lys Thr Thr Lys Lys
 50                  55                  60                  65
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att gtg cta agg ctt gag tgc gtt gag ccc aac tgc aga tct aag aga      298
Ile Val Leu Arg Leu Glu Cys Val Glu Pro Asn Cys Arg Ser Lys Arg
                 70                  75                  80

atg ctg gct att aaa aga tgc aag cat ttt gaa ctg gga gga gat aag      346
Met Leu Ala Ile Lys Arg Cys Lys His Phe Glu Leu Gly Gly Asp Lys
             85                  90                  95

aag aga aag gta tat aat tat ggg tcg gaa ggt gca atc ttt ctc ata      394
Lys Arg Lys Val Tyr Asn Tyr Gly Ser Glu Gly Ala Ile Phe Leu Ile
        100                 105                 110

gct tta tta ttt cga aaa ggt gaa cat cta ttc ctt gtg gca tag agc      442
Ala Leu Leu Phe Arg Lys Gly Glu His Leu Phe Leu Val Ala  *
    115                 120                 125

tcaggggtaa tcctctaaaa atattagatc tatagctaaa gatatgtgag gtcttttgct    502

acaaggagga aaggaagaat gaggaagctt aacagcatgg tgactatttt aggaacagat    562

aatgttctta atggggcagt agttcatggc aaaatacaaa acaacttttt tctgttctgc    622

ttacagggcc aagtgatcca gttttaagtg tcatctttta ttatgaagac aataaaatct    682

tgagtttatg ttcaaaaaaa aaaaa                                          707




     <210> 233
     <211> 824
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (101)..(688)

     <400> 233
attagaaact gatttacatg gagacccaag ctggctagcg tttaaactta agcttggtac     60

cgagctcgga tccactagtc cagtgtggtg gaattccata  atg tat agt att tct     115
                                             Met Tyr Ser Ile Ser
                                              1               5

cct gcc aac tct gag gaa ggc cag gaa ctt tat gtc tgc aca gtc aag      163
Pro Ala Asn Ser Glu Glu Gly Gln Glu Leu Tyr Val Cys Thr Val Lys
                 10                  15                  20

gat gat gtg aac ttg gat aca gta ctt ctc cta ccc ttt ttg aaa gaa      211
Asp Asp Val Asn Leu Asp Thr Val Leu Leu Leu Pro Phe Leu Lys Glu
             25                  30                  35

ata gca gta agc caa ctg gat caa ctg agc cca gag gaa cag ttg ctg      259
Ile Ala Val Ser Gln Leu Asp Gln Leu Ser Pro Glu Glu Gln Leu Leu
         40                  45                  50
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gtc aag tgt gct gca atc att ggt cac tcc ttc cat ata gat ttg ctg      307
Val Lys Cys Ala Ala Ile Ile Gly His Ser Phe His Ile Asp Leu Leu
     55                  60                  65

cag cac ctc ctg cct ggc tgg gat aaa aat aag cta ctt cag gtc ttg      355
Gln His Leu Leu Pro Gly Trp Asp Lys Asn Lys Leu Leu Gln Val Leu
 70                  75                  80                  85

aga gct ctt gtg gat ata cat gtg ctc tgc tgg tct gac aag agc caa      403
Arg Ala Leu Val Asp Ile His Val Leu Cys Trp Ser Asp Lys Ser Gln
                 90                  95                 100

gag ctt cct gct gag ccc ata tta atg cct tcc tct atc gac atc att      451
Glu Leu Pro Ala Glu Pro Ile Leu Met Pro Ser Ser Ile Asp Ile Ile
            105                 110                 115

gat gga acc aaa gag aag aag aca aag tta gat ggt ggg tca gcc tct      499
Asp Gly Thr Lys Glu Lys Lys Thr Lys Leu Asp Gly Gly Ser Ala Ser
        120                 125                 130

ctt ctc agg cta caa gaa gaa tta tcc cta cca cag gca gca ctg aaa      547
Leu Leu Arg Leu Gln Glu Glu Leu Ser Leu Pro Gln Ala Ala Leu Lys
    135                 140                 145

cag aca ata gac agc ttc cac ccc act aca cgc ctg cag caa cac agc      595
Gln Thr Ile Asp Ser Phe His Pro Thr Thr Arg Leu Gln Gln His Ser
150                 155                 160                 165

ccg gct gca cag gct ctc gta tgc gac cat cat gct tgc agt agc ccg      643
Pro Ala Ala Gln Ala Leu Val Cys Asp His His Ala Cys Ser Ser Pro
                170                 175                 180

gtc ttt gca cgg cta cct cta gag cac ctt cag aaa tgc cct taa gca      691
Val Phe Ala Arg Leu Pro Leu Glu His Leu Gln Lys Cys Pro  *
            185                 190                 195

tgctggggtc acgtgtcatg caaaccttgg acagatgact gaacctctct atgccttggt    751

ttcttcatct gtgtagacgc cagtgacgat gtctccttcc tcaggtcggg gactatctgg    811

gacccaaggt tct                                                       824



     <210> 234
     <211> 1077
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (239)..(946)

     <400> 234
tttcgtctgg gcccgcgcgc aggccttaca taggaagtcc ttctaaagag ctgcctgcca     60
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gctgcccttc cccagatccc gaatatcctc ctggccaggt ggagcagaga acagttcctc    120

agctggtcat gctgagctca taccctgatg gctgctccat gaggtcaaga ctgggtctcc    180

tccctcctcc cccttcacca atgcctggtc tcacggggct agttttgacc cccacgct      238
atg gca tca tcg acc tcc ctc cca gct cct ggc tct cgg cct aag aag      286
Met Ala Ser Ser Thr Ser Leu Pro Ala Pro Gly Ser Arg Pro Lys Lys
  1               5                  10                  15

cct cta ggc aag atg gct gac tgg ttc agg cag acc ctg ctg aag aag      334
Pro Leu Gly Lys Met Ala Asp Trp Phe Arg Gln Thr Leu Leu Lys Lys
             20                  25                  30

ccc aag aag agg ccc aac tcc cca gaa agc acc tcc agc gat gct tca      382
Pro Lys Lys Arg Pro Asn Ser Pro Glu Ser Thr Ser Ser Asp Ala Ser
         35                  40                  45

cag cct acc tca cag gac agc cca cta ccc cca agc ctc agc tca gtc      430
Gln Pro Thr Ser Gln Asp Ser Pro Leu Pro Pro Ser Leu Ser Ser Val
     50                  55                  60

acg tct ccc agc ctg cca ccc aca cat gcg agt gac agt ggc agt agt      478
Thr Ser Pro Ser Leu Pro Pro Thr His Ala Ser Asp Ser Gly Ser Ser
 65                  70                  75                  80

cgc tgg agc aaa gac tat gac gtc tgc gtg tgc cac agt gag gaa gac      526
Arg Trp Ser Lys Asp Tyr Asp Val Cys Val Cys His Ser Glu Glu Asp
                 85                  90                  95

ctg gtg gcc gcc cag gac ctg gtc tcc tac ttg gaa ggc agc act gcc      574
Leu Val Ala Ala Gln Asp Leu Val Ser Tyr Leu Glu Gly Ser Thr Ala
            100                 105                 110

agc ctg cgc tgc ttc ctg caa ctc cgg gat gca acc cca ggc ggc gct      622
Ser Leu Arg Cys Phe Leu Gln Leu Arg Asp Ala Thr Pro Gly Gly Ala
        115                 120                 125

ata gtg tcc gag ctg tgc cag gca ctg agc agt agt cac tgc cgg gtg      670
Ile Val Ser Glu Leu Cys Gln Ala Leu Ser Ser Ser His Cys Arg Val
    130                 135                 140

ctg ctc atc acg ccg ggc ttc ctt cag gac ccc tgg tgc aag tac cag      718
Leu Leu Ile Thr Pro Gly Phe Leu Gln Asp Pro Trp Cys Lys Tyr Gln
145                 150                 155                 160

atg ctg cag gcc ctg acc gag gct cca ggg gcc gag ggc tgc acc atc      766
Met Leu Gln Ala Leu Thr Glu Ala Pro Gly Ala Glu Gly Cys Thr Ile
                165                 170                 175

ccc ctg ctg tcg ggc ctc agc aga gct gct tac cca cct gag ctc cga      814
Pro Leu Leu Ser Gly Leu Ser Arg Ala Ala Tyr Pro Pro Glu Leu Arg
            180                 185                 190

ttc atg tac tac gtc gat ggc agg ggc cct gat ggt ggc ttt cgt caa      862
Phe Met Tyr Tyr Val Asp Gly Arg Gly Pro Asp Gly Gly Phe Arg Gln
        195                 200                 205
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gtc aaa gaa gct gtc atg cgt tgt aag cta cta cag gag gga gaa ggg       910
Val Lys Glu Ala Val Met Arg Cys Lys Leu Leu Gln Glu Gly Glu Gly
    210                 215                 220

gaa cgg gat tca gct aca gta ttt gat cta ctt tga cttt taggagacag      960
Glu Arg Asp Ser Ala Thr Val Phe Asp Leu Leu  *
225                 230                 235

ccctgtagcc tagtagttca aagcgcagct tctggaagag gctgtcgggg tttgtatcct   1020

ggctcctgcc cttattaacc cataaaaagt aacttggtca agttaaaaaa aaaaaaa      1077




      <210> 235
      <211> 916
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (169)..(738)

      <400> 235
agctggctag cgtttaaact taagcttggt accgagctcg gatccactag tccagtgtgg     60

tggaattcca cagcccagta actttgctag tacctcttga gtgcaaggtg gagaattaag    120

atctggattt gagacggagc acggaacatt tcactcaggg gaagagct atg aac atg     177
                                                     Met Asn Met
                                                       1

ctg act gcc agc ctg ttg agg gca gtc ata gcc tcc atc tgt gtt gta       225
Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val Val
      5                  10                  15

tcc agc atg gct cag aag gta act caa gcg cag act gaa att tct gtg       273
Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser Val
 20                  25                  30                  35

gtg gag aag gag gat gtg acc ttg gac tgt gtg tat gaa acc cgt gat       321
Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg Asp
                 40                  45                  50

act act tat tac tta ttc tgg tac aag caa cca cca agt gga gaa ttg       369
Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu
             55                  60                  65

gtt ttc ctt att cgt cgg aac tct ttt gat gag caa aat gaa ata agt       417
Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser
         70                  75                  80

ggt cgg tat tct tgg aac ttc cag aaa tcc acc agt tcc ttc aac ttc       465
Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe
     85                  90                  95
```

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acc atc aca gcc tca caa gtc gtg gac tca gca gta tac ttc tgt gct       513
Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala
100                 105                 110                 115

ctg agt gag gcg gcc caa gaa acc agt ggc tct agg ttg acc ttt ggg       561
Leu Ser Glu Ala Ala Gln Glu Thr Ser Gly Ser Arg Leu Thr Phe Gly
                120                 125                 130

gaa gga aca cag ctc aca gtg aat cct gat atc cag aac cct gac cct       609
Glu Gly Thr Gln Leu Thr Val Asn Pro Asp Ile Gln Asn Pro Asp Pro
            135                 140                 145

gcc gtg tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc       657
Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys
        150                 155                 160

cta ttc acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat       705
Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp
    165                 170                 175

tct gat gtg tat atc aca gac aaa ctg tgc tag actgtgag gctagggatt       756
Ser Asp Val Tyr Ile Thr Asp Lys Leu Cys  *
180                 185                 190

tcagaaccac cgggttgggc ctggagcaac aaatctgact ttgcatgggc aacgccttca     816

acaacaggct tatttcagaa gaacccttct tccccagccc caaaaggtcc cttgatggca     876

agctgcccga gaaagctttg aaacagatac caacctaaac                           916




     <210> 236
     <211> 876
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (38)..(547)

     <400> 236
agtgtggtgg aattcgggag ccctgcccca ggggccc atg cag aat gcc acc aag       55
                                         Met Gln Asn Ala Thr Lys
                                           1               5

tat ggc aac atg aca gag gac cat gtg atg cac ctg ctc cag aat gct       103
Tyr Gly Asn Met Thr Glu Asp His Val Met His Leu Leu Gln Asn Ala
             10                  15                  20

gac ccc ctg aag gtg tac ccg cca ctg aag ggg agc ttc ccg gag aac       151
Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly Ser Phe Pro Glu Asn
         25                  30                  35

ctg aga cac ctt aag aac acc atg gag acc ata gac tgg aag gtc ttt       199
Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile Asp Trp Lys Val Phe
```

```
     40                  45                  50

gag agc tgg atg cac cat tgg ctc ctg ttt gaa atg agc agg cac tcc      247
Glu Ser Trp Met His His Trp Leu Leu Phe Glu Met Ser Arg His Ser
 55                  60                  65                  70

ttg gag caa aag ccc act gac gct cca ccg aaa gta ctg acc aag tgc      295
Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys Val Leu Thr Lys Cys
                 75                  80                  85

cag gaa gag gtc agc cac atc cct gct gtc cac ccg ggt tca ttc agg      343
Gln Glu Glu Val Ser His Ile Pro Ala Val His Pro Gly Ser Phe Arg
             90                  95                 100

ccc aag tgc gac gag aac ggc aac tat ctg cca ctc cag tgc tat ggg      391
Pro Lys Cys Asp Glu Asn Gly Asn Tyr Leu Pro Leu Gln Cys Tyr Gly
        105                 110                 115

agc atc ggc tac tgc tgg tgt gtc ttc ccc aac ggc acg gag gtc ccc      439
Ser Ile Gly Tyr Cys Trp Cys Val Phe Pro Asn Gly Thr Glu Val Pro
    120                 125                 130

aac acc aga agc cgc ggg cac cat aac tgc agt gag tca ctg gaa ctg      487
Asn Thr Arg Ser Arg Gly His His Asn Cys Ser Glu Ser Leu Glu Leu
135                 140                 145                 150

gag gac ccg tct tct ggg ctg ggt gtg acc aag cag gat ctg ggc cca      535
Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys Gln Asp Leu Gly Pro
                155                 160                 165

gtc ccc atg tga gag cagcagaggc ggtcttcaac atcctgccag ccccacacag      590
Val Pro Met  *
            170

ctacagcttt cttgctccct tcagccccca gcccctcccc catctcccac cctgtacctc    650

atcccatgag accctggtgc ctggctcttt cgtcaccctt ggacaagaca aaccaagtcg    710

gaacagcaga taacaatgca gcaaggccct gctgcccaat ctccatctgt caacaggggc    770

ggtcgacgcg gccgcgaatt cggatcctcg agagatctct ttttttgggt ttggtggggt    830

gtcttcatca tcggatatac taggtatata catcggccta tcaagg                   876
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<210> 237
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (168)..(419)

<400> 237

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gtccgtgcgc accgcccggc gtccaggtga gtctcccatc tgcagagacg cggacgcgcc       60

ggcccgcagt tggcctgcgg agcgcggtgg acggtttggc gcccaccagg cgatcaatac      120

tttggatttt taatttctag atttggcaat tcttcgctga agtcatc  atg agc ttt      176
                                                     Met Ser Phe
                                                      1

ttc caa ctc ctg atg aaa agg aag gaa ctc att ccc ttg gtg gtg ttc        224
Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile Pro Leu Val Val Phe
     5                  10                  15

atg act gtg gcg gcg ggt gga gcc tca tct ttc gct gtg tat tct ctt        272
Met Thr Val Ala Ala Gly Gly Ala Ser Ser Phe Ala Val Tyr Ser Leu
 20                  25                  30                  35

tgg aaa acc gat gtg atc ctt gat cga aaa aaa aat cca gaa cct tgg        320
Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys Asn Pro Glu Pro Trp
                 40                  45                  50

gaa act gtg gac cct act gta cct caa aag ctt ata aca atc aac caa        368
Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu Ile Thr Ile Asn Gln
             55                  60                  65

caa tgg aaa ccc att gaa gag ttg caa aat gtc caa agg gtg acc aaa        416
Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val Gln Arg Val Thr Lys
         70                  75                  80

tga cgag ccctcgcctc tttcttctga agagtactct ataaatctag tggaaacatt        473
 *


tctgcacaaa ctagattctg gacaccagtg tgcggaaatg cttctgctac atttttaggg      533

tttgtctaca ttttttgggc tctggataag gaattaaagg agtgcagcaa taactgcact      593

gtctaaaagt ttgtgcttat tttcttgtaa atttgaatat tgcatattga aatttttgtt      653

tatgatctat gaatgttttt cttaaaattt acaaagcttt gtaaattaga ttttctttaa      713

taaaatgcca tttgtgcaag atttctcaaa aaaaaaaaaa                            753



     <210> 238
     <211> 1395
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (50)..(1060)

     <400> 238
gagtggtgga attccgctgg cctcgctcgg tgcgcgcctc cctccccgc    atg cag        55
                                                         Met Gln
```

```
                                                           1

ccc gcc gag cgc tcg cgg gtc ccc agg atc gac ccg tac gga ttc gag      103
Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly Phe Glu
          5                  10                  15

cgg cct gag gac ttc gac gac gcc gcc tac gag aag ttt ttc tcc agc      151
Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe Ser Ser
     20                  25                  30

tac ctg gtc acg ctc acc cgc agg gcg atc aaa tgg tcc cgg ctg ctg      199
Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg Leu Leu
 35                  40                  45                  50

cag ggc ggg ggc gtc ccc agg agc cgg aca gtg aag cgc tat gtc cgg      247
Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr Val Arg
                 55                  60                  65

aaa ggg gtc ccg ctg gag cac cgt gcc cgc gtc tgg atg gtg ctg agt      295
Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val Leu Ser
             70                  75                  80

ggg gcc cag gcg cag atg gac cag aat ccc ggc tac tac cac cag ctt      343
Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His Gln Leu
         85                  90                  95

ctc cag gga gag aga aac ccc agg ctg gag gac gcc atc agg aca gac      391
Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg Thr Asp
    100                 105                 110

ctg aac cgg acc ttc ccc gac aac gtg aag ttc cgg aag acc acg gac      439
Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr Thr Asp
115                 120                 125                 130

ccc tgc tta cag agg acc ctg tac aat gtg ctg ctg gca tat ggg cac      487
Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr Gly His
                135                 140                 145

cat aac cag gga gtg ggc tac tgc cag gga atg aat ttt ata gca gga      535
His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile Ala Gly
            150                 155                 160

tat ctg att ctt ata aca aat aat gaa gaa gaa tct ttt tgg ctg tta      583
Tyr Leu Ile Leu Ile Thr Asn Asn Glu Glu Glu Ser Phe Trp Leu Leu
        165                 170                 175

gat gct ctt gtt gga aga ata cta cca gat tac tac agc ccg gcc atg      631
Asp Ala Leu Val Gly Arg Ile Leu Pro Asp Tyr Tyr Ser Pro Ala Met
    180                 185                 190

ctg ggc ctg aag acc gac cag gag gtc ctc ggg gag ctg gtg cgg gcg      679
Leu Gly Leu Lys Thr Asp Gln Glu Val Leu Gly Glu Leu Val Arg Ala
195                 200                 205                 210

aag ctg ccg gct gtg ggg gcc ctg atg gag cgt ctc ggt gtg ctg tgg      727
Lys Leu Pro Ala Val Gly Ala Leu Met Glu Arg Leu Gly Val Leu Trp
                215                 220                 225
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acg ctg ctg gtg tcc cgc tgg ttc atc tgc ctg ttt gtg gac atc ttg        775
Thr Leu Leu Val Ser Arg Trp Phe Ile Cys Leu Phe Val Asp Ile Leu
            230                 235                 240

ccc gtg gag aca gtg ctt cgg atc tgg gac tgt ttg ttt aac gaa ggc        823
Pro Val Glu Thr Val Leu Arg Ile Trp Asp Cys Leu Phe Asn Glu Gly
        245                 250                 255

tcg aag att atc ttc cgg gtg gcc ctg acc tta att aag cag cac cag        871
Ser Lys Ile Ile Phe Arg Val Ala Leu Thr Leu Ile Lys Gln His Gln
    260                 265                 270

gag ttg att ttg gaa gcc acc agc gtt cca gac att tgc gat aag ttt        919
Glu Leu Ile Leu Glu Ala Thr Ser Val Pro Asp Ile Cys Asp Lys Phe
275                 280                 285                 290

aag cag ata acc aaa ggg agt ttc gtg atg gag tgt cac acg ttt atg        967
Lys Gln Ile Thr Lys Gly Ser Phe Val Met Glu Cys His Thr Phe Met
                295                 300                 305

cag aaa ata ttt tca gaa cct gga agc tta tcc atg gcc acc gtc gcc       1015
Gln Lys Ile Phe Ser Glu Pro Gly Ser Leu Ser Met Ala Thr Val Ala
            310                 315                 320

aag ctc cgc gag agc tgc agg gcc cgg ctg ctg gca cag ggg tga gcg       1063
Lys Leu Arg Glu Ser Cys Arg Ala Arg Leu Leu Ala Gln Gly  *
        325                 330                 335

tgcctgtccc ctgcgttgct cgtctctaca ctgacgatgc ccctttccag agttgacact    1123

ggaccaactt tcactgcttt cctttttagt gttgtaaata cttgacatca ctacacttta    1183

gttgtgaatt ttttaaaaga gcagtttaaa atcaggtcat tctaccagct tttgatgatt    1243

agctatgaag tcatactttt taaagaaaac ttatttttac ctgagagatc aataatatat    1303

aaaatgtgag tgtgggtttg tatctaataa agtatgccaa cacctgtgtt tgtgatcagt    1363

ttctcagctg actggaaatt aaaaaaaaaa aa                                  1395
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<210> 239
<211> 767
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (78)..(326)

<220>
<221> misc_feature
<222> (1)...(767)
<223> n = a,t,c or g

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     <400> 239
ccggtccgga attcccgggt cgacccacgc gtccgccctt ctctcttcct tggtgcttct      60

ttttcctgct cggcatc   atg gct gcc ctc aga tcc ctt gtg aag ccc aag      110
                     Met Ala Ala Leu Arg Ser Leu Val Lys Pro Lys
                      1               5                  10

atc gtc aaa aag aga acc aag aaa ttc atc cgg cac cag tca gac cga      158
Ile Val Lys Lys Arg Thr Lys Lys Phe Ile Arg His Gln Ser Asp Arg
            15                  20                  25

tat gtc aaa atc aag atg aga aga ata atg tct ggg gtg aag gtg aag      206
Tyr Val Lys Ile Lys Met Arg Arg Ile Met Ser Gly Val Lys Val Lys
        30                  35                  40

cac cca gcc caa gac tca gca gcc agg aag tgg ccc agc gct ctt tat      254
His Pro Ala Gln Asp Ser Ala Ala Arg Lys Trp Pro Ser Ala Leu Tyr
    45                  50                  55

acc acg ggt gca gga att cac aca gaa aag tgg agg cca agg cgt gag      302
Thr Thr Gly Ala Gly Ile His Thr Glu Lys Trp Arg Pro Arg Arg Glu
 60                  65                  70                  75

aat tcc tca atg act gcc ctc taa aggaagagat ccaaagaaat cctgaggaag     356
Asn Ser Ser Met Thr Ala Leu  *
                80

cacaacaaac aaaaacactc tggatcagaa cttcctgtgc cagcgttaca tcagggtttt    416

ctagcagcaa gggcgggctc cacatggctg aagcaggcaa ccaggaggac caggcttcct    476

gtcagagact gaggacccag gaagaaacat gtctcggccc ctgtccccct ccacaattca    536

gaggccacat tctaacaggg gaggctgacc aattaaacag ataatgacac ctcctagagc    596

taagagctct ccgactatga accagatgcc tggagaacac ggatgaatgg tctgagcatg    656

agcaggggtg ggaggcagcg ttaagggagg catcagagtc agaacctagc aaacaagtgt    716

ttgtgaagaa gaattcatag aanagggcaa tgcgggcatc acatgggcta a             767



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     <211> 526
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (187)..(324)

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gagttttaaa attctttatt taaaaatctc taactgtaat gtttcataaa aaatatacac     60
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gtttctattt acatattcca ttaattctat tagtttgaat tagattttaa gtccaatttt     120

gaaaagcttg cagaatttct tctgaaatta cttaaaatta ctgtatgcat aaacttacaa     180

aaacat   atg cta tac caa ggc aga gaa aag aaa aaa agt gaa gtg gct      228
         Met Leu Tyr Gln Gly Arg Glu Lys Lys Lys Ser Glu Val Ala
           1               5                  10

aca aag gtc cct ggg gca tca cct gct cac cta gga acc agg agt act      276
Thr Lys Val Pro Gly Ala Ser Pro Ala His Leu Gly Thr Arg Ser Thr
 15                  20                  25                  30

gga tac tgt tcc gtt act ggt aac cta tct gga tgt aaa ggt tca taa      324
Gly Tyr Cys Ser Val Thr Gly Asn Leu Ser Gly Cys Lys Gly Ser  *
                35                  40                  45

gttacaatgc ttttttgtt taaaaaaaaa aaaaagtctg tactttacaa gccaaaagtg     384

aaaatgccac acatcctctt tacgctttca tgtacactaa gtcactccat ttggttgata     444

ccaataatga tagctcctgt gtataatatt ttcataaatc atactcagta agcaaatctc     504

tcaagcagcc agcatatgca gc                                              526




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     <211> 3744
     <212> DNA
     <213> Homo sapiens

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     <221> CDS
     <222> (27)..(3161)

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                             Met Val Gln Pro Gln Gly Cys Ser Asp
                               1               5

gag gaa gac cac gcg gag gag ccc tcc aag gac ggc ggt gcc ctg gag      101
Glu Glu Asp His Ala Glu Glu Pro Ser Lys Asp Gly Gly Ala Leu Glu
 10                  15                  20                  25

gag aag gat tcg gac ggg gca gcc tcc aag gag gac agc ggc ccc agc      149
Glu Lys Asp Ser Asp Gly Ala Ala Ser Lys Glu Asp Ser Gly Pro Ser
                30                  35                  40

acc agg cag gct tca gga gag gcc tcc tcg ctg cgg gac tac gcg gcc      197
Thr Arg Gln Ala Ser Gly Glu Ala Ser Ser Leu Arg Asp Tyr Ala Ala
            45                  50                  55

tcc acc atg acc gag ttc ctc ggc atg ttt ggc tat gat gac cag aac      245
Ser Thr Met Thr Glu Phe Leu Gly Met Phe Gly Tyr Asp Asp Gln Asn
        60                  65                  70
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acg cgg gac gag ctg gcc agg aag atc agc ttt gag aag ctg cac gcg       293
Thr Arg Asp Glu Leu Ala Arg Lys Ile Ser Phe Glu Lys Leu His Ala
     75                  80                  85

ggc tcc acc ccg gag gca gcc acc tcc tcc atg ctg ccc acc tcc gag       341
Gly Ser Thr Pro Glu Ala Ala Thr Ser Ser Met Leu Pro Thr Ser Glu
 90                  95                 100                 105

gat acc ctc agc aag cgg gcg cgg ttc tct aag tat gag gag tac atc       389
Asp Thr Leu Ser Lys Arg Ala Arg Phe Ser Lys Tyr Glu Glu Tyr Ile
                110                 115                 120

cgc aag ctc aag gct ggc gag cag ctc tcc tgg ccg gcc ccc agc acc       437
Arg Lys Leu Lys Ala Gly Glu Gln Leu Ser Trp Pro Ala Pro Ser Thr
            125                 130                 135

aag acc gag gag cgg gtg ggc aag gag gtg gtg ggc acc ctg ccc ggc       485
Lys Thr Glu Glu Arg Val Gly Lys Glu Val Val Gly Thr Leu Pro Gly
        140                 145                 150

ctg cgg ctg ccc agc agc acg gcc cac ctg gag acc aag gcc acc atc       533
Leu Arg Leu Pro Ser Ser Thr Ala His Leu Glu Thr Lys Ala Thr Ile
    155                 160                 165

ctg ccc ctg ccg tcg cac agc agt gtc cag atg cag aac ctg gta gcc       581
Leu Pro Leu Pro Ser His Ser Ser Val Gln Met Gln Asn Leu Val Ala
170                 175                 180                 185

cgg gcc tcc aag tac gac ttc ttc atc caa aaa ctg aag acc ggc gag       629
Arg Ala Ser Lys Tyr Asp Phe Phe Ile Gln Lys Leu Lys Thr Gly Glu
                190                 195                 200

aat ctg cgg ccc cag aac ggg agc acc tac aag aag cca tcc aag tac       677
Asn Leu Arg Pro Gln Asn Gly Ser Thr Tyr Lys Lys Pro Ser Lys Tyr
            205                 210                 215

gac ctg gag aat gtc aag tac ctg cac ctc ttc aaa ccc ggg gag ggc       725
Asp Leu Glu Asn Val Lys Tyr Leu His Leu Phe Lys Pro Gly Glu Gly
        220                 225                 230

agc ccc gac atg ggc ggg gcc atc gcc ttc aag aca ggc aag gtg ggg       773
Ser Pro Asp Met Gly Gly Ala Ile Ala Phe Lys Thr Gly Lys Val Gly
    235                 240                 245

cgc cct tcc aag tac gac gtc cgg ggc atc cag aag cca ggc ccc gcc       821
Arg Pro Ser Lys Tyr Asp Val Arg Gly Ile Gln Lys Pro Gly Pro Ala
250                 255                 260                 265

aag gtt ccg ccc acc ccc agc ctg gct ccc gca ccc ctc gcc agc gtg       869
Lys Val Pro Pro Thr Pro Ser Leu Ala Pro Ala Pro Leu Ala Ser Val
                270                 275                 280

ccc agt gcc ccc aac gcc ccc ggg cca ggg cca gag cct cct gcc tcc       917
Pro Ser Ala Pro Asn Ala Pro Gly Pro Gly Pro Glu Pro Pro Ala Ser
            285                 290                 295

ctg tcc ttc aac act ccc gag tac ctg aag tca acc ttc tcc aaa aca       965
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Leu Ser Phe Asn Thr Pro Glu Tyr Leu Lys Ser Thr Phe Ser Lys Thr
        300                 305                 310

gac tcc atc acc acg ggg acc gtc tcc act gtc aag aac gga ctg ccc      1013
Asp Ser Ile Thr Thr Gly Thr Val Ser Thr Val Lys Asn Gly Leu Pro
    315                 320                 325

aca gat aaa cca gcc gtc act gaa gat gta aac att tac cag aaa tat      1061
Thr Asp Lys Pro Ala Val Thr Glu Asp Val Asn Ile Tyr Gln Lys Tyr
330                 335                 340                 345

att gcc agg ttc tcg ggc agc cag cac tgt ggc cac atc cac tgt gcc      1109
Ile Ala Arg Phe Ser Gly Ser Gln His Cys Gly His Ile His Cys Ala
                350                 355                 360

tac cag tac cgc gag cac tac cac tgc ctt gac cct gag tgt aac tac      1157
Tyr Gln Tyr Arg Glu His Tyr His Cys Leu Asp Pro Glu Cys Asn Tyr
            365                 370                 375

cag agg ttc acg agt aag cag gac gtg atc cgc cac tac aac atg cac      1205
Gln Arg Phe Thr Ser Lys Gln Asp Val Ile Arg His Tyr Asn Met His
        380                 385                 390

aag aag cgc gac aac tcc ctg cag cac ggc ttc atg cgt ttc agc ccg      1253
Lys Lys Arg Asp Asn Ser Leu Gln His Gly Phe Met Arg Phe Ser Pro
    395                 400                 405

ctg gac gac tgc agc gtc tac tac cac ggc tgc cac ctc aat ggg aag      1301
Leu Asp Asp Cys Ser Val Tyr Tyr His Gly Cys His Leu Asn Gly Lys
410                 415                 420                 425

agc acc cac tat cac tgc atg cag gtg ggc tgt aac aag gtg tac acg      1349
Ser Thr His Tyr His Cys Met Gln Val Gly Cys Asn Lys Val Tyr Thr
                430                 435                 440

agc acg tct gac gtg atg acc cac gag aac ttc cac aag aag aat acc      1397
Ser Thr Ser Asp Val Met Thr His Glu Asn Phe His Lys Lys Asn Thr
            445                 450                 455

cag ctc att aac gac ggc ttc cag cgc ttc cga gcc acc gaa gac tgt      1445
Gln Leu Ile Asn Asp Gly Phe Gln Arg Phe Arg Ala Thr Glu Asp Cys
        460                 465                 470

ggc aca gcc gac tgc cag ttc tac gga cag aag acc acg cac ttc cac      1493
Gly Thr Ala Asp Cys Gln Phe Tyr Gly Gln Lys Thr Thr His Phe His
    475                 480                 485

tgc agg cgc ccc ggc tgc aca ttc act ttc aag aac aag tgt gac atc      1541
Cys Arg Arg Pro Gly Cys Thr Phe Thr Phe Lys Asn Lys Cys Asp Ile
490                 495                 500                 505

gag aag cac aag agc tac cac atc aag gac gat gcc tac gcc aag gac      1589
Glu Lys His Lys Ser Tyr His Ile Lys Asp Asp Ala Tyr Ala Lys Asp
                510                 515                 520

ggc ttc aag aag ttc tac aag tac gag gag tgc aag tac gag ggc tgc      1637
Gly Phe Lys Lys Phe Tyr Lys Tyr Glu Glu Cys Lys Tyr Glu Gly Cys
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                525                 530                 535

gtg tac agc aag gct acc aac cac ttc cac tgc atc cgc gcc ggc tgc      1685
Val Tyr Ser Lys Ala Thr Asn His Phe His Cys Ile Arg Ala Gly Cys
            540                 545                 550

ggc ttc acc ttc acc tcc acc agc cag atg acc tct cac aag cgc aag      1733
Gly Phe Thr Phe Thr Ser Thr Ser Gln Met Thr Ser His Lys Arg Lys
    555                 560                 565

cat gag cgc cgg cac atc cgc tcc tcg ggc gcg ctg ggg ctg ccg ccc      1781
His Glu Arg Arg His Ile Arg Ser Ser Gly Ala Leu Gly Leu Pro Pro
570                 575                 580                 585

tcg ctg ctg ggc gcc aag gac acg gag cac gag gag tcc agc aac gac      1829
Ser Leu Leu Gly Ala Lys Asp Thr Glu His Glu Glu Ser Ser Asn Asp
                590                 595                 600

gac ctt gtt gac ttc tcc gcc ctg agc agc aag aac tcc agc ctg agc      1877
Asp Leu Val Asp Phe Ser Ala Leu Ser Ser Lys Asn Ser Ser Leu Ser
            605                 610                 615

gcc tcc cct acc agc cag cag tcc tct gcg tcc ctg gct gcc gcc act      1925
Ala Ser Pro Thr Ser Gln Gln Ser Ser Ala Ser Leu Ala Ala Ala Thr
        620                 625                 630

gcc gcc acc gag gct ggg ccc agt gcc acc aaa cct ccc aac agc aag      1973
Ala Ala Thr Glu Ala Gly Pro Ser Ala Thr Lys Pro Pro Asn Ser Lys
    635                 640                 645

atc tcg ggg ctg ctg ccc cag ggc ctg cct ggc tcg atc ccc ctg gcc      2021
Ile Ser Gly Leu Leu Pro Gln Gly Leu Pro Gly Ser Ile Pro Leu Ala
650                 655                 660                 665

ctg gcc ctc tcc aac tcg ggc ctg ccc acc ccc acg ccc tac ttc ccc      2069
Leu Ala Leu Ser Asn Ser Gly Leu Pro Thr Pro Thr Pro Tyr Phe Pro
                670                 675                 680

ata ctg gct ggc cgt ggg agc acc tcc ctg cct gtg ggc acc ccc agc      2117
Ile Leu Ala Gly Arg Gly Ser Thr Ser Leu Pro Val Gly Thr Pro Ser
            685                 690                 695

ctc ctg ggt gcc gtg tcg tct ggg tca gca gcc tca gcc acc cct gac      2165
Leu Leu Gly Ala Val Ser Ser Gly Ser Ala Ala Ser Ala Thr Pro Asp
        700                 705                 710

aca ccc acg ctg gtc gcc tcg gga gct gga gac tca gcc ccc gtg gct      2213
Thr Pro Thr Leu Val Ala Ser Gly Ala Gly Asp Ser Ala Pro Val Ala
    715                 720                 725

gcc gcc tct gtc ccg gca cca ccc gcc tcc atc atg gag agg atc tct      2261
Ala Ala Ser Val Pro Ala Pro Pro Ala Ser Ile Met Glu Arg Ile Ser
730                 735                 740                 745

gca agc aag ggc ctc atc tcg ccc atg atg gcc agg ctg gct gca gct      2309
Ala Ser Lys Gly Leu Ile Ser Pro Met Met Ala Arg Leu Ala Ala Ala
                750                 755                 760
```

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gcc ctc aag ccc tct gcc acc ttt gac cca gga agc ggg cag cag gtc       2357
Ala Leu Lys Pro Ser Ala Thr Phe Asp Pro Gly Ser Gly Gln Gln Val
            765                 770                 775

acc cca gcc agg ttc ccc ccg gcc caa gtg aag ccg gaa ccc ggt gag       2405
Thr Pro Ala Arg Phe Pro Pro Ala Gln Val Lys Pro Glu Pro Gly Glu
        780                 785                 790

agc acc ggc gcc cca ggc ccc cac gaa gcc tcc cag gac cgc agt cta       2453
Ser Thr Gly Ala Pro Gly Pro His Glu Ala Ser Gln Asp Arg Ser Leu
    795                 800                 805

gac ctg act gtg aag gag ccc agc aac gaa tca aat ggc cac gca gtc       2501
Asp Leu Thr Val Lys Glu Pro Ser Asn Glu Ser Asn Gly His Ala Val
810                 815                 820                 825

ccg gca aat tca tct ctt tta tcc tcg ctt atg aat aag atg tct cag       2549
Pro Ala Asn Ser Ser Leu Leu Ser Ser Leu Met Asn Lys Met Ser Gln
                830                 835                 840

ggc aac cct ggc ctg ggc agc ctg ctg aac atc aag gcg gaa gcg gag       2597
Gly Asn Pro Gly Leu Gly Ser Leu Leu Asn Ile Lys Ala Glu Ala Glu
            845                 850                 855

ggg agc ccc gct gcg gag ccc tcg ccc ttc cta ggc aag gcc gtg aag       2645
Gly Ser Pro Ala Ala Glu Pro Ser Pro Phe Leu Gly Lys Ala Val Lys
        860                 865                 870

gcg ctg gtt cag gag aag ttg gca gag ccc tgg aag gtg tac ctg cgc       2693
Ala Leu Val Gln Glu Lys Leu Ala Glu Pro Trp Lys Val Tyr Leu Arg
    875                 880                 885

agg ttt ggt aca aag gac ttc tgt gac ggc cag tgt gac ttc ctc cac       2741
Arg Phe Gly Thr Lys Asp Phe Cys Asp Gly Gln Cys Asp Phe Leu His
890                 895                 900                 905

aag gcc cac ttc cac tgc gtg gtg gag gaa tgc ggc gcg ctc ttc agc       2789
Lys Ala His Phe His Cys Val Val Glu Glu Cys Gly Ala Leu Phe Ser
                910                 915                 920

acc ttg gac ggg gcc atc aag cac gca aac ttc cac ttc cgg aca gag       2837
Thr Leu Asp Gly Ala Ile Lys His Ala Asn Phe His Phe Arg Thr Glu
            925                 930                 935

gga gga gca gca aaa gga aac aca gag gct gcc ttt ccg gcc tcg gcc       2885
Gly Gly Ala Ala Lys Gly Asn Thr Glu Ala Ala Phe Pro Ala Ser Ala
        940                 945                 950

gcc gag acc aaa cct ccc atg gcc ccc tcg tcc cct ccg gtc cct cct       2933
Ala Glu Thr Lys Pro Pro Met Ala Pro Ser Ser Pro Pro Val Pro Pro
    955                 960                 965

gtc acc acg gcc acg gtg tcc tct ctg gag ggg ccc gct ccc agc ccg       2981
Val Thr Thr Ala Thr Val Ser Ser Leu Glu Gly Pro Ala Pro Ser Pro
970                 975                 980                 985
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gcc tcc gtg ccc tcc acc ccc acc ctg ctc gcc tgg aag cag ctg gct 3029
Ala Ser Val Pro Ser Thr Pro Thr Leu Leu Ala Trp Lys Gln Leu Ala
990 995 1000

tcc acc ata ccc cag atg cct cag atc cca gcg tca gtg cct cac ctg 3077
Ser Thr Ile Pro Gln Met Pro Gln Ile Pro Ala Ser Val Pro His Leu
1005 1010 1015

ccc gcc tcg ccc ttg gca acg act tct cta gag aac gcc aag ccc cag 3125
Pro Ala Ser Pro Leu Ala Thr Thr Ser Leu Glu Asn Ala Lys Pro Gln
1020 1025 1030

gtc aaa ccc gga ttc ctc cag ttc cag gag aag tga gtcc ctcgatgagc 3175
Val Lys Pro Gly Phe Leu Gln Phe Gln Glu Lys *
1035 1040 1045

cgggagtccc gcgttcccct cgcgtctcgg gagtaggtgc tagcaagggc gctaggaggc 3235

cctgttcctc actgcggatg gtgctgctgt ccccagcctc tctggggcat ggccatcggg 3295

tgatgtcctt ctagccaaag atgctgctgc tcctacctca ctgcctgtcc cagagcaggc 3355

cagcccgcgt gggccgatgg tggcggcagt ggctactgct cctgcagggc atgtggtgat 3415

cctgccaggg ccaggtgggg tggactgggc gtggtggtcc tcagaggaca actcccagcc 3475

tgacaaggag ggctgcgtct ccctccgagc ctccgtattg gcctcctctg tggctcacac 3535

ccatggctga atctctgcag ggcacgtgaa gtcacgggta ggggccaggc ccctccaggc 3595

cgtcactggc ctgcacagtg gtctgagctc ttgggtggaa gggaccctcc tcactggatg 3655

gtggtggctc cttgcaggga gaacggtgac tttgtattgt catgtgtgcg gcttcctgtt 3715

ctcaataaaa gtaataaatt ggattattt 3744

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atcttttaaa gtatgcatat cattagtgga aaataatagg taacaaaaga aattgggga 120

aaagctttaa gagttctgat gcctatttaa gtaaattaac tcttttcccc ccaaaattct 180

taggcttgaa g atg cag tgg acg cca gag cat gcc cag tgg cca gaa cag 230
Met Gln Trp Thr Pro Glu His Ala Gln Trp Pro Glu Gln

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            1                   5                   10

cac ttt gac atc acc tca acc act cgg tct cct gcc cac aaa gtt gaa       278
His Phe Asp Ile Thr Ser Thr Thr Arg Ser Pro Ala His Lys Val Glu
     15                  20                  25

gcc tac aga ggt cat ctg cag cgc acc tat cag tac gcc tgg gcg aat       326
Ala Tyr Arg Gly His Leu Gln Arg Thr Tyr Gln Tyr Ala Trp Ala Asn
 30                  35                  40                  45

gat gac ata tct gct ctg act gca tcc aac cta cta aaa aaa tat gca       374
Asp Asp Ile Ser Ala Leu Thr Ala Ser Asn Leu Leu Lys Lys Tyr Ala
                 50                  55                  60

gag aag tat tcc ggc att ttg gaa ggt cct gtg gac cga ccc gta ctc       422
Glu Lys Tyr Ser Gly Ile Leu Glu Gly Pro Val Asp Arg Pro Val Leu
             65                  70                  75

agc aac tat tcg gac aca cca tca gga cta gtg aac ggt cgg aaa aat       470
Ser Asn Tyr Ser Asp Thr Pro Ser Gly Leu Val Asn Gly Arg Lys Asn
         80                  85                  90

gaa agt gaa ccc tgg cag cct tcc ttg aat tca gaa gct gtt tat ccc       518
Glu Ser Glu Pro Trp Gln Pro Ser Leu Asn Ser Glu Ala Val Tyr Pro
     95                 100                 105

atg aac tgt gtt ccg gat gtt atc act gcc agc aaa gct gga gtc agt       566
Met Asn Cys Val Pro Asp Val Ile Thr Ala Ser Lys Ala Gly Val Ser
110                 115                 120                 125

tca gcc ctc cct cca gca gat gtc tct gcg agt ata gga agc tct cct       614
Ser Ala Leu Pro Pro Ala Asp Val Ser Ala Ser Ile Gly Ser Ser Pro
                130                 135                 140

ggg gta gcc agc aac ctg aca gaa cct agt tat tca agt agt acc tgt       662
Gly Val Ala Ser Asn Leu Thr Glu Pro Ser Tyr Ser Ser Ser Thr Cys
            145                 150                 155

gga agc cac act gta ccc agt ctt cat gca ggg ctc cca tct cag gaa       710
Gly Ser His Thr Val Pro Ser Leu His Ala Gly Leu Pro Ser Gln Glu
        160                 165                 170

tat gcc cca gga tac aac gga tca tat ttg cat tct act tat agt agc       758
Tyr Ala Pro Gly Tyr Asn Gly Ser Tyr Leu His Ser Thr Tyr Ser Ser
    175                 180                 185

cag cca gca cct gca ctt cct tca cct cat ccg tct cct ttg cat agc       806
Gln Pro Ala Pro Ala Leu Pro Ser Pro His Pro Ser Pro Leu His Ser
190                 195                 200                 205

tct ggg cta cta cag ccc cca cca cca cct cct ccg cca cca gcc ttg       854
Ser Gly Leu Leu Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Leu
                210                 215                 220

gtc cca ggc tac aat ggg act tct aac ctc tcc agt tac agc tat ccg       902
Val Pro Gly Tyr Asn Gly Thr Ser Asn Leu Ser Ser Tyr Ser Tyr Pro
            225                 230                 235
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tct gct agc tat cct cct cag act gct gtg ggg tct ggg tac agc cct        950
Ser Ala Ser Tyr Pro Pro Gln Thr Ala Val Gly Ser Gly Tyr Ser Pro
        240                 245                 250

ggg ggg gca ccg cct ccg cct tca gcg tac ctg cct tca gga att cct        998
Gly Gly Ala Pro Pro Pro Pro Ser Ala Tyr Leu Pro Ser Gly Ile Pro
    255                 260                 265

gct ccc acc ccc cta ccc ccc acc act gtt cct ggc tac acc tac cag       1046
Ala Pro Thr Pro Leu Pro Pro Thr Thr Val Pro Gly Tyr Thr Tyr Gln
270                 275                 280                 285

ggc cat ggt ttg aca cct att gca ccg tcg gct ctg aca aac agt tca       1094
Gly His Gly Leu Thr Pro Ile Ala Pro Ser Ala Leu Thr Asn Ser Ser
                290                 295                 300

gca agt tct ctc aaa agg aaa gct ttc tac atg gca ggg caa gga gat       1142
Ala Ser Ser Leu Lys Arg Lys Ala Phe Tyr Met Ala Gly Gln Gly Asp
            305                 310                 315

atg gac tcc agt tat gga aat tac agc tat ggc caa cag aga tct aca       1190
Met Asp Ser Ser Tyr Gly Asn Tyr Ser Tyr Gly Gln Gln Arg Ser Thr
        320                 325                 330

cag agt cct atg tac aga atg ccc gac aac agc att tca aac aca aat       1238
Gln Ser Pro Met Tyr Arg Met Pro Asp Asn Ser Ile Ser Asn Thr Asn
    335                 340                 345

cgg ggg aat ggc ttt gac aga agt gct gaa aca tca tcc tta gca ttt       1286
Arg Gly Asn Gly Phe Asp Arg Ser Ala Glu Thr Ser Ser Leu Ala Phe
350                 355                 360                 365

aag cca acg aag cag cta atg tcc tct gaa cag caa agg aaa ttc agc       1334
Lys Pro Thr Lys Gln Leu Met Ser Ser Glu Gln Gln Arg Lys Phe Ser
                370                 375                 380

agc cag tcc agt agg gct ctg acc cct cct tcc tac agt act gct aaa       1382
Ser Gln Ser Ser Arg Ala Leu Thr Pro Pro Ser Tyr Ser Thr Ala Lys
            385                 390                 395

aat tca ttg gga tca aga tcc agt gaa tcc ttt ggg aag tac aca tcg       1430
Asn Ser Leu Gly Ser Arg Ser Ser Glu Ser Phe Gly Lys Tyr Thr Ser
        400                 405                 410

cca gta atg agt gag cat ggg gac gag cac agg cag ctc ctc tct cac       1478
Pro Val Met Ser Glu His Gly Asp Glu His Arg Gln Leu Leu Ser His
    415                 420                 425

cca atg caa ggc cct gga ctc cgt gca gct acc tca tcc aac cac tct       1526
Pro Met Gln Gly Pro Gly Leu Arg Ala Ala Thr Ser Ser Asn His Ser
430                 435                 440                 445

gtg gac gag caa ctg aag aat act gac acg cac ctc atc gac ctg gta       1574
Val Asp Glu Gln Leu Lys Asn Thr Asp Thr His Leu Ile Asp Leu Val
                450                 455                 460
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acc aat gag att atc acc caa gga cct cca gtg gac tgg aat gac att      1622
Thr Asn Glu Ile Ile Thr Gln Gly Pro Pro Val Asp Trp Asn Asp Ile
            465                 470                 475

gct ggt ctc gac ctg gtg aag gct gtc att aaa gag gag gtt tta tgg      1670
Ala Gly Leu Asp Leu Val Lys Ala Val Ile Lys Glu Glu Val Leu Trp
        480                 485                 490

cca gtg ttg agg tca gac gcg ttc agt gga ctg acg gcc tta cct cgg      1718
Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr Ala Leu Pro Arg
    495                 500                 505

agc atc ctt tta ttt gga cct cgg ggg aca ggc aaa aca tta ttg ggc      1766
Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys Thr Leu Leu Gly
510                 515                 520                 525

aga tgc atc gct agt cag ctg ggg gcc aca ttt ttc aaa att gcc ggt      1814
Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe Lys Ile Ala Gly
                530                 535                 540

tct gga cta gtc gcc aag tgg tta gga gaa gca gag aaa att atc cat      1862
Ser Gly Leu Val Ala Lys Trp Leu Gly Glu Ala Glu Lys Ile Ile His
            545                 550                 555

gcc tct ttt ctt gtg gcc agg tgt cgc cag ccc tcg gtg att ttt gtt      1910
Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser Val Ile Phe Val
        560                 565                 570

agt gac att gac atg ctt ctc tcc tct caa gtg aat gag gaa cat agt      1958
Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn Glu Glu His Ser
    575                 580                 585

cca gtc agt cgg atg aga acc gaa ttt ctg atg caa ctg gac act gta      2006
Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln Leu Asp Thr Val
590                 595                 600                 605

cta act tcg gct gag gac caa atc gta gta att tgt gcc acc agt aaa      2054
Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys Ala Thr Ser Lys
                610                 615                 620

cca gaa gaa ata gat gaa tcc ctt cgg agg tac ttc atg aaa cga ctt      2102
Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe Met Lys Arg Leu
            625                 630                 635

tta atc cca ctt cct gac agc aca gcg agg cac cag ata ata gta caa      2150
Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln Ile Ile Val Gln
        640                 645                 650

ctg ctc tca cag cac aat tac tgt ctc aat gac aag gag ttt gca ctg      2198
Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys Glu Phe Ala Leu
    655                 660                 665

ctc gtc cag cgc aca gaa ggc ttt tct gga cta gat gtg gct cat ttg      2246
Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp Val Ala His Leu
670                 675                 680                 685

tgt cag gaa gca gtg gtg ggc ccc ctc cat gcc atg cca gcc aca gac      2294
```

```
Cys Gln Glu Ala Val Val Gly Pro Leu His Ala Met Pro Ala Thr Asp
                690                 695                 700

ctt tca gcc att atg ccc agc cag ttg agg ccc gtt aca tat caa gac      2342
Leu Ser Ala Ile Met Pro Ser Gln Leu Arg Pro Val Thr Tyr Gln Asp
            705                 710                 715

ttt gaa aat gct ttc tgc aag att cag cct agc ata tct caa aag gag      2390
Phe Glu Asn Ala Phe Cys Lys Ile Gln Pro Ser Ile Ser Gln Lys Glu
        720                 725                 730

ctt gat atg tat gtt gaa tgg aac aaa atg ttt ggt tgc agt cag tga      2438
Leu Asp Met Tyr Val Glu Trp Asn Lys Met Phe Gly Cys Ser Gln  *
    735                 740                 745

taacttcttt ag                                                        2450



     <210> 243
     <211> 465
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (168)..(437)

     <400> 243
gcatagtaat gatccaaata tatgtatatg ttgctcatgg aatgaaccct ccccagacta      60

aagatgcctg taaatcaaat ttcactataa ttgtaaagaa acctgaggca attagttaaa     120

aagttttaag tattcaggca attcatgata ccttgttgaa ataaagc atg cag act      176
                                                    Met Gln Thr
                                                      1

cat aaa aac ttg tat ata atc aaa ata aag ttc tac aaa tgg gaa aga      224
His Lys Asn Leu Tyr Ile Ile Lys Ile Lys Phe Tyr Lys Trp Glu Arg
    5                   10                  15

gga tta tta tca ggg tat att aag gtg tta gac tta caa aag aag tgc      272
Gly Leu Leu Ser Gly Tyr Ile Lys Val Leu Asp Leu Gln Lys Lys Cys
 20                 25                  30                  35

ata att aat tac tca ttt aaa att aat tct ata ccc att agc ttg gca      320
Ile Ile Asn Tyr Ser Phe Lys Ile Asn Ser Ile Pro Ile Ser Leu Ala
                40                  45                  50

aca gat aaa ata aaa gca tgc aac agt gct ttc tta gtc gac gcg gcc      368
Thr Asp Lys Ile Lys Ala Cys Asn Ser Ala Phe Leu Val Asp Ala Ala
            55                  60                  65

gcg aat tcg gat cct cga gag atc tct ttt ttt ggg ttt ggt ggg gta      416
Ala Asn Ser Asp Pro Arg Glu Ile Ser Phe Phe Gly Phe Gly Gly Val
        70                  75                  80
```

```
tct tca tca tcg aat aga tag ttatatacat catgctcttc aattaaaa          465
Ser Ser Ser Ser Asn Arg  *
    85                  90
```

```
<210> 244
<211> 1080
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (83)..(829)

<400> 244
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ctaggggagc tgaattctgc gtcttccttt aggctgcggc gagacaatcc ccagagcccc      60

gcggcccggc ctcggggcag cc atg gac tcg cag gaa ttg aag act ttg att      112
                         Met Asp Ser Gln Glu Leu Lys Thr Leu Ile
                          1               5                  10

aat tac tat tgt caa gag aga tat ttc cat cat gta tta ctg gtt gcc      160
Asn Tyr Tyr Cys Gln Glu Arg Tyr Phe His His Val Leu Leu Val Ala
                15                  20                  25

agt gaa gga att aag agg tat gga agt gat cca gtc ttc agg ttt tat      208
Ser Glu Gly Ile Lys Arg Tyr Gly Ser Asp Pro Val Phe Arg Phe Tyr
            30                  35                  40

cat gcc tat ggc aca tta atg gaa ggt aaa act caa gaa gct ctt cga      256
His Ala Tyr Gly Thr Leu Met Glu Gly Lys Thr Gln Glu Ala Leu Arg
        45                  50                  55

gaa ttt gag gct att aaa aat aaa caa gat gta tca ctt tgt tct cta      304
Glu Phe Glu Ala Ile Lys Asn Lys Gln Asp Val Ser Leu Cys Ser Leu
    60                  65                  70

ctt gca ctg ata tat gcc cat aaa atg agt cct aat cca gat aga gaa      352
Leu Ala Leu Ile Tyr Ala His Lys Met Ser Pro Asn Pro Asp Arg Glu
 75                  80                  85                  90

gct att ctg gaa tca gat gcc aga gtg aag gaa caa cgt aaa gga gct      400
Ala Ile Leu Glu Ser Asp Ala Arg Val Lys Glu Gln Arg Lys Gly Ala
                95                 100                 105

gga gag aaa gcc tta tac cat gca ggc tta ttt tta tgg cac att ggt      448
Gly Glu Lys Ala Leu Tyr His Ala Gly Leu Phe Leu Trp His Ile Gly
            110                 115                 120

cgc cat gat aaa gca agg gaa tat att gac aga atg atc aaa ata tca      496
Arg His Asp Lys Ala Arg Glu Tyr Ile Asp Arg Met Ile Lys Ile Ser
        125                 130                 135
```

```
gat ggt agt aaa cag gga cac gtt ttg aaa gca tgg ctt gat att aca       544
Asp Gly Ser Lys Gln Gly His Val Leu Lys Ala Trp Leu Asp Ile Thr
    140                 145                 150

aga gga aaa gag cct tac act aaa aaa gca ctg aag tat ttt gaa gag       592
Arg Gly Lys Glu Pro Tyr Thr Lys Lys Ala Leu Lys Tyr Phe Glu Glu
155                 160                 165                 170

gga ctc caa gat ggg aat gat act ttt gct ctg ctg ggt aag gca caa       640
Gly Leu Gln Asp Gly Asn Asp Thr Phe Ala Leu Leu Gly Lys Ala Gln
                175                 180                 185

tgc ctt gag atg cgc cag aat tat tca ggt gcc ctg gag act gtg aac       688
Cys Leu Glu Met Arg Gln Asn Tyr Ser Gly Ala Leu Glu Thr Val Asn
            190                 195                 200

cag ata atc gtg aat ttt ccg agc ttc ctt cct gct ttt gtt aag aaa       736
Gln Ile Ile Val Asn Phe Pro Ser Phe Leu Pro Ala Phe Val Lys Lys
        205                 210                 215

atg aaa tta caa cta gcc ttg cag gat tgg gac cag aca gtt gag aca       784
Met Lys Leu Gln Leu Ala Leu Gln Asp Trp Asp Gln Thr Val Glu Thr
    220                 225                 230

gca aaa ggt tgc tgc tcc aag ata gcc aaa atg tgg aag cac tga gaa       832
Ala Lys Gly Cys Cys Ser Lys Ile Ala Lys Met Trp Lys His  *
235                 240                 245

tgcaggcact ctactatgtg tgtagagagg gggatataga gaaggcttcc accaagctgg     892

aaaacttggg aaatgcattg gatgccatgg aaccacagaa tgctcaactt ttctataaca     952

ttacactcgc cttcagcaga acttgtggac gtagtcaact tattcttcaa aaaattcaaa    1012

cgttacttga gagagctttt agtttaaccc tcagcaatca gaatttgcta cagacttgga    1072

taccaatt                                                             1080



     <210> 245
     <211> 2128
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (107)..(286)

     <400> 245
gagcttagct aacattgcct tttcactcta tttttctcag atattgtaag cattctgttt      60

ttcaatattg tagttaattt tttggctttc aacagcagcc ctagta   atg gtg gag     115
                                                     Met Val Glu
                                                     1
```

```
ttg tta att aat gtg tat att gta ctg aat ttc tgt cag tta agg ggt       163
Leu Leu Ile Asn Val Tyr Ile Val Leu Asn Phe Cys Gln Leu Arg Gly
      5                  10                  15

tca ctg ctt tgg tgg aaa ttg gtg gaa att gct agc agg ttc cac gat       211
Ser Leu Leu Trp Trp Lys Leu Val Glu Ile Ala Ser Arg Phe His Asp
 20                  25                  30                  35

gtt tat ttt ttt ctc cat gtt gta tat cat tac cat ttc aca tac gcg       259
Val Tyr Phe Phe Leu His Val Val Tyr His Tyr His Phe Thr Tyr Ala
                40                  45                  50

ttt cta ttt ttc ttc ctc tcc tcc tga tctcc ttaaaaatga atctagagtt       311
Phe Leu Phe Phe Phe Leu Ser Ser  *
             55                  60

ggtggctttt tccccctcct ctttggccag ttccacagtt cagttcttcc tgaaaacagg    371

gatgatgaac ttgtaggatc aggacaaatg tgtgtttttc aaaaacttaa ggctgggtgt    431

gaaacacctt ctgtggacaa ggatttgtaa acttctctcc tccctccagc tgcggcccca    491

gcctaactga tagttacttg attcagtgtg ctagacactt aaatagcatc tatgtctctt    551

tcaagggaat ttgtcaaata atgctgttta gctaattgtt gcaagcaatt gcatattaac    611

agctgtgatt ttgttggaca gcaagtatta tggccaaagc cagtttcttg gcatttcaaa    671

aataatgcaa taaaaactag ttgaggttag ctgaggctgg aaatgccttt ttcatggtaa    731

atgattcact tctatatttt tctttctttt tcttttttt tctttggttt tcatcctgga     791

ttcatcccct gatcttaaat caaaacgtca gatcaatgaa ctatgaacta aagtattttt    851

cttaagccta ttgagtgatt aattttttaa aaaatgttta aatgcatatg cttttctttc    911

agcacaaaca acagcaaaaa cttttgtaat aactaactta cctttgcatg tatgaagaac    971

tgagtcattt atttccctaa cttactcctc tttcaagtaa caggtggcag atcataaaat   1031

gaattcttta ttgtatctac acactccaca ttctttactg tgtcctacta ctgtatcttg   1091

gctccctgct gtattaaaca ccatcttaag cacttgttcc tgcaggactc cttcttgaca   1151

ttttgtctcc cccttcaaag tcactcaaag agtgggactt catcaaaaga aatgaattag   1211

tctctatcac accgaatact aagatttatt tcctctgatg gtacatagat ttctctctcc   1271

actaagaggg tcactctcat agaggaatgt cttgtcagtt ttatacttgc tgaggctaga   1331

ctgacaataa aaatgagctg ggcagttaaa ttagcatttg ttactatatt ggcctataaa   1391

ggatcaggtt gatgataata cctctaaaaa tatgcaataa taaaacaata gttatgaaag   1451

aaacttgaaa ggtttgcaag gtttctccta tccctgttaa aattatcatt tattatctct   1511

ttgtcagtgt tagtaaggta acccatgaca gaataatttg agtgatagtt catcatgcag   1571
```

```
aggatatgat caagatatta cctaatggtt ttatcctgaa aaaggtgtat acttttaggg   1631

cactgttaac aatgcgagtg aaaccaagat ggtgcaagtt ccctttgcag atggcgtggg   1691

cacacttgat ttttattatg agtgaatgta atctttctgt attttaccag agttacagca   1751

attacctgaa aagtttccta acattttaat aatgttaggg atttcgtttt ggttttagtt   1811

gtcctcaaga gacaacaggt tcacagtaat ttccatgatg ttgggtgtgg ctaagctggg   1871

gattggttct gttcccsctg ctcccgtgta gagaaaagct atatttatac tgcattcttt   1931

ctcaactttc aggtaaaaca aactatgatt taaaaaaaga aaaaagaaaa gacaggtact   1991

tttacttcaa agagtgcttt gctacatttt tatttaaacc aaaaatcaaa taaaataagg   2051

agggggctg ggtatacttt aaacaaaacc agtcctgaaa tgctgttatt ctcaaagtac   2111

attccaaaaa aaaaaaa                                                   2128
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<210> 246
<211> 3373
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (146)..(2254)

<400> 246
agatatgaaa ctggttctgg agtgagatga gctcggctgg ggacgctact tgagaaggcc      60

tttccccaca gggtgactta aatgtcccag gctggaaggt ggagcgagaa gtggatgccc     120

ccagggctct gggtcacact ccagg  atg act tct cgg aac cag ctg gtg cag      172
                             Met Thr Ser Arg Asn Gln Leu Val Gln
                              1               5

aag gtg ctg cag gag ctg cag gaa gca gtg gag tgc gaa ggc ctg gag       220
Lys Val Leu Gln Glu Leu Gln Glu Ala Val Glu Cys Glu Gly Leu Glu
 10                  15                  20                  25

ggt ctc ata ggt gct tcc ttg gag gcc aag cag gtc ctg tct tcc ttc       268
Gly Leu Ile Gly Ala Ser Leu Glu Ala Lys Gln Val Leu Ser Ser Phe
                 30                  35                  40

act ctc ccc acc tgc cgg gag gga ggc cct ggc ctc cag gtg ctg gaa       316
Thr Leu Pro Thr Cys Arg Glu Gly Gly Pro Gly Leu Gln Val Leu Glu
             45                  50                  55

gtg gac tcg gtg gcc ctg agc ctg tat cca gaa gat gct cca cgg aac       364
Val Asp Ser Val Ala Leu Ser Leu Tyr Pro Glu Asp Ala Pro Arg Asn
         60                  65                  70
```

```
atg ctg ccg ctg gtg tgc aag ggg gag ggc agc ctg ctg ttc gag gcg        412
Met Leu Pro Leu Val Cys Lys Gly Glu Gly Ser Leu Leu Phe Glu Ala
     75                  80                  85

gcc agc atg ctg ctg tgg ggt gac gca ggc ctc agc ctg gag ctg cgg        460
Ala Ser Met Leu Leu Trp Gly Asp Ala Gly Leu Ser Leu Glu Leu Arg
 90                  95                 100                 105

gcc cgc acc gtg gta gag atg ctg ctg cac aga cac tac tac ctc cag        508
Ala Arg Thr Val Val Glu Met Leu Leu His Arg His Tyr Tyr Leu Gln
                110                 115                 120

ggc atg atc gac tcc aaa gtg atg ctg cag gcc gtg cgc tac tcc cta        556
Gly Met Ile Asp Ser Lys Val Met Leu Gln Ala Val Arg Tyr Ser Leu
            125                 130                 135

tgc tct gag gag tcc cct gag atg acc agc ttg ccc ccc gcc acg ctg        604
Cys Ser Glu Glu Ser Pro Glu Met Thr Ser Leu Pro Pro Ala Thr Leu
        140                 145                 150

gag gcc atc ttc gat gcc gac gtc aag gcc tcc tgt ttc ccc agc agc        652
Glu Ala Ile Phe Asp Ala Asp Val Lys Ala Ser Cys Phe Pro Ser Ser
    155                 160                 165

ttc tcc aac gtg tgg cac ttg tat gct ctc gcc tct gtc ctc cag cgg        700
Phe Ser Asn Val Trp His Leu Tyr Ala Leu Ala Ser Val Leu Gln Arg
170                 175                 180                 185

aac atc tac tcc atc tac ccc atg cgc aac ctc aag atc cgg ccc tac        748
Asn Ile Tyr Ser Ile Tyr Pro Met Arg Asn Leu Lys Ile Arg Pro Tyr
                190                 195                 200

ttc aac cgt gtc atc cgg ccc cgc cgc tgc gac cac gtg ccc tcc acg        796
Phe Asn Arg Val Ile Arg Pro Arg Arg Cys Asp His Val Pro Ser Thr
            205                 210                 215

ctg cac atc atg tgg gct ggc cag ccc ctc acc agc cac ttc ttc cgc        844
Leu His Ile Met Trp Ala Gly Gln Pro Leu Thr Ser His Phe Phe Arg
        220                 225                 230

cac cag tac ttt gcc cct gtg gtg ggg ctg gaa gag gtg gag gct gaa        892
His Gln Tyr Phe Ala Pro Val Val Gly Leu Glu Glu Val Glu Ala Glu
    235                 240                 245

ggt gcc cct ggc gtg gcc cca gct ctt cca gcc ctg gcc cca ctc tca        940
Gly Ala Pro Gly Val Ala Pro Ala Leu Pro Ala Leu Ala Pro Leu Ser
250                 255                 260                 265

tcg ccg gcc aag acc ctg gag ctg ctc aac cgt gaa cct ggc ctc agc        988
Ser Pro Ala Lys Thr Leu Glu Leu Leu Asn Arg Glu Pro Gly Leu Ser
                270                 275                 280

tac tct cac ctc tgt gag cgc tac agc gtc acc aaa agc acc ttc tac       1036
Tyr Ser His Leu Cys Glu Arg Tyr Ser Val Thr Lys Ser Thr Phe Tyr
            285                 290                 295
```

```
cgc tgg cgg cgg cag tcc cag gag cac cgg cag aag gtt gct gcc cgc       1084
Arg Trp Arg Arg Gln Ser Gln Glu His Arg Gln Lys Val Ala Ala Arg
        300                 305                 310

ttc tcc gcc aag cac ttc ctg cag gac agc ttc cac cgg ggg ggc gtc       1132
Phe Ser Ala Lys His Phe Leu Gln Asp Ser Phe His Arg Gly Gly Val
    315                 320                 325

gtg cca ctt cag cag ttc ctc cag cgg ttc ccg gag atc tcc cgc tca       1180
Val Pro Leu Gln Gln Phe Leu Gln Arg Phe Pro Glu Ile Ser Arg Ser
330                 335                 340                 345

acc tac tat gtc tgg aag cat gag ctg ctg ggc tct ggc acc tgc ccg       1228
Thr Tyr Tyr Val Trp Lys His Glu Leu Leu Gly Ser Gly Thr Cys Pro
                350                 355                 360

gcc ttg ccc ccc agg gag gtg ctg ggc atg gag gag cta gag aag ctg       1276
Ala Leu Pro Pro Arg Glu Val Leu Gly Met Glu Glu Leu Glu Lys Leu
            365                 370                 375

ccg gag gag cag gtg gct gag gag gag ctg gag tgc tcc gca ctg gcg       1324
Pro Glu Glu Gln Val Ala Glu Glu Glu Leu Glu Cys Ser Ala Leu Ala
        380                 385                 390

gtg tca agc cct gga atg gtc tta atg cag cgg gcc aag ttg tac ctg       1372
Val Ser Ser Pro Gly Met Val Leu Met Gln Arg Ala Lys Leu Tyr Leu
    395                 400                 405

gag cat tgc atc tcc ctg aac aca ctg gta ccc tat cgc tgc ttc aaa       1420
Glu His Cys Ile Ser Leu Asn Thr Leu Val Pro Tyr Arg Cys Phe Lys
410                 415                 420                 425

cgc agg ttc cct ggc atc tca cgg tcc act tat tat aat tgg cgg cga       1468
Arg Arg Phe Pro Gly Ile Ser Arg Ser Thr Tyr Tyr Asn Trp Arg Arg
                430                 435                 440

aag gcc ctc cgg agg aac ccc agc ttc aag ccg gca cca gcc ctc tct       1516
Lys Ala Leu Arg Arg Asn Pro Ser Phe Lys Pro Ala Pro Ala Leu Ser
            445                 450                 455

gct gct ggg act ccc cag cta gca tct gtt ggg gaa ggg gct gta att       1564
Ala Ala Gly Thr Pro Gln Leu Ala Ser Val Gly Glu Gly Ala Val Ile
        460                 465                 470

cct tgg aag agt gag gcg gaa gag ggg gca ggg aat gcc aca ggt gag       1612
Pro Trp Lys Ser Glu Ala Glu Glu Gly Ala Gly Asn Ala Thr Gly Glu
    475                 480                 485

gac cct ccc gcc ccc ggg gag ctc ctg cca cta agg atg ccc ctg tcc       1660
Asp Pro Pro Ala Pro Gly Glu Leu Leu Pro Leu Arg Met Pro Leu Ser
490                 495                 500                 505

cgt tgg cag agg cgt ctg cgc agg gct gcc cgc agg cag gtg ctg agt       1708
Arg Trp Gln Arg Arg Leu Arg Arg Ala Ala Arg Arg Gln Val Leu Ser
                510                 515                 520

ggg cat ctc cct ttc tgc cgc ttc cgc ctc cgc tac ccc agc ctg tca       1756
```

```
Gly His Leu Pro Phe Cys Arg Phe Arg Leu Arg Tyr Pro Ser Leu Ser
            525                 530                 535

cct tct gcc ttt tgg gtc tgg aag agt ctt gct cgg ggt tgg ccc aga      1804
Pro Ser Ala Phe Trp Val Trp Lys Ser Leu Ala Arg Gly Trp Pro Arg
        540                 545                 550

ggc ctg tcc aaa ctt cag gtg ccg gtc ccc acc ttg ggc aaa ggg ggg      1852
Gly Leu Ser Lys Leu Gln Val Pro Val Pro Thr Leu Gly Lys Gly Gly
    555                 560                 565

cag gag gct gag gag aag cag gag aag gag gct ggc agg gat gtg aca      1900
Gln Glu Ala Glu Glu Lys Gln Glu Lys Glu Ala Gly Arg Asp Val Thr
570                 575                 580                 585

gct gtg atg gcc cca cct gtg ggg gct tct tca gaa gat gta gag gga      1948
Ala Val Met Ala Pro Pro Val Gly Ala Ser Ser Glu Asp Val Glu Gly
                590                 595                 600

ggg cct tcc aga gag ggg gcc ctg cag gag ggg gcc aca gcc cag ggc      1996
Gly Pro Ser Arg Glu Gly Ala Leu Gln Glu Gly Ala Thr Ala Gln Gly
            605                 610                 615

cag ccc cac agt ggg ccc ttg ctg agc caa cct gtg gtg gca gca gcg      2044
Gln Pro His Ser Gly Pro Leu Leu Ser Gln Pro Val Val Ala Ala Ala
        620                 625                 630

ggt ggc agg gat ggc cgg atg ctg gtg atg gac atg atc gct acc acg      2092
Gly Gly Arg Asp Gly Arg Met Leu Val Met Asp Met Ile Ala Thr Thr
    635                 640                 645

aag ttc aag gcc cag gcc aag ctg ttc ttg cag aag cgc ttc cag tcc      2140
Lys Phe Lys Ala Gln Ala Lys Leu Phe Leu Gln Lys Arg Phe Gln Ser
650                 655                 660                 665

aag agc ttt ccc tcc tac aag gag ttc agt gcc ctc ttt ccc ctc act      2188
Lys Ser Phe Pro Ser Tyr Lys Glu Phe Ser Ala Leu Phe Pro Leu Thr
                670                 675                 680

gcc cgc tcc aca tac tac atg tgg aag cga gcc ctc tat gac ggc ctg      2236
Ala Arg Ser Thr Tyr Tyr Met Trp Lys Arg Ala Leu Tyr Asp Gly Leu
            685                 690                 695

acc ctg gta gat ggc tga caggga ggtacaaaag gggctgggaa gaagggggac      2290
Thr Leu Val Asp Gly  *
        700

cagtttggag agggtcaggg acctgagctg accccaggct tggccaggat gtcctttgct    2350

ctgggtccca cagtgtctac cctaagtcca agggtatatt tgtgttattt tctggctcca    2410

ggacagagaa tgccagaaat cagccatctg gtctcccgta ggaaactgtg ggaccagaga    2470

tatcctcttt cgttgtttgc tggtcatatt tttactgtta tgatttagtt tttggttttg    2530

atttgagtgg gttggttggc ccccttgctg gagttggaag ccgtatgtat gtcagggggt    2590
```

```
ttagaggggg gttggttagc tagagctgct ttcagctttt cctggagaca aaaggagtgt   2650

tatagcatga tcatcggtcc cactgggcag aacgttatct tcagtttctt ttgggggttg   2710

gcatcctctt tactcagttg tttcccaaag gaacattagg ctcgaatatg gggccaggt    2770

gtggtggctt atgcctgtaa tcctagcgct ttgggaggcc aaggcaggag gatcacttga   2830

ggctaggagt tagagaccac cctgggcaat gtagtgagac ctcatctctt agaaaaaaaa   2890

aaagaaagaa aatcaaatgt agagctgatc agcagcttgt gcctggcatc cccaagggag   2950

aaggtgccag gtcagcagga gcagcagcag ggatgtatag aaagaaccac agctggcctc   3010

taaaggatgg cactgaggca ccggagatct tgaggcactg gagatcactg aggggctggc   3070

ctgtcccctg caaggagtgt gggaccaggt ggggcaaggc tgggagatgc aggctctgtt   3130

tgcagattat ggcccagagt ctctgcttgt gggtgcttga tccacctgct gggaccctgc   3190

agtcctcggc cagcctggct gtcagttggg gattccacct ttctgctgag cgtcttctcg   3250

gagctggagg cccatcttca gtgagagatc acaaagcggc caggcaggtg ggagactgaa   3310

tttgccttgt tcgagagtaa cgtttgaaaa ccaaagaaat aaagtgatgc agtgcccaca   3370

aaa                                                                 3373




      <210> 247
      <211> 817
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (90)..(662)

      <400> 247
tttcgtgggc cactgcaggg gccgctaacg gtccggcgcc cctcggcgtc cgcgcgcccc     60

cagcctggcg gacgagcccg gcggcggag  atg ggg gcg acg ggg gcg gcg gag     113
                                 Met Gly Ala Thr Gly Ala Ala Glu
                                 1               5

ccg ctg caa tcc gtg ctg tgg gtg aag cag cag cgc tgc gcc gtg agc      161
Pro Leu Gln Ser Val Leu Trp Val Lys Gln Gln Arg Cys Ala Val Ser
    10                  15                  20

ctg gag ccc gcg cgg gct ctg ctg cgc tgg tgg cgg agc ccg ggg ccc      209
Leu Glu Pro Ala Arg Ala Leu Leu Arg Trp Trp Arg Ser Pro Gly Pro
25                  30                  35                  40

gga gcc ggc gcc ccc ggc gcg gat gcc tgc tct gtg cct gta tct gag      257
Gly Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser Glu
```

```
                 45                  50                  55

atc atc gcc gtt gag gaa aca gac gtt cac ggg aaa cat caa ggc agt       305
Ile Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly Ser
             60                  65                  70

gga aaa tgg cag aaa atg gaa aag cct tac gct ttt aca gtt cac tgt       353
Gly Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys
         75                  80                  85

gta aag aga gca cga cgg cac cgc tgg aag tgg gcg cag gtg act ttc       401
Val Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe
     90                  95                 100

tgg tgt cca gag gag cag ctg tgt cac ttg tgg ctg cag acc ctg cgg       449
Trp Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg
105                 110                 115                 120

gag atg ctg gag aag ctg acg tcc aga cca aag cat tta ctg gta ttt       497
Glu Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe
                125                 130                 135

atc aac ccg ttt gga gga aaa gga caa ggc aag cgg ata tat gaa aga       545
Ile Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg
            140                 145                 150

aaa gtg gca cca ctg ttc acc tta gcc tcc atc acc act gac atc atc       593
Lys Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile
        155                 160                 165

gtt act gaa cat gct aat cag gcc aag gag act ctg tat gag att aac       641
Val Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn
    170                 175                 180

ata gac aaa tac gac ggg tga gt aagccgtctt tcatcgccat caagtccatt       694
Ile Asp Lys Tyr Asp Gly  *
185                 190

gttaatgaaa aagttctacc cacctctcag ttttgagagc tccttttcct aaatccgccc     754

cccgcctcca cccacgacca attgtaaaag taaacatgct tcttacagga aggcaagaaa     814

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actggtgggt tggaggctgt cgtgtggctg accagagatg gccagctgat gggtcacaca     180

gttggggatg gtgtcaggag gtcaacctga ccagcagaga cggctggcag gaaggtcacg     240

gaaggccagc caggcatggt gccactgggt gcaggcaggt ggcggatctg agtggcctga     300

cacattggat ggtcgcttat ttgggcagcg tgattgtcag aacagtgtgg caggggctgc     360

tgcagggagc catttggaca tctgcagggc cccgccggag gcctcggatg gccacgtagg     420

gtctgcctat caagagaacc cccagatgat cacagtcccc cagagacagc cagacccccg     480

gggacccagc ctctcacagt cagtcctccc acccgagtga ccccg    atg gcg gcc      534
                                                     Met Ala Ala
                                                      1

tcc cag ctg gcg gcg ctg gaa gga gtg gac tcc ggt ccc agg gtg ccc      582
Ser Gln Leu Ala Ala Leu Glu Gly Val Asp Ser Gly Pro Arg Val Pro
        5                  10                  15

ggg gcc agc ccc ggc ttc cta tat tcc gag ggc cag cgg ctg gca ctg      630
Gly Ala Ser Pro Gly Phe Leu Tyr Ser Glu Gly Gln Arg Leu Ala Leu
 20                  25                  30                  35

gag gct ctg ttg agc aag ggc gcg gag gcg ttc cag acc tgc gtg cag      678
Glu Ala Leu Leu Ser Lys Gly Ala Glu Ala Phe Gln Thr Cys Val Gln
                 40                  45                  50

cgc gag gag ctg tgg ccc ttc ctc agt gcg gat gag gtt cag ggc ttg      726
Arg Glu Glu Leu Trp Pro Phe Leu Ser Ala Asp Glu Val Gln Gly Leu
             55                  60                  65

gca gcg gca gct gaa gac tgg aca gtg gcc aag cag gag ccc agc ggg      774
Ala Ala Ala Ala Glu Asp Trp Thr Val Ala Lys Gln Glu Pro Ser Gly
         70                  75                  80

atg gca gag gga gcc acc acc gcc gat gtg gac gcg ggc agc ctg agc      822
Met Ala Glu Gly Ala Thr Thr Ala Asp Val Asp Ala Gly Ser Leu Ser
     85                  90                  95

tac tgg cct ggg cag tcg gag cag ccg gcg ccc gtc ctg cgg ctg ggc      870
Tyr Trp Pro Gly Gln Ser Glu Gln Pro Ala Pro Val Leu Arg Leu Gly
100                 105                 110                 115

tgg cca gtg gac tct gcg tgg aaa ggc atc acc cgg gcg cag ctg tac      918
Trp Pro Val Asp Ser Ala Trp Lys Gly Ile Thr Arg Ala Gln Leu Tyr
                120                 125                 130

acc cag cct cct gga gag ggt cag ccg ccc ctc aag gag ctg gtg cgg      966
Thr Gln Pro Pro Gly Glu Gly Gln Pro Pro Leu Lys Glu Leu Val Arg
            135                 140                 145

ctg gag atc cag gct gcc cac aag ctg gtg gcc gtg gtc atg gac gtc     1014
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Leu Glu Ile Gln Ala Ala His Lys Leu Val Ala Val Val Met Asp Val
        150                 155                 160

ttc act gac cca gac ctg ctt ttg gac ttg gtg gat gct gcc acg cgc      1062
Phe Thr Asp Pro Asp Leu Leu Leu Asp Leu Val Asp Ala Ala Thr Arg
    165                 170                 175

cgc tgg gta cct gtc tac ctg ctc ctg gac cgc cag cag ctg cct gcc      1110
Arg Trp Val Pro Val Tyr Leu Leu Leu Asp Arg Gln Gln Leu Pro Ala
180                 185                 190                 195

ttc ctg gaa ctg gcc cag cag ctg ggg gtg aac ccc tgg aac acg gag      1158
Phe Leu Glu Leu Ala Gln Gln Leu Gly Val Asn Pro Trp Asn Thr Glu
                200                 205                 210

aac gtg gat gtc cgt gtc gtg cgg ggc tgc agc ttc cag agc cgc tgg      1206
Asn Val Asp Val Arg Val Val Arg Gly Cys Ser Phe Gln Ser Arg Trp
            215                 220                 225

cga cgg cag gtg agc ggc acc gtg cgg gag aag ttt gtg ctg ctg gac      1254
Arg Arg Gln Val Ser Gly Thr Val Arg Glu Lys Phe Val Leu Leu Asp
        230                 235                 240

ggc gag agg gtc atc tca gga tcc tac agc ttc acg tgg agt gac gca      1302
Gly Glu Arg Val Ile Ser Gly Ser Tyr Ser Phe Thr Trp Ser Asp Ala
    245                 250                 255

cgc ctg cac cga ggc ctg gtg acc ctg ctg act ggt gaa att gtt gac      1350
Arg Leu His Arg Gly Leu Val Thr Leu Leu Thr Gly Glu Ile Val Asp
260                 265                 270                 275

gcc ttc agc ctt gag ttc cgg acg ctg tac gcg gcc tcc tgc ccg ctc      1398
Ala Phe Ser Leu Glu Phe Arg Thr Leu Tyr Ala Ala Ser Cys Pro Leu
                280                 285                 290

cca cct gcg ccc ccc cag aaa ccc tcg gtc ata ggt ggc ctg cag cgg      1446
Pro Pro Ala Pro Pro Gln Lys Pro Ser Val Ile Gly Gly Leu Gln Arg
            295                 300                 305

ggc cgc agc ctg cac cgc gtg tcc cgc cgc cgc tcc gtg gcc ccc gcg      1494
Gly Arg Ser Leu His Arg Val Ser Arg Arg Arg Ser Val Ala Pro Ala
        310                 315                 320

tcg cct ccg ccg cct gac ggc ccg ctg gcc cac cgc ctg gcc gcc tgc      1542
Ser Pro Pro Pro Pro Asp Gly Pro Leu Ala His Arg Leu Ala Ala Cys
    325                 330                 335

cgc gtc tcc cct gct acc ccg ggg ccg gca ctc agt gac att cta agg      1590
Arg Val Ser Pro Ala Thr Pro Gly Pro Ala Leu Ser Asp Ile Leu Arg
340                 345                 350                 355

agt gtg cag cgc gcc cgg acc ccc agc ggc ccc ccg gcc cgg ccc agc      1638
Ser Val Gln Arg Ala Arg Thr Pro Ser Gly Pro Pro Ala Arg Pro Ser
                360                 365                 370

cgc tcc atg tgg gac cta agc cgc ctg tcc cag ctg tct ggc tcc agt      1686
Arg Ser Met Trp Asp Leu Ser Arg Leu Ser Gln Leu Ser Gly Ser Ser
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              375                 380                 385

gat ggg gac aac gag ctc aag aaa tcc tgg ggc tcc aag gac act cca      1734
Asp Gly Asp Asn Glu Leu Lys Lys Ser Trp Gly Ser Lys Asp Thr Pro
        390                 395                 400

gcc aag gct ctg atg agg cag cgg ggc act gga gga ggc ccc tgg ggg      1782
Ala Lys Ala Leu Met Arg Gln Arg Gly Thr Gly Gly Gly Pro Trp Gly
    405                 410                 415

gaa gtg gac tcc cga cct ccg tgg ggc ggt gcc ctg ccc ctg ccc ccc      1830
Glu Val Asp Ser Arg Pro Pro Trp Gly Gly Ala Leu Pro Leu Pro Pro
420                 425                 430                 435

gcc cac cgc ctc cgc tat ctg tcc cca gcc cga agg cgg ttc ggt ggg      1878
Ala His Arg Leu Arg Tyr Leu Ser Pro Ala Arg Arg Arg Phe Gly Gly
                440                 445                 450

gat gct aca ttc aaa ctt caa gag ccc aga ggc gtc agg ccg tca gac      1926
Asp Ala Thr Phe Lys Leu Gln Glu Pro Arg Gly Val Arg Pro Ser Asp
            455                 460                 465

tgg gcc ccc cgg gca gga ctt ggg ggg caa ccc tga acag gagcccaagc      1976
Trp Ala Pro Arg Ala Gly Leu Gly Gly Gln Pro  *
        470                 475

caaatctgct ggcccaccca aggagcagtg ccggacaact gtcggctcag agccctctgc    2036

ctcaatgccc tgccttggac aaggcttctg gcctcggcgt ctgtcaagca gaagggatgt    2096

ttgtcacttg ttctgcaact tgggccggga gtggtggctc atgcctgtaa tccctgcact    2156

ttgggaggct aaggtgggag ggttgcttaa ggccaggagt tggagaccag cctgggcaac    2216

atagtgagac cccatctcta caattaaaaa aacaaattag ttgggtgtgg tggcgcacgc    2276

ctgtggtccc agctacgcag gaggctgagg tgggaggatc cctcgagctc aggaggtgga    2336

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cctgggaagc tgccagtgag atttcagaga ccaagagcgc gaaggggcgg gcgatgtggc    180

aatccgtctg ggatgtgaaa agcgtggagc gcatttagag gcattcgacg aaaacacagg    240

aaatcactcc tctcccgctc ctgggcgccg ctgccactgg ggcagaggac tgggaaccgc    300

ggcagcggga taagtggccc agccagagag cgcagctccc gcgcccggtc ctgccctgcg    360

aaccagcgcg gccccctggc gctgaggctg ctccggcc    atg gcc cct cgg ccc     413
                                             Met Ala Pro Arg Pro
                                               1               5

cgc gcc cgc cca ggg gtc gct gtc gcc tgc tgc tgg ctc ctc act gtt      461
Arg Ala Arg Pro Gly Val Ala Val Ala Cys Cys Trp Leu Leu Thr Val
                 10                  15                  20

gtt cta cgc tgc tgc gta tca ttc aat gtt gat gtg aaa aat tca atg      509
Val Leu Arg Cys Cys Val Ser Phe Asn Val Asp Val Lys Asn Ser Met
             25                  30                  35

act ttc agc ggc ccg gtg gaa gac atg ttt gga tat act gtt caa caa      557
Thr Phe Ser Gly Pro Val Glu Asp Met Phe Gly Tyr Thr Val Gln Gln
         40                  45                  50

tat gaa aat gaa gaa gga aaa tgg gtg ctt att ggt tct ccg tta gtt      605
Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile Gly Ser Pro Leu Val
     55                  60                  65

ggc caa ccc aaa aac aga act gga gat gtc tat aag tgt cca gtt ggg      653
Gly Gln Pro Lys Asn Arg Thr Gly Asp Val Tyr Lys Cys Pro Val Gly
 70                  75                  80                  85

aga ggt gaa tca tta cct tgc gta aag ttg gat cta cca gtt aat aca      701
Arg Gly Glu Ser Leu Pro Cys Val Lys Leu Asp Leu Pro Val Asn Thr
                 90                  95                 100

tca att ccc aat gtc aca gaa gta aag gag aac atg aca ttt gga tca      749
Ser Ile Pro Asn Val Thr Glu Val Lys Glu Asn Met Thr Phe Gly Ser
            105                 110                 115

act tta gtc acc aac cca aat gga gga ttt ctg gct tgt ggg ccc tta      797
Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu Ala Cys Gly Pro Leu
        120                 125                 130

tat gcc tat aga tgt gga cat ttg cat tac aca act gga atc tgt tct      845
Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr Thr Gly Ile Cys Ser
    135                 140                 145

gac gtc agc ccc aca ttt caa gtc gtg aat tcc att gcc cct gta caa      893
Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser Ile Ala Pro Val Gln
150                 155                 160                 165

gaa tgc agc act caa ctg gac ata gtc ata gtg ctg gat ggt tcc aac      941
Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val Leu Asp Gly Ser Asn
                170                 175                 180
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agt att tac cca tgg gac agt gtt aca gct ttt tta aat gac ctc ttg       989
Ser Ile Tyr Pro Trp Asp Ser Val Thr Ala Phe Leu Asn Asp Leu Leu
            185                 190                 195

aaa aga atg gat att ggt cct aaa cag aca cag gtt gga att gta cag      1037
Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln Val Gly Ile Val Gln
        200                 205                 210

tat gga gaa aac gtg acc cat gag ttc aac ctc aat aag tat tct tcc      1085
Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu Asn Lys Tyr Ser Ser
    215                 220                 225

acc gaa gag gta ctt gtt gca gca aag aaa ata gtc cag aga ggt ggc      1133
Thr Glu Glu Val Leu Val Ala Ala Lys Lys Ile Val Gln Arg Gly Gly
230                 235                 240                 245

cgc cag act atg aca gct ctt gga aca gac aca gca aga aag gag gca      1181
Arg Gln Thr Met Thr Ala Leu Gly Thr Asp Thr Ala Arg Lys Glu Ala
                250                 255                 260

ttc acg gaa gcc cgg ggt gcc cga aga gga gtt aaa aaa gtc atg gtt      1229
Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val Lys Lys Val Met Val
            265                 270                 275

att gtg aca gat gga gag tct cat gac aat cat cga ctg aag aag gtc      1277
Ile Val Thr Asp Gly Glu Ser His Asp Asn His Arg Leu Lys Lys Val
        280                 285                 290

atc caa gac tgt gaa gat gaa aac att caa cgg ttt tcc ata gct att      1325
Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg Phe Ser Ile Ala Ile
    295                 300                 305

ctt ggc agc tat aac cga gga aat tta agc act gaa aaa ttt gtg gag      1373
Leu Gly Ser Tyr Asn Arg Gly Asn Leu Ser Thr Glu Lys Phe Val Glu
310                 315                 320                 325

gaa ata aaa tca att gca agt gaa ccc act gaa aag cat ttc ttc aat      1421
Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu Lys His Phe Phe Asn
                330                 335                 340

gtc tct gat gaa ttg gct cta gtc acc att gtt aaa act ctg gga gaa      1469
Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val Lys Thr Leu Gly Glu
            345                 350                 355

aga ata ttt gcc ctg gaa gcc aca gct gac cag tca gca gct tca ttt      1517
Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln Ser Ala Ala Ser Phe
        360                 365                 370

gaa atg gaa atg tct cag act ggc ttc agt gct cat tat tca cag gac      1565
Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala His Tyr Ser Gln Asp
    375                 380                 385

tgg gtc atg ctt gga gca gta gga gcc tat gat tgg aat gga aca gtt      1613
Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp Trp Asn Gly Thr Val
390                 395                 400                 405
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gtc atg cag aag gct agt caa atc ata atc cct cga aac aca acc ttt      1661
Val Met Gln Lys Ala Ser Gln Ile Ile Ile Pro Arg Asn Thr Thr Phe
                410                 415                 420

aat gtt gag tct acc aaa aag aat gaa ccg ctt gct tct tat tta ggt      1709
Asn Val Glu Ser Thr Lys Lys Asn Glu Pro Leu Ala Ser Tyr Leu Gly
            425                 430                 435

tac act gta aac tct gct act gct tct tct gga gat gtg ctc tat att      1757
Tyr Thr Val Asn Ser Ala Thr Ala Ser Ser Gly Asp Val Leu Tyr Ile
        440                 445                 450

gct gga cag cct cgg tac aat cat aca ggc cag gtc att atc tac agg      1805
Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val Ile Ile Tyr Arg
    455                 460                 465

atg gaa gat gga aac atc aaa att ctc cag acg ctc agt gga gaa cag      1853
Met Glu Asp Gly Asn Ile Lys Ile Leu Gln Thr Leu Ser Gly Glu Gln
470                 475                 480                 485

att ggt tcc tac ttt ggc agt att tta aca aca act gac att gac aag      1901
Ile Gly Ser Tyr Phe Gly Ser Ile Leu Thr Thr Thr Asp Ile Asp Lys
                490                 495                 500

gat tct aat act gac att ctt cta gtc gga gcc cct atg tac atg gga      1949
Asp Ser Asn Thr Asp Ile Leu Leu Val Gly Ala Pro Met Tyr Met Gly
            505                 510                 515

aca gag aag gag gag caa gga aaa gtg tat gtg tat gct ctc aat cag      1997
Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr Ala Leu Asn Gln
        520                 525                 530

aca agg ttt gaa tat caa atg agc ctg gaa cct att aag cag acg tgc      2045
Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile Lys Gln Thr Cys
    535                 540                 545

tgt tca tct cgg cag cac aat tca tgc aca aca gaa aac aaa aat gag      2093
Cys Ser Ser Arg Gln His Asn Ser Cys Thr Thr Glu Asn Lys Asn Glu
550                 555                 560                 565

cca tgc ggg gct cgt ttt gga act gca att gct gct gta aaa gac ctc      2141
Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala Val Lys Asp Leu
                570                 575                 580

aat ctt gat gga ttt aat gac atc gtg ata gga gct ccg ctg gaa gat      2189
Asn Leu Asp Gly Phe Asn Asp Ile Val Ile Gly Ala Pro Leu Glu Asp
            585                 590                 595

gat cac ggg gga gct gtg tac att tat cat gga agt ggc aag act ata      2237
Asp His Gly Gly Ala Val Tyr Ile Tyr His Gly Ser Gly Lys Thr Ile
        600                 605                 610

agg aaa gag tat gca caa cgt att cca tca ggt ggg gat ggt aag aca      2285
Arg Lys Glu Tyr Ala Gln Arg Ile Pro Ser Gly Gly Asp Gly Lys Thr
    615                 620                 625

ctg aaa ttt ttt ggc cag tct atc cac gga gaa atg gat tta aat ggt      2333
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Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met Asp Leu Asn Gly
630                 635                 640                 645

gac ggt ctg aca gat gtg act att ggg ggc ctt ggt ggt gct gcc ctc       2381
Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly Gly Ala Ala Leu
                650                 655                 660

ttc tgg tcc cga gat gtg gcc gta gtt aaa gtg acc atg aat ttt gag       2429
Phe Trp Ser Arg Asp Val Ala Val Val Lys Val Thr Met Asn Phe Glu
            665                 670                 675

cca aat aaa gtg aat att caa aag aaa aac tgc cat atg gag gga aag       2477
Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys His Met Glu Gly Lys
        680                 685                 690

gaa aca gta tgc ata aat gct aca gtg tgt ttt gag gtt aaa tta aag       2525
Glu Thr Val Cys Ile Asn Ala Thr Val Cys Phe Glu Val Lys Leu Lys
    695                 700                 705

tct aaa gaa gac acg att tat gaa gct gat ttg cag tac cgt gtc acc       2573
Ser Lys Glu Asp Thr Ile Tyr Glu Ala Asp Leu Gln Tyr Arg Val Thr
710                 715                 720                 725

cta gat tca cta aga caa ata tca cga agt ttt ttc tct gga act caa       2621
Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe Ser Gly Thr Gln
                730                 735                 740

gag aga aag gtt caa agg aac atc aca gtt cga aaa tca gaa tgc act       2669
Glu Arg Lys Val Gln Arg Asn Ile Thr Val Arg Lys Ser Glu Cys Thr
            745                 750                 755

aag cac tcc ttc tac atg ttg gac aag cat gac ttt cag gac tct gtg       2717
Lys His Ser Phe Tyr Met Leu Asp Lys His Asp Phe Gln Asp Ser Val
        760                 765                 770

aga ata acg ttg gac ttt aat ctt acc gat cca gaa aat ggg cct gtt       2765
Arg Ile Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu Asn Gly Pro Val
    775                 780                 785

ctt gat gat tct cta cca aac tca gta cat gaa tat att ccc ttt gcc       2813
Leu Asp Asp Ser Leu Pro Asn Ser Val His Glu Tyr Ile Pro Phe Ala
790                 795                 800                 805

aaa gat tgt gga aat aag gaa aaa tgt atc tca gac ctc agc ctg cat       2861
Lys Asp Cys Gly Asn Lys Glu Lys Cys Ile Ser Asp Leu Ser Leu His
                810                 815                 820

gtc gcc acc act gaa aag gac ctg ctg att gtc cga tcc cag aat gat       2909
Val Ala Thr Thr Glu Lys Asp Leu Leu Ile Val Arg Ser Gln Asn Asp
            825                 830                 835

aag ttc aac gtt agc ctc aca gtc aaa aat aca aag gac agt gcc tat       2957
Lys Phe Asn Val Ser Leu Thr Val Lys Asn Thr Lys Asp Ser Ala Tyr
        840                 845                 850

aac acc agg aca ata gtg cat tat tct cca aat cta gtt ttt tca gga       3005
Asn Thr Arg Thr Ile Val His Tyr Ser Pro Asn Leu Val Phe Ser Gly
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    855                 860                 865

att gag gct atc caa aaa gac agt tgt gaa tct aat cat aat atc aca      3053
Ile Glu Ala Ile Gln Lys Asp Ser Cys Glu Ser Asn His Asn Ile Thr
870                 875                 880                 885

tgt aaa gtt gga tat ccc ttc ctg aga aga gga gag atg gta act ttc      3101
Cys Lys Val Gly Tyr Pro Phe Leu Arg Arg Gly Glu Met Val Thr Phe
                890                 895                 900

aaa ata ttg ttt cag ttt aac aca tcc tat ctc atg gaa aat gtg acc      3149
Lys Ile Leu Phe Gln Phe Asn Thr Ser Tyr Leu Met Glu Asn Val Thr
            905                 910                 915

att tat tta agt gca aca agt gac agc gaa gaa cct cct gaa acc ctt      3197
Ile Tyr Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro Pro Glu Thr Leu
        920                 925                 930

tct gat aat gta gta aac att tct atc ccg gta aaa tat gaa gtt gga      3245
Ser Asp Asn Val Val Asn Ile Ser Ile Pro Val Lys Tyr Glu Val Gly
    935                 940                 945

cta cag ttt tac agc tct gca agt gaa tac cac att tca att gct gcc      3293
Leu Gln Phe Tyr Ser Ser Ala Ser Glu Tyr His Ile Ser Ile Ala Ala
950                 955                 960                 965

aat gag aca gtc cct gaa gtt att aat tct act gag gac att gga aat      3341
Asn Glu Thr Val Pro Glu Val Ile Asn Ser Thr Glu Asp Ile Gly Asn
                970                 975                 980

gaa att aat atc ttc tac ttg att aga aaa agt gga tct ttt cca atg      3389
Glu Ile Asn Ile Phe Tyr Leu Ile Arg Lys Ser Gly Ser Phe Pro Met
            985                 990                 995

cca gag ctt aag ctg tca att tca ttc ccc aat atg aca tca aat ggt      3437
Pro Glu Leu Lys Leu Ser Ile Ser Phe Pro Asn Met Thr Ser Asn Gly
       1000                1005                1010

tac cct gtg ctg tac cca act gga ttg tca tct tct gag aat gca aac      3485
Tyr Pro Val Leu Tyr Pro Thr Gly Leu Ser Ser Ser Glu Asn Ala Asn
   1015                1020                1025

tgc aga ccc cat atc ttt gag gat cct ttc agt atc aac tct gga aag      3533
Cys Arg Pro His Ile Phe Glu Asp Pro Phe Ser Ile Asn Ser Gly Lys
1030                1035                1040                1045

aaa atg act aca tca act gac cat ctc aaa cga ggc aca att ctg gac      3581
Lys Met Thr Thr Ser Thr Asp His Leu Lys Arg Gly Thr Ile Leu Asp
               1050                1055                1060

tgc aat aca tgt aaa ttt gct acc atc aca tgt aat ctc act tct tct      3629
Cys Asn Thr Cys Lys Phe Ala Thr Ile Thr Cys Asn Leu Thr Ser Ser
           1065                1070                1075

gac atc agc caa gtc aat gtt tcg ctt atc ttg tgg aaa cca act ttt      3677
Asp Ile Ser Gln Val Asn Val Ser Leu Ile Leu Trp Lys Pro Thr Phe
       1080                1085                1090
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 ata aaa tca tat ttt tcc agc tta aat ctt act ata agg gga gaa ctt     3725
 Ile Lys Ser Tyr Phe Ser Ser Leu Asn Leu Thr Ile Arg Gly Glu Leu
    1095                1100                1105

 cgg agt gaa aat gca tct ctg gtt tta agt agc agc aat caa aaa aga     3773
 Arg Ser Glu Asn Ala Ser Leu Val Leu Ser Ser Ser Asn Gln Lys Arg
1110                1115                1120                1125

 gag ctt gct att caa ata tcc aaa gat ggg cta ccg ggc aga gtg cca     3821
 Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly Leu Pro Gly Arg Val Pro
                1130                1135                1140

 tta tgg gtc atc ctg ctg agt gct ttt gcc gga ttg ttg ctg tta atg     3869
 Leu Trp Val Ile Leu Leu Ser Ala Phe Ala Gly Leu Leu Leu Leu Met
            1145                1150                1155

 ctg ctc att tta gca ctg tgg aag att gga ttc ttc aaa aga cca ctg     3917
 Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly Phe Phe Lys Arg Pro Leu
        1160                1165                1170

 aaa aag aaa atg gag aaa tga aa tattttatga aagaaaataa taacaattat     3970
 Lys Lys Lys Met Glu Lys  *
    1175                1180

 tcaataatct atcctcaggt ttgcctcaaa tatgtgacaa gaaatgtata attcatgaca   4030

 tagtcatgta actatgtaat ccatcaggga ttcattactt ggaaaatgac aggtcatgca   4090

 ttatccaaaa acaataccaa aaagacatat tttataaaat gacaaaaaat attttacata   4150

 attactcatt tttgttgagt aagcaaaatt acaaagtgtt tttaaaaaaa cctgtacaaa   4210

 tatgtttatg tattaaatca ccatccaaaa tatttaagga atatataaaa agatttttat   4270

 gatcatagaa acatctattt tcaaaacaat ataaattaag cttttcccct tgattcctgt   4330

 tggatatcca tgttcagcat gacagtcagc actcgtaaat gccaagaaaa gaattacctg   4390

 aaaaagatca tttctcccta ttcaaatgag aatattttcc ctcggtagaa tccatataca   4450

 atatggattg aaaattaagt cacgaagaat acatttagca tctttgtgtt gggttctata   4510

 cctaaaaatt ttccctcccg gcccaag                                       4537
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<210> 250
<211> 1203
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (608)..(832)

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     <400> 250
gagatcctca aggtagcggc agctcggggc ttgtgttcag tttcctcttc ccagacgccc      60

ccagccccgt ttccctgaac gactgttggg tgtcccgacg gctcctgtgg ctggcagaaa     120

gagaaagagg ataacactga ccaggtttgg gtctggtcag agcccccgcc tcttcagggc     180

aggtgctgag ttgtggaaat ttgaggagcc tattttcgtg tttagttttc aaactaagac     240

tgctgcttct gcttctctga cgggcttcag ctgggaacag attaactagg ttgctaaagg     300

aacaaatatt tcttccgtgc actgaagaca ggcaggaaga caacagataa cgtacctgca     360

gtggagaggt taagctcctg tacggaagcg taattcataa atagataaat ataggaaagg     420

acaacaaaga aaatagggat agaataacgg gcagagaatt tagagatgat gtcaggtgat     480

tagttttctc atctaaaagc ttgaaaatcc tgcatgtttg tggagtggtc aagcaggtgg     540

tgaagagggc aaactctttg attctacaat agctgatgag ggaacatgga ctttggagga     600

cagaaaa  atg gtt cgt att gtt ctt aca aag aca aag aga gat gca gca      649
         Met Val Arg Ile Val Leu Thr Lys Thr Lys Arg Asp Ala Ala
           1               5                  10

aat tgt tgg act tct cta cta gaa tct gaa tat gca gcg gat cct tgg       697
Asn Cys Trp Thr Ser Leu Leu Glu Ser Glu Tyr Ala Ala Asp Pro Trp
 15                  20                  25                  30

gtg caa gac caa atg cag aga aag ctt aca tta gag aga ttc caa aaa       745
Val Gln Asp Gln Met Gln Arg Lys Leu Thr Leu Glu Arg Phe Gln Lys
                 35                  40                  45

gaa aat cct ggt ttt gac ttc agt gga gca gaa atc tca gga aac tac       793
Glu Asn Pro Gly Phe Asp Phe Ser Gly Ala Glu Ile Ser Gly Asn Tyr
             50                  55                  60

act aaa ggt gga cca gat ttc tca aac ctt gag aaa taa ctgctttttt        842
Thr Lys Gly Gly Pro Asp Phe Ser Asn Leu Glu Lys  *
         65                  70                  75

tcctgcattc tgtggatcct agcagatatt gccaacttaa tcagataaac agattatgta     902

atggaagaaa aatgcggatg cctacagtta acagattgca aaatgtatct taaaatggtt     962

ctaaaaattg cattcaaaca taatttacat aggaaatgta ctgtgggaac tattctatgg    1022

atatatgggt aagttgtttt ggacttgttt ttgctcagca tgaagtttta tatgctgcat    1082

tttactaatt ccatatttaa ccatatgttt aatacaaaag aacattagag tatagatcat    1142

gtgaaatgaa gggtgccttc ggggaaaatt aactttttct tttgatagta tgatattcac    1202

t                                                                    1203
```

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<210> 251
<211> 935
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (36)..(362)

<400> 251
atttggccct cgaggccaag aattcggcac gaggc atg acc cca tcg agg ctt      53
                                      Met Thr Pro Ser Arg Leu
                                       1               5

ccc tgg ttg ctt agc tgg gtc tcg gcc acg gcg tgg aga gcg gca aga     101
Pro Trp Leu Leu Ser Trp Val Ser Ala Thr Ala Trp Arg Ala Ala Arg
            10                  15                  20

tca ccc ctt ctg tgt cat tct ctg agg aaa aca agt tct tct caa gga     149
Ser Pro Leu Leu Cys His Ser Leu Arg Lys Thr Ser Ser Ser Gln Gly
        25                  30                  35

gga aag tct gaa ctt gtc aaa cag tcc ctt aag aag ccg aag tta cca     197
Gly Lys Ser Glu Leu Val Lys Gln Ser Leu Lys Lys Pro Lys Leu Pro
    40                  45                  50

gaa ggt cgt ttt gat gca cca gag gat tcc cat tta gag aaa gaa cca     245
Glu Gly Arg Phe Asp Ala Pro Glu Asp Ser His Leu Glu Lys Glu Pro
55                  60                  65                  70

ctg gaa aaa ttt cca gat gat gtt aat cca gtg acc aaa gaa aaa ggt     293
Leu Glu Lys Phe Pro Asp Asp Val Asn Pro Val Thr Lys Glu Lys Gly
                75                  80                  85

gga ccc agg ggc cca gaa cct acc cga tat gga gat tgg gaa cga aaa     341
Gly Pro Arg Gly Pro Glu Pro Thr Arg Tyr Gly Asp Trp Glu Arg Lys
            90                  95                  100

gga cgc tgt att gat ttt taa gt cgcatattct ttaacttcaa tattgttttc     394
Gly Arg Cys Ile Asp Phe  *
        105

tgaatatgta catctgaatt aacttatttc tgattatttt ctttctttat atcctttatg   454

tcgtgtagtt tgtataatgt gtttaaatat atatatatat atatatatat atatatatat   514

atgatggctt tggaagaaaa tatgctgctg taaattagga aagggagacc agcctgacca   574

atatggagaa atctcgcctt tgctagagat acaaaattag ccaggcgtgg tggcatgcac   634

ctgtaatcag cctcctgagt agctgggatt acagacaccc accattgcgc ctggctaatt   694

tttgtatttt tagtaaagac aaggtttcac catgttagcc aggctggtct cgaactcctg   754

acctcagttg atccacctgc ctcagcctcc caaagtgctg ggattgcagg tgtgagccac   814
```

```
cacgcccagc ctagaaatga ttcttagagc tgtaggcctt tacttcatca tttttcagtt    874

taaattaatc agttgcttat aaaatgcata cataaataaa ataattttta aaaaaaaaaa    934

a                                                                     935




     <210> 252
     <211> 1219
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (41)..(532)

     <400> 252
ggcgcaggag ggggcggggg cgcggctcgt cccccagcgg  atg agc tgc cgc gga      55
                                             Met Ser Cys Arg Gly
                                              1               5

cgg ggc gcg ggc gga cga tgg aac tcc aca tcc tgg agc acc ggc tgc      103
Arg Gly Ala Gly Gly Arg Trp Asn Ser Thr Ser Trp Ser Thr Gly Cys
                 10                  15                  20

aag ttg cca gcg tcg cca agg aga gta tcc cgc tgt tca cct acg ggc      151
Lys Leu Pro Ala Ser Pro Arg Arg Val Ser Arg Cys Ser Pro Thr Gly
             25                  30                  35

ctg atc aaa ctt gcc ttc ctg ttc tcc aag acc agg tgc aag ttc ttc      199
Leu Ile Lys Leu Ala Phe Leu Phe Ser Lys Thr Arg Cys Lys Phe Phe
         40                  45                  50

agt ctg act gag aca cca gag gat tac act atc att gtc gat gag gaa      247
Ser Leu Thr Glu Thr Pro Glu Asp Tyr Thr Ile Ile Val Asp Glu Glu
     55                  60                  65

gga ttc cta gag ctg ccc tcc tca gag cac ctg agt gtg gcg gat gcc      295
Gly Phe Leu Glu Leu Pro Ser Ser Glu His Leu Ser Val Ala Asp Ala
 70                  75                  80                  85

acc tgg ctg gcc ctg aac gtg gtg tcc ggc ggt ggc agc ttc tcc agc      343
Thr Trp Leu Ala Leu Asn Val Val Ser Gly Gly Gly Ser Phe Ser Ser
                 90                  95                 100

tcc cag cct att ggc atg acc aag atc gcc aag tca gtc atc gcc cca      391
Ser Gln Pro Ile Gly Met Thr Lys Ile Ala Lys Ser Val Ile Ala Pro
            105                 110                 115

ctg gct gac cag aac ata tcc gtg ttc atg ctg tcc acg tat cag aca      439
Leu Ala Asp Gln Asn Ile Ser Val Phe Met Leu Ser Thr Tyr Gln Thr
        120                 125                 130

gac ttc atc ctg gtg ctc aag cgg gac ctg ccc ttt gtc acc cac acg      487
Asp Phe Ile Leu Val Leu Lys Arg Asp Leu Pro Phe Val Thr His Thr
```

```
    135                 140                 145

ttg tca tca gag ttc acc atc ctg tgg tca gtg gct aga ctg tag cag      535
Leu Ser Ser Glu Phe Thr Ile Leu Trp Ser Val Ala Arg Leu  *
150                 155                 160

ccgagaacct cggcatcacc agtggcttcg tgaagcccaa gctggtccag atgccggtca    595

tccacccact gtccagcccg agcaacaggt tctgtgtcac cagcctggac cccgacacgc    655

tgcctgctgt tgccacactc ctcatggatg tcatgtccta cttcaatggg tgaggataca    715

actagaagcc agcagtctac aggctggaag aaggccctca ccagaaccca acccttggac    775

ttcagcctcc agaactgtga gaaatacata cctgctgttt gtcagacacc agtctatgga    835

attctgttac agtagcctga actcagacat agcccttttc catttataag gtggttttac    895

cttatatttt atgtaaaagg tccattttat ttatttttga attgttgatt ttttttaag     955

agacacgtgt ttactatgtt acccaggctg gactccaact cctggactat tgatcctcct   1015

gtctccacct cccgagttgc tggaactaca ggctaacagc tctgttttaa agatgagaaa   1075

atgggcccga cgcagtggct cacacctgta atcccagcac ttagggtagc tgagccaggt   1135

ggagccactt gaggtcaggt gttcgagatt agcctggcca acatggcaaa accccgtctc   1195

tactaaaaat acaaaaaaaa aaaa                                          1219



      <210> 253
      <211> 421
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (211)..(363)

      <400> 253
cccacgcgtc cgcccacgcg tccgacagca cccctggcct ggtctgattc cactgaaaga     60

tggggccatg atggtagctg attgctaaat ttacataact cagttcatcg tcacaggagc    120

cctaagaggt tgatacgacc atgagtccat tttcactgag gaaaaccgaa gaaaagaaat    180

tgtaaatggc cagagatgta tggctggtga     atg gcc ctg tgt gga ggc agg    231
                                     Met Ala Leu Cys Gly Gly Arg
                                      1               5

gcc aag gtg aat gct cct gct atg cag atg atg cag ccc aga gag ccg      279
Ala Lys Val Asn Ala Pro Ala Met Gln Met Met Gln Pro Arg Glu Pro
        10                  15                  20
```

```
cag cca cct ctg cga gtc cca cag ctg gaa gga gca ccc agt cct ccc      327
Gln Pro Pro Leu Arg Val Pro Gln Leu Glu Gly Ala Pro Ser Pro Pro
     25                  30                  35

aca cta gcc gga cag gcc cgc agc ctg cac tac tga gctg tcacggagga      377
Thr Leu Ala Gly Gln Ala Arg Ser Leu His Tyr  *
 40                  45                  50

ctctaccaag ccccagtgcg gagccacaag tggaggacat cctg                     421
```

```
     <210> 254
     <211> 636
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (250)..(516)

     <400> 254
gtcttttgag agctctaggt cccacccagc tctcagattt tataatacta tggtcatctt     60

ccctgcaggt tgggggacag ggaaggggga ataaggcctc gggagaagga agatgagcta    120

ggaggcctgg tgcactacac agctcctttg tgcctccagg ccacctgccc aagctggtgt    180

gcctcccttc taaggtcctg tcccactggg cacaggaggc agatccagca gcgtggaatc    240

ccagataac    atg tcc cac aga ctc tgg caa cgt cac aga tca cat gga      288
             Met Ser His Arg Leu Trp Gln Arg His Arg Ser His Gly
               1               5                  10

gag gca agt gca ggc caa cga cat ccg cat ccg ggt cct aca gga gga      336
Glu Ala Ser Ala Gly Gln Arg His Pro His Pro Gly Pro Thr Gly Gly
     15                  20                  25

gaa cgg gcg gct cca atc aat gct gtc caa aat ccg gga agt ggc cca      384
Glu Arg Ala Ala Pro Ile Asn Ala Val Gln Asn Pro Gly Ser Gly Pro
 30                  35                  40                  45

gca ggg tgg cct caa ggt ggg cct gag agg gcg ggc cct tgg gga cca      432
Ala Gly Trp Pro Gln Gly Gly Pro Glu Arg Ala Gly Pro Trp Gly Pro
                 50                  55                  60

gga gga agc ccc tat cca gca gca ggt ctt cag act ctg ccc cgg gaa      480
Gly Gly Ser Pro Tyr Pro Ala Ala Gly Leu Gln Thr Leu Pro Arg Glu
             65                  70                  75

ctt gtg gag agc cca cct cat cac atg agg cct tag gctg tgcttttgtg      530
Leu Val Glu Ser Pro Pro His His Met Arg Pro  *
         80                  85

aaacattttt cacatttcca gaaggcgtga ggatgttatg gattcgatgc cttccagttc    590
```

```
cataagccct ttgtagctgt cattccttta agtgcagcaa caagcc                     636




     <210> 255
     <211> 718
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (414)..(695)

     <400> 255
ggaattcccg ggtcgacgat ttcgtagcga ggcctctttc cccctcgctc ccactcagac      60

cacccccaag cctggactgg aagtgtgttg agcccctggg tcaggctggc gagccagctc     120

ggccctgccc acccaggggt ttccgagatc acccctggtg aggcggcgtg ccagtccctt     180

gctttcttac ttgttctgca gagcggggag ctgaggctgc atgagggaag actcccgtac     240

cccagcacgg tggagggtgg gatggggtca cgcctgtgcg acccaggagg tggccagcag     300

aaggaaacag tagtgtccac catggtctgc gtctccccac cacggattgt cttggctccg     360

gatttgagac atggcagggc cagatgagga caacttgatg acagtttaca gag   atg     416
                                                              Met
                                                               1

gag gca ggg tgc cag gaa gcc acg ggg gag ccc cca ggg cac tca gca       464
Glu Ala Gly Cys Gln Glu Ala Thr Gly Glu Pro Pro Gly His Ser Ala
              5                  10                  15

gtc cag gca ggg ctg ggc gtc ctg gca agg agc agg gac ctt ctg ccc       512
Val Gln Ala Gly Leu Gly Val Leu Ala Arg Ser Arg Asp Leu Leu Pro
         20                  25                  30

agg ggt gtg gcc agc ctg tgg gtg ctg tgt gca gga ccc cag gaa cca       560
Arg Gly Val Ala Ser Leu Trp Val Leu Cys Ala Gly Pro Gln Glu Pro
     35                  40                  45

agg ccg cag tct ctt ccc tcg ctc cag cat cct ccc aag gcc acc ctt       608
Arg Pro Gln Ser Leu Pro Ser Leu Gln His Pro Pro Lys Ala Thr Leu
 50                  55                  60                  65

ggc tgc act cag cca gag agc tgg ggc aca ggg acc cca cag gtt tcc       656
Gly Cys Thr Gln Pro Glu Ser Trp Gly Thr Gly Thr Pro Gln Val Ser
                 70                  75                  80

ctg gag gct gtc agg ggc tcc ggt ggg ggc ggg ggg tga gcccgctggg        705
Leu Glu Ala Val Arg Gly Ser Gly Gly Gly Gly Gly  *
             85                  90

ttcactgcac ctc                                                        718
```

```
     <210> 256
     <211> 1767
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (251)..(1609)

     <400> 256
aactaggcta ggtagcgagg cctgggtggt ggggggctca ggcggcggcg gcctcgacgc      60

gagtgagtgt cgtggttggg gtgctggacc cagagtgcct accctcgcct gcctgggcct     120

cagtttccac atctgcacaa tgggggtgac catccctgcc ctgctggctg ccaggagcgg     180

ctgtgagtct tcaggcgtgg atgcagcctg ggggaagcca tagggcgctt tcacaggcct     240

ggccttcacc   atg gcg gga ggg aga ccg cat ctg aag agg agt ttc tcc         289
             Met Ala Gly Gly Arg Pro His Leu Lys Arg Ser Phe Ser
               1               5                  10

atc atc ccc tgc ttt gtc ttc gtg gag tcg gtg ctg ctg ggc att gtg      337
Ile Ile Pro Cys Phe Val Phe Val Glu Ser Val Leu Leu Gly Ile Val
     15                  20                  25

atc ctg ctt gct tac cgc ctg gag ttc acg gac acc ttc cct gtg cac      385
Ile Leu Leu Ala Tyr Arg Leu Glu Phe Thr Asp Thr Phe Pro Val His
 30                  35                  40                  45

acc cag gga ttc ttc tgc tat gac agt acc tac gcc aag ccc tac cca      433
Thr Gln Gly Phe Phe Cys Tyr Asp Ser Thr Tyr Ala Lys Pro Tyr Pro
                 50                  55                  60

ggg cct gag gct gcc agc cga gtg cct cct gct ctt gtc tac gca ctg      481
Gly Pro Glu Ala Ala Ser Arg Val Pro Pro Ala Leu Val Tyr Ala Leu
             65                  70                  75

gtc act gcc ggg ccc acc ctc acg atc ctg ctg gga gag ctg gcg cgt      529
Val Thr Ala Gly Pro Thr Leu Thr Ile Leu Leu Gly Glu Leu Ala Arg
         80                  85                  90

gcc ttt ttc cct gca cca cct tca gcc gtc cca gtc atc ggg gag agc      577
Ala Phe Phe Pro Ala Pro Pro Ser Ala Val Pro Val Ile Gly Glu Ser
     95                 100                 105

acc atc gtg tct ggg gcc tgc tgc cgc ttc agc ccc cca gtg cgg agg      625
Thr Ile Val Ser Gly Ala Cys Cys Arg Phe Ser Pro Pro Val Arg Arg
110                 115                 120                 125

ctg gtc cgc ttc ctg ggg gtc tac tcc ttc ggc ctc ttc acc acg acc      673
Leu Val Arg Phe Leu Gly Val Tyr Ser Phe Gly Leu Phe Thr Thr Thr
                130                 135                 140
```

```
atc ttc gcc aac gcg ggg cag gtg gtg acc ggc aat ccc acg cca cac       721
Ile Phe Ala Asn Ala Gly Gln Val Val Thr Gly Asn Pro Thr Pro His
            145                 150                 155

ttc ctg tcc gtg tgc cgc ccc aac tac acg gcc ctg ggc tgc ctg cca       769
Phe Leu Ser Val Cys Arg Pro Asn Tyr Thr Ala Leu Gly Cys Leu Pro
        160                 165                 170

cct tct ccg gat cgg cca ggt ccc gac cgc ttt gtc act gac cag ggt       817
Pro Ser Pro Asp Arg Pro Gly Pro Asp Arg Phe Val Thr Asp Gln Gly
    175                 180                 185

gcc tgc gct ggc agt ccc agc ctc gtg gcc gcc gcg cgc cgc gcc ttc       865
Ala Cys Ala Gly Ser Pro Ser Leu Val Ala Ala Ala Arg Arg Ala Phe
190                 195                 200                 205

ccc tgc aag gat gcg gcc ctc tgc gcc tac gcg gtc acc tac aca gcg       913
Pro Cys Lys Asp Ala Ala Leu Cys Ala Tyr Ala Val Thr Tyr Thr Ala
                210                 215                 220

atg tac gtg act ctc gtg ttc cgc gtg aag ggc tcc cgc ctg gtc aaa       961
Met Tyr Val Thr Leu Val Phe Arg Val Lys Gly Ser Arg Leu Val Lys
            225                 230                 235

ccc tcg ctc tgc ctg gcc ttg ctg tgc ccg gcc ttc ctg gtg ggc gtg      1009
Pro Ser Leu Cys Leu Ala Leu Leu Cys Pro Ala Phe Leu Val Gly Val
        240                 245                 250

gtc cgc gtg gcc gag tac cga aac cac tgg tcg gac gtg ctg gct ggc      1057
Val Arg Val Ala Glu Tyr Arg Asn His Trp Ser Asp Val Leu Ala Gly
    255                 260                 265

ttc ctg aca ggg gcg gcc atc gcc acc ttt ttg gtc acc tgc gtt gtg      1105
Phe Leu Thr Gly Ala Ala Ile Ala Thr Phe Leu Val Thr Cys Val Val
270                 275                 280                 285

cat aac ttt cag agc cgg cca ccc tct ggc cga agg ctc tct ccc tgg      1153
His Asn Phe Gln Ser Arg Pro Pro Ser Gly Arg Arg Leu Ser Pro Trp
                290                 295                 300

gag gac ctg ggc caa gcc ccc acc atg gat agc ccc ctc gaa aag tta      1201
Glu Asp Leu Gly Gln Ala Pro Thr Met Asp Ser Pro Leu Glu Lys Leu
            305                 310                 315

agt gtg gcg cag gaa ccc gag gtc tgc agg ccg cat tcg aca ccg gca      1249
Ser Val Ala Gln Glu Pro Glu Val Cys Arg Pro His Ser Thr Pro Ala
        320                 325                 330

cgg ctc acc cca tcc aag tcg cag aac tgc gcc cgc cgt ggc cac ctg      1297
Arg Leu Thr Pro Ser Lys Ser Gln Asn Cys Ala Arg Arg Gly His Leu
    335                 340                 345

atc ccc agc tgt gtc tcc tcc agg gcc cca gcc atg tgt tcg tcg ccc      1345
Ile Pro Ser Cys Val Ser Ser Arg Ala Pro Ala Met Cys Ser Ser Pro
350                 355                 360                 365

cgt gtg ccc cgt cct cga ttg agg tct gag ccg acg ccc ttg ccc ctg      1393
```

```
Arg Val Pro Arg Pro Arg Leu Arg Ser Glu Pro Thr Pro Leu Pro Leu
                370                 375                 380

ccc cta ccc ctg cca gcg ccc acc ccc agc cag ggc ccc tcg cct tcc      1441
Pro Leu Pro Leu Pro Ala Pro Thr Pro Ser Gln Gly Pro Ser Pro Ser
            385                 390                 395

tcc cct gga cct ggg ggg cca ggc ggg ggt ggt gga cgt ggc cgg aag      1489
Ser Pro Gly Pro Gly Gly Pro Gly Gly Gly Gly Gly Arg Gly Arg Lys
        400                 405                 410

ctg ctg ctg ccc acg ccc ctg ctg cgg gac ctg tac acc ctg agt gga      1537
Leu Leu Leu Pro Thr Pro Leu Leu Arg Asp Leu Tyr Thr Leu Ser Gly
    415                 420                 425

ctc tat ccc tcc ccc ttc cac cgg gac aac ttc agc cct tac ctg ttt      1585
Leu Tyr Pro Ser Pro Phe His Arg Asp Asn Phe Ser Pro Tyr Leu Phe
430                 435                 440                 445

gcc agc cgt gac cac ctg ctg tga ggcccgacca cccacccaga atctgcccag     1639
Ala Ser Arg Asp His Leu Leu  *
                450

tccccacttc ttccctgcca cgcgtgtgtg tgcgtgtgcc acgtgagtgc caaagtcccc   1699

agcaccccaa gccagccaga cccagattgt attgcggccg ctcagaggat caaactacgt   1759

cgcggcca                                                             1767



     <210> 257
     <211> 2367
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (379)..(1332)

     <400> 257
tcaatttaag ctccctaaag ggaatttggc cctcaggcca agatcgcccc aggcccggcc      60

caggaaaggg cccgaggggt aggttggact gcgggccagg acctaacgcg gggtcgggc     120

cgcctcaggt gcttgggagt cggggactcg aaggacgcaa gtgttgagct cgcgcccttc    180

tcgaagccgt ttgggcggac gctggggtcc ttcgggctcc gccccagggg gtggggctat    240

atgttcggac aatgaccggc cgtccttgcg gtcccgcccc ctcccсgccc ccggaagccg    300

cggcctcgct gagtgcccag ccgcccggcg cccaggcctg gggcaccgcg agtgccgaac    360

cttcggctgg acaccaag  atg cct ggc gaa cag cag gca gag gaa gag gag     411
                     Met Pro Gly Glu Gln Gln Ala Glu Glu Glu Glu
                      1               5                  10
```

```
gag gaa gag atg cag gag gag atg gtg ctg ctg gtg aag ggt gag gag      459
Glu Glu Glu Met Gln Glu Glu Met Val Leu Leu Val Lys Gly Glu Glu
             15                  20                  25

gat gag ggt gag gag aag tat gag gtg gtg aaa ctc aag atc ccc atg      507
Asp Glu Gly Glu Glu Lys Tyr Glu Val Val Lys Leu Lys Ile Pro Met
         30                  35                  40

gac aac aag gag gtc ccg ggc gag gcg ccc gcg ccg tcc gcc gac ccg      555
Asp Asn Lys Glu Val Pro Gly Glu Ala Pro Ala Pro Ser Ala Asp Pro
     45                  50                  55

gcg cgt ccc cac gcg tgc ccc gac tgc ggc cgc gcc ttc gcg cgc cgc      603
Ala Arg Pro His Ala Cys Pro Asp Cys Gly Arg Ala Phe Ala Arg Arg
 60                  65                  70                  75

tcc acg ctg gcg aag cac gcg cgc acg cac acg ggc gaa cgg ccc ttc      651
Ser Thr Leu Ala Lys His Ala Arg Thr His Thr Gly Glu Arg Pro Phe
                 80                  85                  90

ggg tgc acc gag tgc ggg cgg cgc ttc tca cag aag tcg gcg ctg acc      699
Gly Cys Thr Glu Cys Gly Arg Arg Phe Ser Gln Lys Ser Ala Leu Thr
             95                 100                 105

aaa cac ggc cgc acg cac acg ggc gag cgg ccc tac gag tgc ccc gag      747
Lys His Gly Arg Thr His Thr Gly Glu Arg Pro Tyr Glu Cys Pro Glu
        110                 115                 120

tgc gac aaa cgc ttc tcg gcc gcc tcg aac ctg cgg cag cac cgg cgg      795
Cys Asp Lys Arg Phe Ser Ala Ala Ser Asn Leu Arg Gln His Arg Arg
    125                 130                 135

cgg cac acg ggc gag aag ccg tac gca tgc gcg cac tgc ggc cgc cgc      843
Arg His Thr Gly Glu Lys Pro Tyr Ala Cys Ala His Cys Gly Arg Arg
140                 145                 150                 155

ttc gcg cag agc tcc aac tac gca cag cac ctg cgc gtg cac acg ggc      891
Phe Ala Gln Ser Ser Asn Tyr Ala Gln His Leu Arg Val His Thr Gly
                160                 165                 170

gag aag ccg tac gcg tgc ccg gac tgc gga cgc gcc ttt ggc ggc agc      939
Glu Lys Pro Tyr Ala Cys Pro Asp Cys Gly Arg Ala Phe Gly Gly Ser
            175                 180                 185

tcg tgc ctg gcg cgc cac cga cgc acg cac acg ggc gag cgg ccc tac      987
Ser Cys Leu Ala Arg His Arg Arg Thr His Thr Gly Glu Arg Pro Tyr
        190                 195                 200

gct tgc gcc gac tgc ggc acg cgc ttc gct cag agc tcg gcg ctg gcc     1035
Ala Cys Ala Asp Cys Gly Thr Arg Phe Ala Gln Ser Ser Ala Leu Ala
    205                 210                 215

aag cac cgg cgc gtg cac acg ggc gag aag ccg cac cgc tgc gct gtg     1083
Lys His Arg Arg Val His Thr Gly Glu Lys Pro His Arg Cys Ala Val
220                 225                 230                 235
```

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tgt ggc cgt cgc ttc ggc cac cgc tcc aac ctg gcg gag cac gcg cgc      1131
Cys Gly Arg Arg Phe Gly His Arg Ser Asn Leu Ala Glu His Ala Arg
                240                 245                 250

acg cac aca ggc gag cgg ccc tac ccc tgc gcc gag tgc ggc cgc cgc      1179
Thr His Thr Gly Glu Arg Pro Tyr Pro Cys Ala Glu Cys Gly Arg Arg
            255                 260                 265

ttc cgc cta agc tcg cac ttc att cgc cac cga cgc gcg cac atg cgg      1227
Phe Arg Leu Ser Ser His Phe Ile Arg His Arg Arg Ala His Met Arg
        270                 275                 280

cgc cgc ctg tat att tgc gcc ggc tgc ggc agg gac ttc aag ctg ccc      1275
Arg Arg Leu Tyr Ile Cys Ala Gly Cys Gly Arg Asp Phe Lys Leu Pro
    285                 290                 295

cct ggc gcc acg gcc gcc act gcc acc gag cgt tgc ccg gag tgt gag      1323
Pro Gly Ala Thr Ala Ala Thr Ala Thr Glu Arg Cys Pro Glu Cys Glu
300                 305                 310                 315

ggc agc tga gtcccgc agggctgcgg aggggcgcgc tggggcttcg acctggctgc      1379
Gly Ser  *


actaacccag gctcctcctc gccccggcct ccgggtctgg gaaattgagg ggacggcagg    1439

cccggctgcc ctggaactgg gagacaggga gaatcccctg ccggggtccc tggaaacagt    1499

gcccacccca catcactaca ttccctcggc ccgtgttagt gaataaagta ttatatcctc    1559

accccacccg tgcctgtgag tgaggtgggt gggagaggaa gaaagttggg gttctccagg    1619

ctcaggtgcc aagtgagttg tcaaggaacc aaatggggat gtaaacctaa aaggggttcc    1679

cggcacctcg gtttgtgttg gttggaggtg atcgcacact tggcccttgg ttacgtcctc    1739

ataaccttag acctgaaagg gcccataaat atactatgtt cacgatcaga cacgcactgc    1799

attcggcaga gctccagtga gcaaggcacg accctcagat ctcagtctag tgaaggagag    1859

aaaactgtaa taacactacg ttaaaggttt taactgcttt gttatgtaag cttacccagc    1919

ccggcgcaca gtgactcacg cctgtaatcc cagcactttg ggagggcgag gctagcagat    1979

cacttgaggt taggagttcg ataccagcct ggccaacatg gtgaaacccg gtctctacta    2039

aaaatacaaa aattaactgg gtgtggtggc gggcgcctgt aatcccagct actgaggggg    2099

ctgaggcatg agaatcactt gaacctggga gacagaggtt gcaatgaacc gagatagtgc    2159

cattgcactc cggcctgggc aacagaggaa gactgcctca aacaaacaaa aaacaacaaa    2219

ccaaaccaaa ccaaaaaaat ctcaaagcga ttggacctag cagctcatgc ctgtaatctc    2279

cagcactttg ggaggcggag gcaggaggat ctcttgaagt caagagtttg agatcagcct    2339

ggagaacaaa gtgagacccc catctatt                                       2367
```

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     <210> 258
     <211> 581
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (97)..(525)

     <400> 258
cacaatgagg cagggagaca tgggtttgct atcacatcac cgggggctgg tgagtgcagt      60

tgagacaggt gttttaatca tcgtttttgc acccag atg aac aag gag agg gca       114
                                        Met Asn Lys Glu Arg Ala
                                         1               5

ttc agg cat ggc gac ccg cct gag cca cct cca ggg gca aga gat gag       162
Phe Arg His Gly Asp Pro Pro Glu Pro Pro Pro Gly Ala Arg Asp Glu
            10                  15                  20

cag att tac ttt aga aag gac aac agc atc agc cac tgc cac agc ccc       210
Gln Ile Tyr Phe Arg Lys Asp Asn Ser Ile Ser His Cys His Ser Pro
        25                  30                  35

ccc cag atc atc tgt act ggc tgt cag aac agt cct gct gaa acg cca       258
Pro Gln Ile Ile Cys Thr Gly Cys Gln Asn Ser Pro Ala Glu Thr Pro
    40                  45                  50

atc aca cct gtc att cac tgc tct gcc cag gac tct tca gtg ggc tcc       306
Ile Thr Pro Val Ile His Cys Ser Ala Gln Asp Ser Ser Val Gly Ser
55                  60                  65                  70

cca gcg cta agc att tgg cct gac act cca ggc gcc atg tgc cct ggt       354
Pro Ala Leu Ser Ile Trp Pro Asp Thr Pro Gly Ala Met Cys Pro Gly
                75                  80                  85

ccc cac cta cct ctc cac tgc aaa ttc tgg cca tac acc cct gca ccc       402
Pro His Leu Pro Leu His Cys Lys Phe Trp Pro Tyr Thr Pro Ala Pro
            90                  95                  100

cca aac agt gca ctc cca tct cag tcc aca ttc tcc cct tac aac atg       450
Pro Asn Ser Ala Leu Pro Ser Gln Ser Thr Phe Ser Pro Tyr Asn Met
        105                 110                 115

att cat cca aga cca tgg att cgt ggc ctt aag ttt act tct ggt ctg       498
Ile His Pro Arg Pro Trp Ile Arg Gly Leu Lys Phe Thr Ser Gly Leu
    120                 125                 130

gac ttc tgt gtc agc tcc aga gta tag ttgtc tcactgaccc cttcacttgg       550
Asp Phe Cys Val Ser Ser Arg Val  *
135                 140

gtgccagaga acactggata ttccagaccc c                                    581
```

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     <210> 259
     <211> 317
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (39)..(317)

     <400> 259
aacaaaattc ggagcccggc ccacggcgcg cgctgctg   atg ggt ctg ggc ccg       53
                                            Met Gly Leu Gly Pro
                                             1               5

cct acc gac ggc cca gga ccc atc gac cca cga gtc ggt ccg gcc gcc      101
Pro Thr Asp Gly Pro Gly Pro Ile Asp Pro Arg Val Gly Pro Ala Ala
                10                  15                  20

ggg tgc aca atg ggt ggc tcc tcc agc gtc gcc gct atg aag aaa gtg      149
Gly Cys Thr Met Gly Gly Ser Ser Ser Val Ala Ala Met Lys Lys Val
            25                  30                  35

gtt caa cag ctc cgg ctg gag gcc gga ctc aac cgc gta aaa gtt tcc      197
Val Gln Gln Leu Arg Leu Glu Ala Gly Leu Asn Arg Val Lys Val Ser
        40                  45                  50

cag gca gct gca gac ttg aaa cag ttc tgt ctg cag aat gct caa cat      245
Gln Ala Ala Ala Asp Leu Lys Gln Phe Cys Leu Gln Asn Ala Gln His
    55                  60                  65

gac cct ctg ctg act gga gta tct tca agt aca aat ccc ttc aga ccc      293
Asp Pro Leu Leu Thr Gly Val Ser Ser Ser Thr Asn Pro Phe Arg Pro
 70                 75                  80                  85

cag aaa gtc tgt tcc ttt ttg tag                                      317
Gln Lys Val Cys Ser Phe Leu  *
                90




     <210> 260
     <211> 1480
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (239)..(961)

     <220>
     <221> misc_feature
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    <222> (1)...(1480)
    <223> n = a,t,c or g

    <400> 260
agctagtctg cggacgctgt ataccctcct ccacttcccg ctgcagccaa taaaggccgt      60

tcctaccata gtctgtgtcc gcgttctttt ttccgggact gcagagttcg gggaagctgt     120

acgccgcctt tcgctacgcg gaatttgcag atcttcccct ggacctcagg cctctccggc     180

tggagtaggg tggacgcttc acataagctt ctctggtcga acttacccga atctccag       238
atg gcc gcg ctg cgt cga atg ctc cac ttg ccg agc ctg atg atg ggg       286
Met Ala Ala Leu Arg Arg Met Leu His Leu Pro Ser Leu Met Met Gly
  1               5                  10                  15

acg tgc cgc ccc ttt gcg ggc tca ctg gct gat agt tgc ctg gcg gac       334
Thr Cys Arg Pro Phe Ala Gly Ser Leu Ala Asp Ser Cys Leu Ala Asp
             20                  25                  30

cgc tgt ctc tgg gat cgg ctg cat gcc cag cct cgt ttg ggc act gtc       382
Arg Cys Leu Trp Asp Arg Leu His Ala Gln Pro Arg Leu Gly Thr Val
         35                  40                  45

ccc acc ttc gac tgg ttc ttt gga tac gac gaa gtc cag ggg ctc cta       430
Pro Thr Phe Asp Trp Phe Phe Gly Tyr Asp Glu Val Gln Gly Leu Leu
     50                  55                  60

ctg cca ttg ctg cag gag gca cag gct gcc agt cct ctg cga gtg ctg       478
Leu Pro Leu Leu Gln Glu Ala Gln Ala Ala Ser Pro Leu Arg Val Leu
 65                  70                  75                  80

gat gtg ggc tgt ggg act tcc agc cta tgt aca ggc ctc tac acc aaa       526
Asp Val Gly Cys Gly Thr Ser Ser Leu Cys Thr Gly Leu Tyr Thr Lys
                 85                  90                  95

tct cca cac cca gtg gat gtg ctg ggg gtg gac ttt tct cct gtg gct       574
Ser Pro His Pro Val Asp Val Leu Gly Val Asp Phe Ser Pro Val Ala
            100                 105                 110

gtg gcc cac atg aat agc ctc ctg gag ggt ggc cca agc caa aca cct       622
Val Ala His Met Asn Ser Leu Leu Glu Gly Gly Pro Ser Gln Thr Pro
        115                 120                 125

cta tgc cct gga cac cct gcc tca agc ctc cac ttc atg cac gcc gat       670
Leu Cys Pro Gly His Pro Ala Ser Ser Leu His Phe Met His Ala Asp
    130                 135                 140

gct cag aac ctg ggg gct gtg gct tct tca ggc tct ttc caa cta ctg       718
Ala Gln Asn Leu Gly Ala Val Ala Ser Ser Gly Ser Phe Gln Leu Leu
145                 150                 155                 160

ctg gac aaa ggc aca tgg gat gct gtt gcc cgg gga ggt ctg cct agg       766
Leu Asp Lys Gly Thr Trp Asp Ala Val Ala Arg Gly Gly Leu Pro Arg
                165                 170                 175

gct tac cag ctt cta tca gaa tgc ttg agg gtt cta aac cct cag ggg       814
Ala Tyr Gln Leu Leu Ser Glu Cys Leu Arg Val Leu Asn Pro Gln Gly
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```
            180                 185                 190

acc ctg att cag ttc tca gat gag gac cct gat gtg cga ctg ccc tgc      862
Thr Leu Ile Gln Phe Ser Asp Glu Asp Pro Asp Val Arg Leu Pro Cys
        195                 200                 205

ctg gaa caa ggg tcc tat ggc tgg act gtg act gtg cag gag cta ggc      910
Leu Glu Gln Gly Ser Tyr Gly Trp Thr Val Thr Val Gln Glu Leu Gly
    210                 215                 220

ccg ttc agg ggc atc acc tac ttt gct tac ttg att caa ggc tct cat      958
Pro Phe Arg Gly Ile Thr Tyr Phe Ala Tyr Leu Ile Gln Gly Ser His
225                 230                 235                 240

taa agac atttagtag tcctgaccct agtatttctg tgggcaagga gagggctgaa     1015
 *

gaactgtctt tgcaagctat ctggctgcaa agtgagaatt tgagtcctgg cttccacatt   1075

tactagctgg gtgccatatt gctgaatgtt tctgttcccc agtttactca tctgcagagt   1135

gagaataact tggagttacg gagattacat acaatgatgt gcgcaatatt tagcacaaaa   1195

tgaatgctga aaagagaagg tacaattggg tcattcccca gtttcaacta actggagctc   1255

ctaaaagcag cagacaggaa ctgaatcaaa acccctgcgc tgactgactt gtataatcta   1315

gtggcctaac ctgtaagcct cattnttgtc acctgtaaaa ggagattgta agaggatggg   1375

tataacgagc ttcataaacc tcgatgagat atttgagggg gagggaacaa tacttaccct   1435

caaagctatt aggaggccgg agatgggaat atttccacaa gcccg                    1480



     <210> 261
     <211> 1645
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (389)..(1030)

     <400> 261
atttggccct cgaggccaag aattcggcac gagatcgttt cgagggggcgt ccgccgggtt     60

aggaagccac tgcctggcag cttgtggaag cctcatttgc aaagccaccc ctcagatgtt    120

ttgaagatcg tgacgtcttg taactagcag tgtgtgcaca gaatcctact caaggaacgt    180

cttggcccag cgatgcaaag aactgaagtt tcaagctgga agagcctgta ttgtcctcac    240

aatagtatag aagaattcaa gagaggagag agagacagca ccgaatgaag actgtaaaag    300
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aaaagaagga atgccagaga ttgagaaaat ctgccaagac taggagggta acccagagga    360

aaccgtcttc agggcctgtt tgctggct  atg ctt cga gaa cct ggg gat ccc      412
                                Met Leu Arg Glu Pro Gly Asp Pro
                                 1               5

gaa aaa tta ggg gaa ttt ctt cag aaa gac aat atc agc gtg cat tat      460
Glu Lys Leu Gly Glu Phe Leu Gln Lys Asp Asn Ile Ser Val His Tyr
    10                  15                  20

ttc tgt ctt atc tta tct agt aag ctg cct cag agg ggc cag tcc aac      508
Phe Cys Leu Ile Leu Ser Ser Lys Leu Pro Gln Arg Gly Gln Ser Asn
25                  30                  35                  40

aga ggt ttc cat gga ttt ctg cct gaa gac atc aaa aag gag gca gcc      556
Arg Gly Phe His Gly Phe Leu Pro Glu Asp Ile Lys Lys Glu Ala Ala
                45                  50                  55

cgg gct tct agg aag atc tgc ttt gtg tgc aag aaa aag gga gct gct      604
Arg Ala Ser Arg Lys Ile Cys Phe Val Cys Lys Lys Lys Gly Ala Ala
            60                  65                  70

atc aac tgc cag aag gat cag tgc ctc aga aac ttc cat ctg cct tgt      652
Ile Asn Cys Gln Lys Asp Gln Cys Leu Arg Asn Phe His Leu Pro Cys
        75                  80                  85

ggc caa gaa agg ggt tgc ctt tca caa ttt ttt gga gag tac aaa tca      700
Gly Gln Glu Arg Gly Cys Leu Ser Gln Phe Phe Gly Glu Tyr Lys Ser
    90                  95                  100

ttt tgt gac aaa cat cgc cca aca cag aac atc caa cat ggg cat gtg      748
Phe Cys Asp Lys His Arg Pro Thr Gln Asn Ile Gln His Gly His Val
105                 110                 115                 120

ggg gag gaa agc tgc atc tta tgt tgt gaa gac tta tcc caa cag agt      796
Gly Glu Glu Ser Cys Ile Leu Cys Cys Glu Asp Leu Ser Gln Gln Ser
                125                 130                 135

gtt gag aac atc cag agc ccg tgt tgt agt caa gcc atc tac cac cgc      844
Val Glu Asn Ile Gln Ser Pro Cys Cys Ser Gln Ala Ile Tyr His Arg
            140                 145                 150

aag tgc ata cag aaa tat gcc cac aca tca gca aag cat ttc ttc aaa      892
Lys Cys Ile Gln Lys Tyr Ala His Thr Ser Ala Lys His Phe Phe Lys
        155                 160                 165

tgt cca cag tgt aac aat cga aaa gag ttt cct caa gaa atg ctg aga      940
Cys Pro Gln Cys Asn Asn Arg Lys Glu Phe Pro Gln Glu Met Leu Arg
    170                 175                 180

atg gga att cat att cca gac agg agg tgg tgc ctc att ctg tgt gct      988
Met Gly Ile His Ile Pro Asp Arg Arg Trp Cys Leu Ile Leu Cys Ala
185                 190                 195                 200

act gcg gat ccc acg gaa ccc aca gga ctg ctc ctc tct tag atctaac     1037
Thr Ala Asp Pro Thr Glu Pro Thr Gly Leu Leu Leu Ser  *
                205                 210
```

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agtaagaaat gggagtgtga ggagtgttca cctgctgcag ccacagacta catacctgaa   1097

aactcagggg acatcccttg ctgcagcagc accttccacc ctgaggaaca tttctgcaga   1157

gacaacacct tggaagagaa tccgggcctt tcttggactg attggccaga accttcctta   1217

ttagaaaagc cagagtcctc tcgtggcagg aggagctact cctggaggtc caagggtgtc   1277

agaatcacta acagctgcaa aaaatccaag taacaccttc tgagtagctg ctgtcccaca   1337

caatagggta tgaagctgcg ctcctccatc gggtttgggg agggagcact ctgggactgt   1397

gagacaagga agcagggcca gcagtgagac tatgagccaa gcaaagagaa gtctcagtgg   1457

agcatgagga gggagcagtc cagatgccaa caaggaaatg cgtttatggc tacaagagtg   1517

cctctgcttt ctcctcctct cctcccacca aggattcttc caccttaatc ttgttttcat   1577

atgcctcttc ttacttcacc catgtttgtt gttatgcaaa taaaggtttt ctctccaaaa   1637

aaaaaaaa                                                            1645
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<210> 262
<211> 694
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (166)..(672)

<400> 262
gcggtggaat tcgtcaaaca aaatccctta ccctcttcat tccctggtaa aaagatcaca      60

atcagattag ctgctcctgt gtgttcttct aagactctgc aggctgaggt ccctttgtca     120

gactgtgtcc aaaaagcaag taaacccact tcaagcacac aaatc atg gtg aag         174
                                                  Met Val Lys
                                                  1

acc aac atg tat cat aat gaa aag gtg aac ttt cat gtt gaa tgt aaa       222
Thr Asn Met Tyr His Asn Glu Lys Val Asn Phe His Val Glu Cys Lys
    5                   10                  15

gac tat gta aaa aag gca aag gta aag atc aac cca gtg caa cag agc       270
Asp Tyr Val Lys Lys Ala Lys Val Lys Ile Asn Pro Val Gln Gln Ser
20                  25                  30                  35

cgg ccc ttg ttg agc cag att cac aca gat gca gca aag gag aac acc       318
Arg Pro Leu Leu Ser Gln Ile His Thr Asp Ala Ala Lys Glu Asn Thr
                40                  45                  50

tgc tac tgt ggt gca gtg gca aag aga caa gag aaa aaa ggg atg gag       366
```

```
Cys Tyr Cys Gly Ala Val Ala Lys Arg Gln Glu Lys Lys Gly Met Glu
            55                  60                  65

cct ctt caa ggt cat gcc act ccc gct ttg cct ttt aaa gaa acc cag       414
Pro Leu Gln Gly His Ala Thr Pro Ala Leu Pro Phe Lys Glu Thr Gln
        70                  75                  80

gaa cta tta cta agt ccc ctg ccc cag gaa ggt cct ggg tca ctt gca       462
Glu Leu Leu Leu Ser Pro Leu Pro Gln Glu Gly Pro Gly Ser Leu Ala
    85                  90                  95

gca gga gag agc agc agt ctt tct gcc agt aca tca gtc tca gat tca       510
Ala Gly Glu Ser Ser Ser Leu Ser Ala Ser Thr Ser Val Ser Asp Ser
100                 105                 110                 115

tcc cag aaa aaa gaa gag cac aat tat tct ctt ttt gtc tcc gac aac       558
Ser Gln Lys Lys Glu Glu His Asn Tyr Ser Leu Phe Val Ser Asp Asn
                120                 125                 130

ttg ggt gaa cag cca act aaa tgc agt cct gaa gaa gat gag gag gac       606
Leu Gly Glu Gln Pro Thr Lys Cys Ser Pro Glu Glu Asp Glu Glu Asp
            135                 140                 145

gag gag gat gtt gat gat gag gac cat gat gaa gga ttc ggc agt gag       654
Glu Glu Asp Val Asp Asp Glu Asp His Asp Glu Gly Phe Gly Ser Glu
        150                 155                 160

cat tac atc att ata taa tggtacttcc tcaagttgct gg                      694
His Tyr Ile Ile Ile  *
    165




    <210> 263
    <211> 1540
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (1033)..(1188)

    <400> 263
cccaggagga agtgaacttc ctgagcactt acatggacca tgagtattcc atcaagtctg      60

tccagatctc cactcttatg cgccagctgc agcaggttaa ggacagccag caggatgagc     120

tggatgacct cggtgagatg cgcagaaagg tcctggaatc cttgtctgac aagattcaga     180

agaagaagaa aaaaattctg agttctgtgg tggcggaaac ccagcgtccc tatgaagagg     240

ctctcctaca gaagatgtgg gaaagccagg acttcctgaa atgcatgcaa aggttcagag     300

aagtgcgtgg gcaaggaagg tggtggtccc tgtagggaag cagtggatgg gcagtcccca     360
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cggcctgtgg gaatgagtca ggcttctcct gatctggcgc tcaggaggtc tctgattctg     420

gtgttggcct ccctccttgc cggtgccatt actgtcactt gtctttcatc tgggaaggcg     480

attggcactg acctaggcct tgcctcatta gccagcaatg ctggctaatg acccatttac     540

aaccatcacc aaacatcacc tattcagcca ttaaccaccg tgcatcttta ccccttgatt     600

cttgttactg cccaccaccc attatcagtg ttaatgaact tcaccatcac tgccttcttg     660

aattaatttt cattatcttg cctcttcact ggtttttaat gtgcatgccc ttcactatct     720

ctgccagcct ccattcattc ccacgattga gcattccccg ccactttgta acctgtctcc     780

attctccatg atccctcacc tgtttcagca ccactgaata ttgtcactaa cttggaagcc     840

agccgcaccc tgcatgggga agtcccctct ctggagtcca gcaagtccca gtgacagaac     900

ccataccatt tccccagata gctttgctcc tcgttcattt tggcctttct ccctttggtt     960

gggggccatt tgcctctccc ttctcccctg ctgtgccttt cctctcagtt tattgaccag    1020

tttgaggaga ac    atg cct gta tta agg gcc gag gtg gaa gag ctc caa     1068
                 Met Pro Val Leu Arg Ala Glu Val Glu Glu Leu Gln
                   1               5                  10

gcc cag acc cgg gaa ccc cga gag gtc ata ttt gag gat gtt ctg ctt      1116
Ala Gln Thr Arg Glu Pro Arg Glu Val Ile Phe Glu Asp Val Leu Leu
         15                  20                  25

cgg aga ccc aag tgc acc cca gac atg gat gtc atc ctc aac att cct      1164
Arg Arg Pro Lys Cys Thr Pro Asp Met Asp Val Ile Leu Asn Ile Pro
     30                  35                  40

gtg gaa gag cca cta ccc ttc tag atggcagtgc catgggccgc cctcccctcc     1218
Val Glu Glu Pro Leu Pro Phe  *
 45                  50

tgctctcttc ccagcacctg gagccttgga tcatttactt ccaggaccgg atctccattc    1278

agaccctgat ctacagtctc cctgctccct ctgcccttcc tccctctttc tttccctccc    1338

tccctccctc ccttcttccc cccttccctt ccctcctcct tccttcctcc tctccctccc    1398

tccctccttt ctttcttcct gtggtttttt cctctcttct tcccttcttt ctggttggtg    1458

ctgctgggcc aggtgggaat ttctgattaa atctgctatt ccttttttac caataaagct    1518

ggatttacat ttaaaaaaaa aa                                             1540
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<210> 264
<211> 583
<212> DNA
<213> Homo sapiens

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     <220>
     <221> CDS
     <222> (216)..(464)

     <400> 264
gtgctgagag gtgagttagc tgcagaagaa atgctggaag ctggcaaaga tcagttcgtg      60

aggtttaaca agtcatttcc ataacataaa agtacaaagt gaagtagcaa ttgctgatgt     120

ggaatctgca gcaagcattt ccagaatatc tagataaatg gcagaggtag ctctactaga     180

gttttaacag agacaaaaca gccttacttc aggag atg cca ttt agg act ttc        233
                                       Met Pro Phe Arg Thr Phe
                                        1               5

aca gct cta ggt aag cta ata tct gac ttc aaa gat tca aag gac ggg       281
Thr Ala Leu Gly Lys Leu Ile Ser Asp Phe Lys Asp Ser Lys Asp Gly
            10                  15                  20

ctg act ctt tac ttt gta gag aca gcg tca cgc tct gtt gtg ctg gct       329
Leu Thr Leu Tyr Phe Val Glu Thr Ala Ser Arg Ser Val Val Leu Ala
        25                  30                  35

ggt ctt gaa ctc ttg acc tca agt gat cct cca acc tca gcc tcc caa       377
Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Thr Ser Ala Ser Gln
    40                  45                  50

agc act gga att aca ggt gta agc cac ttt tcc cag cct ggg ctg gct       425
Ser Thr Gly Ile Thr Gly Val Ser His Phe Ser Gln Pro Gly Leu Ala
55                  60                  65                  70

ttc ttg tta gag gtc aat gca gtt ggt gac ttt aaa tga atgctaatat        474
Phe Leu Leu Glu Val Asn Ala Val Gly Asp Phe Lys  *
                75                  80

tcaattacca ttccaaaaat ccaagagcca gttaagaatt atgctacatc ctcgtgccga     534

attcattgcc tcgagggcca aattccctat agtgatcgta ttaaattca                 583



     <210> 265
     <211> 2077
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (154)..(834)

     <400> 265
cggcacgagg acagcataga ggaagtcaag gaagatagaa acaggcatcc tccagcaaac      60

ctgcccactc cagccagtac ccggattctt agaaaatatt ccaatattcg aggaaagctc     120
```

```
agagcccagc aacgtttaat caagaatgag aaa atg gaa tgc cca gat gct ctg      174
                                     Met Glu Cys Pro Asp Ala Leu
                                      1               5

gct gtg gaa agt aag cca agt cgt aag agc gta tgc atc aac cct ctg       222
Ala Val Glu Ser Lys Pro Ser Arg Lys Ser Val Cys Ile Asn Pro Leu
        10                  15                  20

atg tcc ccc aag ctt gcc ctg caa gtg gat gca gat ggg ttt cct gtt       270
Met Ser Pro Lys Leu Ala Leu Gln Val Asp Ala Asp Gly Phe Pro Val
    25                  30                  35

aag ccc aag agt act gaa gga atg aag gga agg aag ggg aag cag gtg       318
Lys Pro Lys Ser Thr Glu Gly Met Lys Gly Arg Lys Gly Lys Gln Val
40                  45                  50                  55

tct gaa atc ttg cct aaa gca gaa gtt cag agt aaa cgc aag aga aca       366
Ser Glu Ile Leu Pro Lys Ala Glu Val Gln Ser Lys Arg Lys Arg Thr
                60                  65                  70

gaa ggc agc agc cct cca gat agt aag aac aag ggg cct acg gtg aaa       414
Glu Gly Ser Ser Pro Pro Asp Ser Lys Asn Lys Gly Pro Thr Val Lys
            75                  80                  85

gcc agc aaa gaa aag cat gct gat gga gcc acc aaa acc cct gct gcc       462
Ala Ser Lys Glu Lys His Ala Asp Gly Ala Thr Lys Thr Pro Ala Ala
        90                  95                  100

aag agg cca gct gca agg gac aga agc agc caa ccc ccc aaa aag acg       510
Lys Arg Pro Ala Ala Arg Asp Arg Ser Ser Gln Pro Pro Lys Lys Thr
    105                 110                 115

tct ttg aaa gag aat aaa gtg aag atc cct aaa aag tcc gct ggg aag       558
Ser Leu Lys Glu Asn Lys Val Lys Ile Pro Lys Lys Ser Ala Gly Lys
120                 125                 130                 135

agc tgc cct ccc tcc agg aaa gaa aaa gag aat aca aac aaa agg cct       606
Ser Cys Pro Pro Ser Arg Lys Glu Lys Glu Asn Thr Asn Lys Arg Pro
                140                 145                 150

tcc cag tct att gcc tcg gaa aca ctg acg aaa cct gca aaa cag aag       654
Ser Gln Ser Ile Ala Ser Glu Thr Leu Thr Lys Pro Ala Lys Gln Lys
            155                 160                 165

ggg gcc ggt gaa tcc tct tca agg cct cag aaa gcc acg aat agg aag       702
Gly Ala Gly Glu Ser Ser Ser Arg Pro Gln Lys Ala Thr Asn Arg Lys
        170                 175                 180

cag agt agt gga aag act cgg gcc aga ccc tca acg aaa acc cca gag       750
Gln Ser Ser Gly Lys Thr Arg Ala Arg Pro Ser Thr Lys Thr Pro Glu
    185                 190                 195

agc agt gca gct cag aga aag cga aag ctg aag gca aag ctg gac tgt       798
Ser Ser Ala Ala Gln Arg Lys Arg Lys Leu Lys Ala Lys Leu Asp Cys
200                 205                 210                 215

tcg cac ggc aaa cgg agg cgg ctg gat gca aag tga ttgg aaagatggta       848
```

```
Ser His Gly Lys Arg Arg Arg Leu Asp Ala Lys  *
                220                 225

gccaagagta aaactgttct atagaagtaa ccttttattt tgcattaact aaatctgctt     908

ttataagctt atcaagcctt tcaaatttac agttaatgga gaacaccgta atttgagatg     968

tcagaaaatg catctcagat ggagaaggga acttgcagag tccttctctg aggctaaggg    1028

aagttatata ttatattctg gttgttcctt gggttttaaa cttggaacca agcagttttc    1088

gtttttaaaa gtacagtgcc ttatttatcc tttttgtttt taaatttaca aaagctaaaa    1148

agctgatcta tgtgattaaa ggcttgtatt ttatacttga tgcacaagca cttgtactgt    1208

agccgagaag accaccatca tgcacataaa aggagctttt cagcagccac cctgcagcat    1268

ctgcccacga acagatgccc ttctttgcaa accccagcag tgaacttccc tctctgtctt    1328

gtttgtttgt ttagatgatg tttgaaagct aaaccaaatc attttatggt atgcagagga    1388

tttataatta taaaagatta ctatttctgt taccccccttt taaaaaagat catgttcatt   1448

gttggtccct cctctcacct ttgatgtttt gtcatttgag agcatgtatt ctaaattatg    1508

tgcccatggg acaagagata tgtcacaagt gttaattttt gtttacaaac tctaaaaaat    1568

catttgcatc cccaaactgt attactaatt ctcaccatct tcttcatttc tggtcttgct    1628

agcactcctg caaggcttcc atcctacttc gggaggaaaa agcctaggat ttttttttc     1688

catcttgtag ctgtaatttg atgattagga tgaaaatgac tcttattttc tttcttaccc    1748

agagtacttc catattcaaa gaaagccgaa ctattatttc cagtaataga aaggtttaag    1808

aatatgtatg tccatgtgtg tttgggtgca tttgcatgtg gttatcagcc acaaatgtct    1868

cccaatccca attttacagt aaaatttttt ccctatgcag tgtgcttggg tgtccctgag    1928

ttgagtaatt agcaaaggac agatggttta aaagtagccc agtgtctctg tgagcatccc    1988

caataccact ttggtaccag actcagaaag atctaaaaca gcatggagtt atgtaaaggt    2048

tagagcagcc ttgcagttgg aggaagcag                                      2077


     <210> 266
     <211> 1175
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (116)..(685)
```

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<400> 266
cccacgcgtc cgtccactag caacagtctc cccaggcaca acacagctaa cacaaggccc     60

cgcaggcagg actctgggac agacgcaggc cagctgccca gagcccagac caagc atg     118
                                                             Met
                                                               1

gac gcc gtg gat gcc acc atg gag aaa ctc cgg gca cag tgc ctg tcc      166
Asp Ala Val Asp Ala Thr Met Glu Lys Leu Arg Ala Gln Cys Leu Ser
              5                  10                  15

cgc ggg gcc tcg ggc atc cag ggc ctg gcc agg ttt ttc cgc caa cta      214
Arg Gly Ala Ser Gly Ile Gln Gly Leu Ala Arg Phe Phe Arg Gln Leu
         20                  25                  30

gac cgg gac ggg agc aga tcc ctg gac gct gat gag ttc cgg cag ggt      262
Asp Arg Asp Gly Ser Arg Ser Leu Asp Ala Asp Glu Phe Arg Gln Gly
     35                  40                  45

ctg gcc aaa ctc ggg ctg gtg ctg gac cag gcg gag gca gag ggt gtg      310
Leu Ala Lys Leu Gly Leu Val Leu Asp Gln Ala Glu Ala Glu Gly Val
 50                  55                  60                  65

tgc agg aag tgg gac cgc aat ggc agc ggg acg ctg gat ctg gag gag      358
Cys Arg Lys Trp Asp Arg Asn Gly Ser Gly Thr Leu Asp Leu Glu Glu
                 70                  75                  80

ttc ctt cgg gcg ctg cgg ccc ccc atg tcc cag gcc cgg gag gct gtc      406
Phe Leu Arg Ala Leu Arg Pro Pro Met Ser Gln Ala Arg Glu Ala Val
             85                  90                  95

atc gca gct gca ttt gcc aag ctg gac cgc agt ggg gac ggc gtc gtg      454
Ile Ala Ala Ala Phe Ala Lys Leu Asp Arg Ser Gly Asp Gly Val Val
        100                 105                 110

acg gtg gac gac ctc cgc ggg gtg tac agt ggc cgt gcc cac ccc aag      502
Thr Val Asp Asp Leu Arg Gly Val Tyr Ser Gly Arg Ala His Pro Lys
    115                 120                 125

gtg cgc agt ggg gag tgg acc gag gac gag gtg ctg cgc cgc ttc ctg      550
Val Arg Ser Gly Glu Trp Thr Glu Asp Glu Val Leu Arg Arg Phe Leu
130                 135                 140                 145

gac aac ttc gac tcc tct gag aag gac ggg cag gtc aca ctg gcg gaa      598
Asp Asn Phe Asp Ser Ser Glu Lys Asp Gly Gln Val Thr Leu Ala Glu
                150                 155                 160

ttc cag gac tac tac agc ggc gtg agt gcc tcc atg aac acg gat gag      646
Phe Gln Asp Tyr Tyr Ser Gly Val Ser Ala Ser Met Asn Thr Asp Glu
            165                 170                 175

gag ttc gtg gcc atg atg acc agt gcc tgg cag ctg tga gcagctccgg       695
Glu Phe Val Ala Met Met Thr Ser Ala Trp Gln Leu  *
        180                 185                 190

ctcagccctg ctgccctggc ctgtcactcc ccacccctgc cggagacctc ccttccctgg    755
```

```
gccccttctc tcctgggcag ccacaccaca gagcggggag gggcaggtgg gggaatggag    815

gctgcaggac tggctagacc aggtccctgc cggtccacca ggcggaggtg ggacaaaggt    875

cctaacagga gtcactggct caggacccca gggagaaacg ctctccccac ccacgccatg    935

ctgaccagag gtcttgcagc ccctgtggat gcccccgccg aggtcccccg atccccgcac    995

ccggactgct gctccctgcc cctcccttgc gggtccccca ggaagccagg tgaccccagg   1055

tgggaggctg tgtgtggagg ccatcctgga aggaagttta gacctgccca ggtgtggagc   1115

gaggggcaca ggggcatcct aacctcagaa actgaaataa agcctttgaa aaaaaaaaaa   1175




     <210> 267
     <211> 1094
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (116)..(604)

     <400> 267
cccacgcgtc cgtccactag caacagtctc cccaggcaca acacagctaa cacaaggccc     60

cgcaggcagg actctgggac agacgcaggc cagctgccca gagcccagac caagc atg     118
                                                             Met
                                                             1

gac gcc gtg gat gcc acc atg gag aaa ctc cgg gca cag tgc ctg tcc      166
Asp Ala Val Asp Ala Thr Met Glu Lys Leu Arg Ala Gln Cys Leu Ser
            5                   10                  15

cgc ggg gcc tcg ggc atc cag ggc ctg gcc agg ttt ttc cgc caa cta      214
Arg Gly Ala Ser Gly Ile Gln Gly Leu Ala Arg Phe Phe Arg Gln Leu
        20                  25                  30

gac cgg gac ggg agc aga tcc ctg gac gct gat gag ttc cgg cag ggt      262
Asp Arg Asp Gly Ser Arg Ser Leu Asp Ala Asp Glu Phe Arg Gln Gly
    35                  40                  45

ctg gcc aaa ctc ggg ctg gtg ctg gac cag gcg gag gca gag ggt gtg      310
Leu Ala Lys Leu Gly Leu Val Leu Asp Gln Ala Glu Ala Glu Gly Val
50                  55                  60                  65

tgc agg aag tgg gac cgc aat ggc agc ggg acg ctg gat ctg gag gag      358
Cys Arg Lys Trp Asp Arg Asn Gly Ser Gly Thr Leu Asp Leu Glu Glu
                70                  75                  80

ttc ctt cgg gcg ctg cgg ccc ccc atg tcc cag gcc cgg gag gct gtc      406
Phe Leu Arg Ala Leu Arg Pro Pro Met Ser Gln Ala Arg Glu Ala Val
            85                  90                  95
```

```
atc gca gct gca ttt gcc aag ctg gac cgc agt ggg gac ggc gtc gtg      454
Ile Ala Ala Ala Phe Ala Lys Leu Asp Arg Ser Gly Asp Gly Val Val
        100                 105                 110

acg gtg gac gac ctc cgc ggg gtg tac agt ggc cgt gcc cac ccc aag      502
Thr Val Asp Asp Leu Arg Gly Val Tyr Ser Gly Arg Ala His Pro Lys
    115                 120                 125

gtc aca ctg gcg gaa ttc cag gac tac tac agc ggc gtg agt gcc tcc      550
Val Thr Leu Ala Glu Phe Gln Asp Tyr Tyr Ser Gly Val Ser Ala Ser
130                 135                 140                 145

atg aac acg gat gag gag ttc gtg gcc atg atg acc agt gcc tgg cag      598
Met Asn Thr Asp Glu Glu Phe Val Ala Met Met Thr Ser Ala Trp Gln
                150                 155                 160

ctg tga gcagctccgg ctcagccctg ctgccctggc ctgtcactcc ccacccctgc       654
Leu  *


cggagacctc ccttccctgg gccccttctc tcctgggcag ccacaccaca gagcggggag    714

gggcaggtgg gggaatggag gctgcaggac tggctagacc aggtccctgc cggtccacca    774

ggcggaggtg ggacaaaggt cctaacagga gtcactggct caggacccca gggagaaacg    834

ctctccccac ccacgccatg ctgaccagag gtcttgcagc cctgtggat gcccccgccg     894

aggtcccccg atccccgcac ccggactgct gctccctgcc cctcccttgc gggtccccca    954

ggaagccagg tgaccccagg tgggaggctg tgtgtggagg ccatcctgga aggaagttta   1014

gacctgccca ggtgtggagc gaggggcaca ggggcatcct aacctcagaa actgaaataa   1074

agcctttgaa aaaaaaaaaa                                               1094



     <210> 268
     <211> 485
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (169)..(387)

     <400> 268
ccctcttcat agaggagccg gaagcatcgg gagccgcggt acccgcccat cttccggcca     60

ggatgtgtgg tcctggtgag cgattgtcct gtggcgtccg ggaccgagtt tgtggcccag    120

ggttatgtgt gcacttcaca cctctgactt ttttcagggt tcctattg atg gtt agg     177
                                                     Met Val Arg
                                                       1
```

```
agc agg att tcg ggg atg aag gcg gca gca gca aga gga ggc tgc gac       225
Ser Arg Ile Ser Gly Met Lys Ala Ala Ala Ala Arg Gly Gly Cys Asp
     5                   10                  15

tgc gga ccc cag att cgt ccc cct cca cca cac aca acg cca aga cgg       273
Cys Gly Pro Gln Ile Arg Pro Pro Pro Pro His Thr Thr Pro Arg Arg
 20                  25                  30                  35

gcc cca gga ggg cgt gaa gag aag act tcc ttt cct ctc ctc tcg cct       321
Ala Pro Gly Gly Arg Glu Glu Lys Thr Ser Phe Pro Leu Leu Ser Pro
                40                  45                  50

cct ggc gct ggc cgt atg aag gtg tct ccc aga agc att agc aga gga       369
Pro Gly Ala Gly Arg Met Lys Val Ser Pro Arg Ser Ile Ser Arg Gly
            55                  60                  65

gcc ctg tgg gag aaa tga ggagtg acccaaaaga aacttgctca aggacagcct       423
Ala Leu Trp Glu Lys  *
        70

ccttaaagca gacttccata taccccaacc tgcaaaagaa gactttacgt gaaatgttac     483

ag                                                                    485




     <210> 269
     <211> 1170
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (168)..(611)

     <220>
     <221> misc_feature
     <222> (1)...(1170)
     <223> n = a,t,c or g

     <400> 269
attcagccgc ctttttatgt caccgggcgc cacatggacc cagccggccc gagcgcgccc      60

cgccgctgac cgcccgcgcc ccgggaagga agaacactcg ctcccggcca tacttgcgtg     120

tgagttctga cccctggagg agccactgtg gaagcagagc aatcgcc  atg gag ttt      176
                                                      Met Glu Phe
                                                        1

gtg atg aag cag gct cta gga ggg gcc acc aag gac atg ggg aag atg       224
Val Met Lys Gln Ala Leu Gly Gly Ala Thr Lys Asp Met Gly Lys Met
     5                   10                  15

ctg ggg ggt gac gag gag aag gac cca gac gcc gcc aag aag gag gag       272
Leu Gly Gly Asp Glu Glu Lys Asp Pro Asp Ala Ala Lys Lys Glu Glu
 20                  25                  30                  35
```

```
gag cgg cag gag gcg ctg cgc cag gcg gag gag gag cgc aag gcc aag       320
Glu Arg Gln Glu Ala Leu Arg Gln Ala Glu Glu Glu Arg Lys Ala Lys
                40                  45                  50

tac gcc aag atg gag gcg gag cgc gag gcc gtg cgc cag ggc atc cga       368
Tyr Ala Lys Met Glu Ala Glu Arg Glu Ala Val Arg Gln Gly Ile Arg
            55                  60                  65

gac aag tac ggc atc aag aag aag gag gag cgc gag gcc gag gcc cag       416
Asp Lys Tyr Gly Ile Lys Lys Lys Glu Glu Arg Glu Ala Glu Ala Gln
        70                  75                  80

gcc gcc atg gag gcc aac tcc gag ggg agc ttg acg cgg ccc aag aag       464
Ala Ala Met Glu Ala Asn Ser Glu Gly Ser Leu Thr Arg Pro Lys Lys
    85                  90                  95

gcc atc ccg ccg ggc tgc ggg gac gag gtg gag gag gag gac gag agc       512
Ala Ile Pro Pro Gly Cys Gly Asp Glu Val Glu Glu Glu Asp Glu Ser
100                 105                 110                 115

atc ctg gac acc gtc atc aag tac ctg ccc ggg ccg ctg cat gac atg       560
Ile Leu Asp Thr Val Ile Lys Tyr Leu Pro Gly Pro Leu His Asp Met
                120                 125                 130

ctc aag atg tat ccc cgc gcg gga cag ctg ccc cgc gga gcc ggc cat       608
Leu Lys Met Tyr Pro Arg Ala Gly Gln Leu Pro Arg Gly Ala Gly His
            135                 140                 145

tga acac tgcaccctcc acaggagccg cagaggccct gaggcaccgg actgcttgga       665
 *


gaccctgcgc ccctgcccag cacctcctcc gtgggcagct cctcggtgtg gggcctgcgg    725

ggttccctgc ggcgcagccg ggcgcgtgtg tggcctaatc cacctggtgg ccctgcgggg    785

cggcatccga gcccctgttt ctcctccatt catgtttatt ttgcatcaca atttgttgaa    845

tctcaggtag atgaggtctt tgcatttagt gagttttatc ttgacagggc gcgctcgccc    905

ccggtccctt tcgtccacat caaaaatgca tcacgtctcc acgtgtttcg ggccagggcg    965

gggcttggca ttgaccttca tgaccttaca tagctttaga gaagccataa cgcttgactg   1025

caatactaac gaccgacgcc cctccggaca gagaccaccg cgcccctctg cgccccatcg   1085

acgctgtccg cggngacgtc gctgaccgcc ctgctcgccc tgagccctct cactgacttc   1145

tcccgggtcg tgtcttatta aaact                                         1170


     <210> 270
     <211> 1116
     <212> DNA
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     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (497)..(766)

     <400> 270
gatgacctct ttcttccttc cgttttgcca gtgtcactct gtgatgatag gtgtaagttg      60

actgtgtgca ttgcccgtct gtgaccgttt tcgactcaca gaaatggcag tctgaagtgg     120

ctcggcctct tgcttgagag acagattgga gcagagtctt tgtggatgca aagccacctg     180

ggccactgcc gtgtgtgcca ccctgaactt caagctgccc tgaaccgcgt gcgtttctca     240

gtgtcacgta cagctcggcc tgaccgtttg ccttttagtg ttctcttcct tctcggtgtc     300

ctcctcctct tcctcactaa cattcatcca gagcctttca gtgcagaaat caggtagctg     360

ctgaactcgg cagctgcgtc ctttttccca tcatctcttc tgtcctttgc tagctgtcat     420

ttcttccctc ttggcttcaa ctgcacatcc ctgggtttgt cctaataggg aatttttccc     480

acttgagtag acaagc    atg aga ata tca tta ttt tta tat gtt ata tgt      529
                     Met Arg Ile Ser Leu Phe Leu Tyr Val Ile Cys
                       1               5                  10

tat att ttt agc aga gaa aaa agt gga aaa tgt gtg caa act tgc aga      577
Tyr Ile Phe Ser Arg Glu Lys Ser Gly Lys Cys Val Gln Thr Cys Arg
            15                  20                  25

agg ccc ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc      625
Arg Pro Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly
        30                  35                  40

ccc gga gga ggg tcg tcc ctg tgc cca tgc tgt cag gaa ggc ccc gga      673
Pro Gly Gly Gly Ser Ser Leu Cys Pro Cys Cys Gln Glu Gly Pro Gly
    45                  50                  55

gga ggg tcg tcc ctg tgc cca tgc ggt cag aaa ggc ccc gga gga ggg      721
Gly Gly Ser Ser Leu Cys Pro Cys Gly Gln Lys Gly Pro Gly Gly Gly
 60                  65                  70                  75

tca tct ctg tgc cca tgc ggt cag gtt ggg gct gag gca ctt tga tca      769
Ser Ser Leu Cys Pro Cys Gly Gln Val Gly Ala Glu Ala Leu  *
                80                  85                  90

ttgctcctcc tcagagtgtt cttttcctgc cctctcagat tataataacg aggtagttac     829

agagtgagct ccagcctaga tcgtctgggt ttgaatccag ctccatgact gtggccgtgt     889

tgcctaatct ctctgagtct cagcttcctt ttctgtaaag tgggtataat agtagagtct     949

acactgtggg gctgtggtgg gattcattgt gttcacacgt gtgcagggct gagaacaggg    1009

ccccaaacag ggtaggcaca atgaagcatg agtcagaata ataatacaga tgacagtttc    1069
```

```
tctatcacta atttgaacat tgcagacagt gcaaagaaga aaattag                  1116




     <210> 271
     <211> 2569
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (15)..(596)

     <400> 271
cgcgccccca ttga  atg gat gct gtg gta ccg gac cgg aat tcc cgg gtc       50
                 Met Asp Ala Val Val Pro Asp Arg Asn Ser Arg Val
                   1               5                  10

gac cca cgc gtc cgg ttt ccc agc gcg gtg ccc gcc cct cat cct cct        98
Asp Pro Arg Val Arg Phe Pro Ser Ala Val Pro Ala Pro His Pro Pro
         15                  20                  25

cca gtc tcc ctc ccc tcg ccg act gcc gcc cca ggc tcc gcc atg ggg       146
Pro Val Ser Leu Pro Ser Pro Thr Ala Ala Pro Gly Ser Ala Met Gly
     30                  35                  40

aat gtg cca tcc gcg gtg aag cac tgc ctc agc tac cag cag ctt ctc       194
Asn Val Pro Ser Ala Val Lys His Cys Leu Ser Tyr Gln Gln Leu Leu
 45                  50                  55                  60

cgg gag cat ctc tgg atc ggg gat tca gtg gca ggg gcg ctc gac ccc       242
Arg Glu His Leu Trp Ile Gly Asp Ser Val Ala Gly Ala Leu Asp Pro
                 65                  70                  75

gcg cag gaa aca tcc cag tta tct gga ctc cct gag ttt gtt aaa ata       290
Ala Gln Glu Thr Ser Gln Leu Ser Gly Leu Pro Glu Phe Val Lys Ile
             80                  85                  90

gta gaa gtt ggg cct agg gat gga ttg cag aat gaa aag gtt ata gtt       338
Val Glu Val Gly Pro Arg Asp Gly Leu Gln Asn Glu Lys Val Ile Val
         95                 100                 105

cct aca gat ata aaa att gaa ttt atc aat cga ctt tcc caa act ggc       386
Pro Thr Asp Ile Lys Ile Glu Phe Ile Asn Arg Leu Ser Gln Thr Gly
    110                 115                 120

ttg tct gta ata gaa gtg act agc ttt gtg tct tcc aga tgg gta cca       434
Leu Ser Val Ile Glu Val Thr Ser Phe Val Ser Ser Arg Trp Val Pro
125                 130                 135                 140

cag gtt gct gct gga gct act gag ata tca gtt ttt gga gct gca tct       482
Gln Val Ala Ala Gly Ala Thr Glu Ile Ser Val Phe Gly Ala Ala Ser
                145                 150                 155

gaa tcc ttt agc aag aag aat att aac tgt tcc att gaa gaa agt atg       530
Glu Ser Phe Ser Lys Lys Asn Ile Asn Cys Ser Ile Glu Glu Ser Met
```

```
         160                 165                 170

gga aaa ttt gag gag gtt gtt aag tct gca aga cac atg aat att cca      578
Gly Lys Phe Glu Glu Val Val Lys Ser Ala Arg His Met Asn Ile Pro
    175                 180                 185

gca cga ggg tac tta tga aatccc acaaattctg ttttgttaat gtttattgtt      632
Ala Arg Gly Tyr Leu  *
190

aaagcttact caaaaattat ctagagattc ttatatcatt tataaaaata tacatagaat    692

atcatatttc tattttgttt aatcagggta atcactatat agttacatct cattaacatc    752

actgctgatt attagtgagt atctagcttg tggaatgtgt catgcaattg aaatcagagg    812

tactagcatg caaatctggc attattaact attttattaa cactctagca cccaaatgca    872

gccctcttat ctcagcctac atgtgctgat aagttggtat aaactcacaa cagcttttgg    932

aaaagaatca cctaatgtgg ttttcaaatt ttttttaaaa catgactttt tcttcaaaga    992

gtattttatg tagaacttca atagaataca gcagatataa aattgagctg ctctgggaaa   1052

tcattttatc cattctttct ccccctcaat ggctgacttt tctacttcct ctgggtgatc   1112

ccaaagcacc tccatagtat cttgcagaac actgtttaaa aatacttgat aaattgctta   1172

tagaagataa atataaactt tcagttctct actattttct attatatgtg atttctataa   1232

atttaggagt atcagagata tcaatccctt tctcctcgcc ttgccttttt cttgtggaaa   1292

cttatcagct gttcattcta agagatgttg attacaggac atggaaaata aaaactgacc   1352

caagatccac aaacctaatt ttctctctca ggagtttaga aatggtatac caaacatggt   1412

tacttgtatt gaaagattat gtgattttgt cactgagttc actattttgg ggttcctagg   1472

atggagccac atgcaaacca gtgacaggac agagtagtag aaagcagaaa tggaaaaagg   1532

aggctcctag cggtgatgag aggtatgggg gagggaggag agggaaaaat ctgccttggt   1592

gcttgtctgc ttccaggacc aatagttgcc tcaagtatta taaccaggcc tatgtgctgt   1652

gaaacctata atgcattttt gtgtgtgttt gtttcttaag gaagaatttg tttctaagac   1712

attagctact ttttctatta attttataaa tatggagata tgatgaacac acatcttaac   1772

aagttaaagt gcatagcgat tggtaataga aggttgaaag ctggggatgg atttgggtgc   1832

aggctgtact tcccttagtt gaggtgagca aagttcatgg tagcgggaaa gattcaacag   1892

ttaatgagaa agataagtga gtcaattgtg actgaaaata ttagtgaaat gattggaatt   1952

tcaatcaagg tgttttgggg gaacaattag agttagacta tacctagtaa aatattttgt   2012

tagtttgttt tctatttata tttttcctgt cctccatagt aagtctacat gagtttctaa   2072
```

```
aatttgaaat tacttttgta attaagatag atgcatatca tgtaaggact atatgagaaa   2132

aatttaaaat ccaaggcaat gtacttccaa agacataaaa taaaggatat ttatttttca   2192

ggcaaaagtt acaaaaccac aatcaaaaag gagagatata ctattggttt ctcaattcga   2252

atataaataa gttgtctcaa ttttctttaa aataaagaga aagatgaaga ccctattcta   2312

cttcaatatg tgtttaaagt gtggagtata agctttaaag taattctcat tgggaagtta   2372

aaaagtatgt gactataaga agtaaattgc ttatgtagct tgctcttcaa ataggaaggg   2432

ttttttagt gttgaaagat ggatgcaaat ataagttgta ggaagtaacc ttttattatc    2492

ttagctttct gttgtaaaat ggaatagtta atgtaactgg gctaataaaa atcttaaacc   2552

ctcttaaaaa aaaaaaa                                                  2569



      <210> 272
      <211> 1204
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (64)..(630)

      <400> 272
tttcgtaaat agttgctccg tgggctttcc gcatttcacc ctgctccagg cagcgtggtc      60

tgt  atg gct ccg ccc tgg gca gga gga gaa aga aga ggg cca ggc acc      108
     Met Ala Pro Pro Trp Ala Gly Gly Glu Arg Arg Gly Pro Gly Thr
       1               5                  10                  15

acg tgc ctg cac tct ccc tgg atg ctg gag gct gct ccg ccg tgg gca      156
Thr Cys Leu His Ser Pro Trp Met Leu Glu Ala Ala Pro Pro Trp Ala
                 20                  25                  30

gga gga gaa gga aga gaa ctg ggt gcc gcc tgc ctg cac tct ctc cgg      204
Gly Gly Glu Gly Arg Glu Leu Gly Ala Ala Cys Leu His Ser Leu Arg
             35                  40                  45

atg ctg gag gct gga ggc agt gag gca gca aca gcg cga ggg cga ggc      252
Met Leu Glu Ala Gly Gly Ser Glu Ala Ala Thr Ala Arg Gly Arg Gly
         50                  55                  60

gac ttt gga gct gcc tca tgc agc gac ctc gcc ttc cgc tgc gcc tcc      300
Asp Phe Gly Ala Ala Ser Cys Ser Asp Leu Ala Phe Arg Cys Ala Ser
     65                  70                  75

tcc cag aac cca aga agc ctg gaa cct gtg gcg tcc agc cct gaa agg      348
Ser Gln Asn Pro Arg Ser Leu Glu Pro Val Ala Ser Ser Pro Glu Arg
 80                  85                  90                  95
```

```
agg aga cgg caa ccc agc cgc gct ttt gcc tgc act ctc cct gga tgc      396
Arg Arg Arg Gln Pro Ser Arg Ala Phe Ala Cys Thr Leu Pro Gly Cys
                100                 105                 110

tgg agg ctg gag gca gtg acg cag caa cag cgc gag gcg act ttg gag      444
Trp Arg Leu Glu Ala Val Thr Gln Gln Gln Arg Glu Ala Thr Leu Glu
            115                 120                 125

cgg cct cat ata gcg acc tcg cct tcc gct gcg cgt cct ccc aga gcc      492
Arg Pro His Ile Ala Thr Ser Pro Ser Ala Ala Arg Pro Pro Arg Ala
        130                 135                 140

caa gaa gcc cgg aac ctg tgg cat cca tct ctg aaa gga gaa gac ggc      540
Gln Glu Ala Arg Asn Leu Trp His Pro Ser Leu Lys Gly Glu Asp Gly
    145                 150                 155

aac cca gcc gag gca cta ctg ggt tgg ggt ctc cac gac cga gct ggt      588
Asn Pro Ala Glu Ala Leu Leu Gly Trp Gly Leu His Asp Arg Ala Gly
160                 165                 170                 175

ctc atc aag tgg cgt cca aca agg ggc tca aac ccg ggt tga ggggttg      637
Leu Ile Lys Trp Arg Pro Thr Arg Gly Ser Asn Pro Gly  *
                180                 185

ctggagcgac ggagaacgtg gaactacact ggaggacacc agagtactct taagcaatcc     697

cttggccaaa accagcaact gatttggata ccatcaagac acctgaaatc ttgtcatgag     757

ccagatactg aggaagagat tttgggaaga acccaaggac cccccagttg cagccatgtc     817

aagactgaca ataaggaaga catcagtccc agcaagcaac attcatcggg cacagccacc     877

catgtggggc cagatcaaga agttgacaca gacggcggaa gaaaatctga agaaagcgga     937

tgaccagcta caatgagtaa tctaatggta gctatgatgg ctgtgctcac cattgccatg     997

agtattcccc cagcacctgc tgaaacaaaa aacattatac ttattgggca tatattcctt    1057

ttccaccagt ttcatggcca gtgacatggt tagacccccc agtggaggta tacactaatg    1117

atagcttttg gatacctggt tctacagatg atagaggccc atctcacccc caaaaggagg    1177

gaacattatg aatatttcgt tgggatt                                        1204


<210> 273
<211> 943
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (356)..(610)
```

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     <400> 273
gagaagggat ggcgggcgct ggctgctgag catgctggca ggcccgggac tctgcgttgc       60

tgccaccctc tcctcagggt cacctccccc tggagccaga ggcaccgtag tcaagagaca      120

acacgaggag cctccactcc gggcagctgt tcgggttcgt ctcagttgcc aaacggaata      180

atttcacact ctgataacct gattgttttt taagccttgt ggtattctta attgcccggt      240

gttagataaa ctgtgattta aagagcacaa acccagatag cagacacaca aaacactggc      300

ttgggaatag caaggagtga cttatttact ttagcaaagc cttttataag gtttt atg       358
                                                             Met
                                                              1

gct gca cta tca gag tgt cac cca gaa gtc act ctg gga ggt gaa cgc        406
Ala Ala Leu Ser Glu Cys His Pro Glu Val Thr Leu Gly Gly Glu Arg
            5                   10                  15

aca ggg cag gac caa ggt agc acc agg cag aca caa gcc tcc ctg tgg        454
Thr Gly Gln Asp Gln Gly Ser Thr Arg Gln Thr Gln Ala Ser Leu Trp
        20                  25                  30

gga gcc tct ctc atc tgt cgg ggg cct gcg ggc agg gga gag gag gtg        502
Gly Ala Ser Leu Ile Cys Arg Gly Pro Ala Gly Arg Gly Glu Glu Val
    35                  40                  45

ccc cta cag gca agc ctg tgg ggg cgg cac cca gac ctc tgg aga cca        550
Pro Leu Gln Ala Ser Leu Trp Gly Arg His Pro Asp Leu Trp Arg Pro
 50                  55                  60                  65

agc acc act gcc acc cag tgc tgg gga gaa ggg atg gag aga atc aaa        598
Ser Thr Thr Ala Thr Gln Cys Trp Gly Glu Gly Met Glu Arg Ile Lys
                70                  75                  80

agc cag cac tag gaa ggctgttgtc tctgcatgac ccatggcggg gcaggtggag        653
Ser Gln His  *
            85

gggaagccgg acacaggaga gctcctgggg ccagacacgc cacctctgcc aggtgagccc      713

acgtcctgag ctgcagcctc aggaacccag ggttcttcca agaactccct tcaccccaca      773

tggtcacttc ccagcctcct gacccacact caggcccagc tccttcccag actgtcatcc      833

tctttctaga aggaaacagg gaccccctgg ggtccgggat ggccctgagc tcccctgtgt      893

gccccacacc ctggcggtct ttgcccccat gtgccctgag tctgatgcct                 943



     <210> 274
     <211> 803
     <212> DNA
     <213> Homo sapiens
```

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<220>
<221> CDS
<222> (27)..(488)

<400> 274
aatttaggtg acactataga agagct atg acg tcg cat gca cgc gta cgt aag       53
                             Met Thr Ser His Ala Arg Val Arg Lys
                              1               5

ctt gga tcc tct aga gcg gcc gct gtc gtt gtt ctg agg aga aac ctt       101
Leu Gly Ser Ser Arg Ala Ala Ala Val Val Val Leu Arg Arg Asn Leu
 10                  15                  20                  25

aca agt gta ata aat gtg cga agg ttt tta atc aaa aag gaa tcc ttg       149
Thr Ser Val Ile Asn Val Arg Arg Phe Leu Ile Lys Lys Glu Ser Leu
                 30                  35                  40

cac aac atc aga gag ttc ata ctg gag aga aac ctt aca agt gta atg       197
His Asn Ile Arg Glu Phe Ile Leu Glu Arg Asn Leu Thr Ser Val Met
             45                  50                  55

aat gtg gca agg ttt tta atc aaa aag caa gcc ttg caa aac atc aga       245
Asn Val Ala Arg Phe Leu Ile Lys Lys Gln Ala Leu Gln Asn Ile Arg
         60                  65                  70

gag ttc ata ctg cag aga aac ctt aca agt gta atg agt gtg gca aag       293
Glu Phe Ile Leu Gln Arg Asn Leu Thr Ser Val Met Ser Val Ala Lys
     75                  80                  85

cct tta ctg gac agt caa cac tta ttc acc atc aag caa tcc atg ggt       341
Pro Leu Leu Asp Ser Gln His Leu Phe Thr Ile Lys Gln Ser Met Gly
 90                  95                 100                 105

gta ggg aaa ctt tac aaa tgt aat gat tgt cac aaa gtc ttc agt aat       389
Val Gly Lys Leu Tyr Lys Cys Asn Asp Cys His Lys Val Phe Ser Asn
                110                 115                 120

gct aca acc att gca aat cat tac aga atc cat att gaa gag aga tct       437
Ala Thr Thr Ile Ala Asn His Tyr Arg Ile His Ile Glu Glu Arg Ser
            125                 130                 135

aca agt gta ata aat gtg gca aat ttt tca gac gtc att cat aac ttg       485
Thr Ser Val Ile Asn Val Ala Asn Phe Ser Asp Val Ile His Asn Leu
        140                 145                 150

tag ttca tcagtgaact catactggag agaaacctta caaatatcat gactgtgaca       542
 *

aggtcttcag tcaagcttca tcctatgcaa aacatagaat tcatacagga gagaaacctc     602

acaagtgtga tgattgtggc aaagccttta cttcatgttc acacctcatt agacatcaga     662

gaattcatac tggacagatg ccttacaaat gtaagggtgg caaggtcttc actctgtggt     722

cattccatgc agaacatcag aaaattcatt tttgagataa ttgttccaaa taaaatgaat     782
```

```
ataaaaaatc aaaaaaaaaa a                                                 803



      <210> 275
      <211> 1078
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (357)..(713)

      <220>
      <221> misc_feature
      <222> (1)...(1078)
      <223> n = a,t,c or g

      <400> 275
acgccccccc actgagacta cagtccagng ncggcgaant cgagaaaaca cagcaacgag      60

gtgaatgaca tgggagacag acctggggtc ttttagggac ggaaagcctc agccaagacc     120

cagactccca gggtcatcaa cctcctcggg tcactaaccc tccccagtgt ctgtctaccc     180

ctaagtccag agaacacgtc ctctctaggc tcgagccgga atcaatatag gctacaaggg     240

catcagttca ggctgcgcgg aggagagaag gaagtgctga tgtggagtcc tccctccccc     300

ttctccttca cccccaagtg tctcccacga ctgccctccc cgacctctag ctgacc         356
atg gca tca gag gca gaa aaa aca ttc cat cgg ttt gct gcg ttt gga       404
Met Ala Ser Glu Ala Glu Lys Thr Phe His Arg Phe Ala Ala Phe Gly
  1               5                  10                  15

gaa tca tca agc agt ggc act gaa atg aac aac aag aac ttc tcc aag       452
Glu Ser Ser Ser Ser Gly Thr Glu Met Asn Asn Lys Asn Phe Ser Lys
            20                  25                  30

ctg tgc aaa gac tgt ggc atc atg gat ggc aag aca gtc acc tcc acg       500
Leu Cys Lys Asp Cys Gly Ile Met Asp Gly Lys Thr Val Thr Ser Thr
        35                  40                  45

gac gtg gac atc gtg ttc agc aaa gtc aag gcc aag aac gcc cga acc       548
Asp Val Asp Ile Val Phe Ser Lys Val Lys Ala Lys Asn Ala Arg Thr
    50                  55                  60

atc acg ttt caa cag ttc aaa gag gca gtg aag gaa ctg ggc cag aag       596
Ile Thr Phe Gln Gln Phe Lys Glu Ala Val Lys Glu Leu Gly Gln Lys
 65                  70                  75                  80

cgc ttc aaa ggg aag agt cca gat gaa gtc ctg gag aac att tat gga       644
Arg Phe Lys Gly Lys Ser Pro Asp Glu Val Leu Glu Asn Ile Tyr Gly
                85                  90                  95

ctc atg gag ggc aaa gac cca gcc acc act ggc gct act ttt ccc tgg       692
Leu Met Glu Gly Lys Asp Pro Ala Thr Thr Gly Ala Thr Phe Pro Trp
```

```
            100                 105                 110

tta cct atg caa gaa acc tga aa gtgatcctag acccctccac ctccccaatc      745
Leu Pro Met Gln Glu Thr  *
        115

ccagctacgg ggaggcggtc ctgcatggtg gttaagatca aggcttttga gtgaaacaga    805

ccaggaattg aatcctgcct ctgcagctta caaactgcac accatctatc tgtttacgaa    865

accactgaaa gcttccttgt ttcatctgtt catgaggata gtattttta ctcacggcag     925

tatgaggatc cattaagatg tatatcaaga gtttttagac cagtgcccgg cacatgtgga    985

tgctctcgtc tcgcctggac agcacacaca ctccaactcc agtaagactc aactcaaata   1045

tatctcttat acaacttcaa gaaaaaaaaa aaa                                1078



     <210> 276
     <211> 724
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (74)..(223)

     <400> 276
aaaaatgaaa catttaccct agtgtctaag tgtctaataa ggaagaactt aaaatgtggg      60

cacctatgta aaa atg tca aaa ttg aaa atg cgg agg ggg cat ctg gaa       109
               Met Ser Lys Leu Lys Met Arg Arg Gly His Leu Glu
               1               5                   10

tca aac tgg tgg cct ctc ggt ctg cag tct tat gct cta acc ctg agc      157
Ser Asn Trp Trp Pro Leu Gly Leu Gln Ser Tyr Ala Leu Thr Leu Ser
        15                  20                  25

tat acc cct tcc tgc tgc tgt ggg ggt caa tta atg cct ttg act tgt      205
Tyr Thr Pro Ser Cys Cys Cys Gly Gly Gln Leu Met Pro Leu Thr Cys
    30                  35                  40

gcg gtc aca ccc aga tga ccagtc acctgtgtgt tgccacttca caatggaagc      259
Ala Val Thr Pro Arg  *
45                  50

tcctaggagc tgccaggtct acctcagtga aaactcattg accttgtgca tagcaagagg    319

cagtccccgc tcctcagata acccccgtgc ctgtgtcttc cctgccttga gtccttagtt    379

atgggcagca ggctggaaaa gcactgccag cagccactag aatggccttg agagtcatcc    439

tccagtaact gtttatggtg ggcacataca agagaaactt tgtgtgactg aggtgtctgt    499
```

```
tctaaaacac ttaatgacag agttgggcct ggctctcctg gtccagtgtt ccattcaggg    559

cagattcagc acaactgcag tctaggacaa aagatgattc tttcaacttt tacttcttca    619

gttaatacaa atgaagaatg ttagagaagg agcaactcca agaaatagtg agaagtgtgt    679

agctgagtag atttcccaaa agcattaata gggccagtgt tacca                    724
```

```
<210> 277
<211> 1007
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119)..(682)

<400> 277
```

```
tttcgtcagt tcgcggcagt tcgcgcggga gcggggcgcc tgggtggatg ggcgcttggg     60

cgcctgggct gccggacggt gggaacggaa gtcgctgtgg gacgctgagg aagccagg      118
atg gcg act ccg agc aag aag acg tca act cca agc ccc cag cct tcc      166
Met Ala Thr Pro Ser Lys Lys Thr Ser Thr Pro Ser Pro Gln Pro Ser
1               5                   10                  15

aag aga gct ctc ccg aga gac cct tcg tcg gag gtc ccg agc aag agg      214
Lys Arg Ala Leu Pro Arg Asp Pro Ser Ser Glu Val Pro Ser Lys Arg
            20                  25                  30

aag aat tcg gcc ccg cag ctg ccg ctg ttg cag tcg tcc ggg cct ttc      262
Lys Asn Ser Ala Pro Gln Leu Pro Leu Leu Gln Ser Ser Gly Pro Phe
        35                  40                  45

gtg gaa ggc tct atc gtc cgc atc tcg atg gag aac ttc cta aca tat      310
Val Glu Gly Ser Ile Val Arg Ile Ser Met Glu Asn Phe Leu Thr Tyr
    50                  55                  60

gat att tgt gaa gta tct cct gga ccc cac ttg aat atg atc gtt gga      358
Asp Ile Cys Glu Val Ser Pro Gly Pro His Leu Asn Met Ile Val Gly
65                  70                  75                  80

gcc aat gga aca ggg aag tcg agc att gtg tgt gcc att tgc ctt ggt      406
Ala Asn Gly Thr Gly Lys Ser Ser Ile Val Cys Ala Ile Cys Leu Gly
                85                  90                  95

tta gct gga aaa cct gct ttc atg gga cga gca gat aag gtt ggg ttt      454
Leu Ala Gly Lys Pro Ala Phe Met Gly Arg Ala Asp Lys Val Gly Phe
            100                 105                 110

ttt gtg aag aga gga tgt tct aga ggc atg gtt gaa att gaa ttg ttc      502
Phe Val Lys Arg Gly Cys Ser Arg Gly Met Val Glu Ile Glu Leu Phe
        115                 120                 125

agg gct tct gga aat ctt gta atc acc cgt gag att gat gtg gca aaa      550
```

```
Arg Ala Ser Gly Asn Leu Val Ile Thr Arg Glu Ile Asp Val Ala Lys
    130                 135                 140

aat cag tcc ttt tgg ttc atc aac aaa aaa tct aca acc cag aaa ata      598
Asn Gln Ser Phe Trp Phe Ile Asn Lys Lys Ser Thr Thr Gln Lys Ile
145                 150                 155                 160

gtg gaa gag aaa gtt gca gcc tta aat att cag tgg gga atc ttt gcc      646
Val Glu Glu Lys Val Ala Ala Leu Asn Ile Gln Trp Gly Ile Phe Ala
                165                 170                 175

agt ttc tcc tca gga caa gtt gga gga att tgc taa actc agcaaattgg      696
Ser Phe Ser Ser Gly Gln Val Gly Gly Ile Cys  *
            180                 185

actcctcgaa gcactggaaa gttcaatggg cccccagaaa ttgcgcaata tcctgtgtac    756

tccaaactgt ggagaagaag aacagtcccg acccctgcgc agagaaactg ctgtctctcg    816

cgaaatggtg tgcccgcttc gaggattata cccccggtgg gagggcttct agcagggccg    876

cacatattcg agctgccacc cacagcacgc tggacaaaag ctcgcgcctc agagacatat    936

tgacgcggag cgcatcacag gcactccact catgcacagg agccctgcgg cgcggaacgg    996

cgcacacacc g                                                        1007



     <210> 278
     <211> 439
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (18)..(131)

     <400> 278
cgacgatttc gtccaaa   atg gcg gca gcg atg gat gtg gat acc ccg agc       50
                     Met Ala Ala Ala Met Asp Val Asp Thr Pro Ser
                       1               5                  10

ggc acc aac agc ggc gcg ggc aag aag cgc ttt gaa gtg aaa aag gtt       98
Gly Thr Asn Ser Gly Ala Gly Lys Lys Arg Phe Glu Val Lys Lys Val
             15                  20                  25

ggg tct cgc cag cgc ctt cct cag gga agc tag agaggcgc ggatctggct      149
Gly Ser Arg Gln Arg Leu Pro Gln Gly Ser  *
         30                  35

ggcaggcccg aggatggtcg aggcgcggag taaagggttt catttcaggg cgttcctggg    209

accgggtacc acgaaaggaa gccgggggc gggtcttaga gttgatcggc gtgacggcgg     269

cccactgttg ggggaagtgt tggtttcgct gtgaggctaa ggggccaatc acagagctgc    329
```

```
ttattgagat acgcggggtt gcgacttggc ggcgggagcc aagcgcttga gctgtcactg      389

gagtggttga gaggtggggg aaggacaggg tatggtggag tggggtgggt                 439
```

<210> 279
<211> 1771
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (24)..(1049)

<400> 279

```
tttcgtcacg ggccttgttc acc    atg tcg gtg ctg gat gcg ctt tgg gag        50
                             Met Ser Val Leu Asp Ala Leu Trp Glu
                              1               5

gat cgg gat gtc cgt ttc gac ctg tcc gcg cag caa atg aaa aca aga        98
Asp Arg Asp Val Arg Phe Asp Leu Ser Ala Gln Gln Met Lys Thr Arg
 10                  15                  20                  25

cct gga gaa gtc ctt att gat tgt tta gat tcc att gaa gac acc aaa       146
Pro Gly Glu Val Leu Ile Asp Cys Leu Asp Ser Ile Glu Asp Thr Lys
                 30                  35                  40

gga aat aat gga gat aga ggt aga ctc ttg gta aca aat tta aga att       194
Gly Asn Asn Gly Asp Arg Gly Arg Leu Leu Val Thr Asn Leu Arg Ile
             45                  50                  55

ctc tgg cac tct ttg gca tta tca aga gtc aat gtt tct gtc ggt tac       242
Leu Trp His Ser Leu Ala Leu Ser Arg Val Asn Val Ser Val Gly Tyr
         60                  65                  70

aat tgc ata ttg aat att aca aca agg act gct aac tct aaa tta cga       290
Asn Cys Ile Leu Asn Ile Thr Thr Arg Thr Ala Asn Ser Lys Leu Arg
     75                  80                  85

ggc caa act gaa gct ctc tat ata cta aca aaa tgt aac agt act cgt       338
Gly Gln Thr Glu Ala Leu Tyr Ile Leu Thr Lys Cys Asn Ser Thr Arg
 90                  95                 100                 105

ttt gaa ttt ata ttt aca aat ttg gtt cct gga agc cct aga ctt ttt       386
Phe Glu Phe Ile Phe Thr Asn Leu Val Pro Gly Ser Pro Arg Leu Phe
                110                 115                 120

act tct gtg atg gca gta cac aga gct tat gaa act tct aaa atg tat       434
Thr Ser Val Met Ala Val His Arg Ala Tyr Glu Thr Ser Lys Met Tyr
            125                 130                 135

cgt gat ttt aaa tta aga agt gca cta att cag aac aag caa cta aga       482
Arg Asp Phe Lys Leu Arg Ser Ala Leu Ile Gln Asn Lys Gln Leu Arg
        140                 145                 150
```

```
ctg ttg cca caa gaa cat gta tat gat aaa ata aat gga gtt tgg aat       530
Leu Leu Pro Gln Glu His Val Tyr Asp Lys Ile Asn Gly Val Trp Asn
    155                 160                 165

tta tcc agt gat cag ggc aat tta gga acc ttt ttt att acc aat gtg       578
Leu Ser Ser Asp Gln Gly Asn Leu Gly Thr Phe Phe Ile Thr Asn Val
170                 175                 180                 185

aga att gtg tgg cat gca aat atg aat gat agt ttt aat gtc agt ata       626
Arg Ile Val Trp His Ala Asn Met Asn Asp Ser Phe Asn Val Ser Ile
                190                 195                 200

cca tat ctg caa att cgt tca ata aag att aga gat tca aaa ttt ggt       674
Pro Tyr Leu Gln Ile Arg Ser Ile Lys Ile Arg Asp Ser Lys Phe Gly
            205                 210                 215

tta gct ctt gtc ata gaa agc tct cag cag agt ggt gga tat gtt ctt       722
Leu Ala Leu Val Ile Glu Ser Ser Gln Gln Ser Gly Gly Tyr Val Leu
        220                 225                 230

ggc ttt aaa ata gat cct gtg gaa aaa cta caa gaa tca gtt aag gaa       770
Gly Phe Lys Ile Asp Pro Val Glu Lys Leu Gln Glu Ser Val Lys Glu
    235                 240                 245

atc aat tca ctt cac aaa gtc tat tct gcc agt ccc ata ttt gga gtt       818
Ile Asn Ser Leu His Lys Val Tyr Ser Ala Ser Pro Ile Phe Gly Val
250                 255                 260                 265

gat tat gag atg gaa gaa aag ccc cag ccg ctc gaa gct ctg aca gtc       866
Asp Tyr Glu Met Glu Glu Lys Pro Gln Pro Leu Glu Ala Leu Thr Val
                270                 275                 280

gaa caa att caa gat gat gta gaa ata gac tct gat ggt cac acg gat       914
Glu Gln Ile Gln Asp Asp Val Glu Ile Asp Ser Asp Gly His Thr Asp
            285                 290                 295

gct ttt gtg gct tat ttt gct gat ggc aat aag caa caa gat cgt gaa       962
Ala Phe Val Ala Tyr Phe Ala Asp Gly Asn Lys Gln Gln Asp Arg Glu
        300                 305                 310

cct gta ttt tca gaa gaa ctg ggg ctt gca ata gag aaa ttg aag gat      1010
Pro Val Phe Ser Glu Glu Leu Gly Leu Ala Ile Glu Lys Leu Lys Asp
    315                 320                 325

gga ttc acc cta cag gga ctt tgg gaa gta atg agt tga ttgaccttga       1059
Gly Phe Thr Leu Gln Gly Leu Trp Glu Val Met Ser  *
330                 335                 340

gttgagatgg atttctatta aagatatctc tagtttaaag atactagtca cctgccataa    1119

gtcatggaat agtttttata tttacagctt ttatatttaa aacttgtaag agttttttta    1179

atgattgagg aaaaagtcat ttagaaaact tcagttttcg gccagcgcgt cgagggaggg    1239

gccagcgaca catggcctag taaccgtccg gccgcggcgc tggcttaagc catggctgag    1299
```

```
ggtagccgga ttcctcaggc ccgggcgctc ctacagcagt gcctgcacgc ccggctgcaa   1359

attcgcccag ccgatgggga cgtcgcggcc cagtgggtgg aggtccaaag aggactggtg   1419

atctacgtgt gctttttcaa gggagctgat aaagaacttc ttcccaaaat ggatctacga   1479

ctctggctcc actgattacc ttaaccatat tacatggaat gatgtaaggg agaaacagaa   1539

gactcttgtt gaacagctcc tgtctttgtt gaacagctcc ccagggcctc ctacccgcaa   1599

actgcttgct aagaatctag ccatacttta tagtattgga gacacattct ccgttcatga   1659

agcaatcgat aaatgtaatg atcttattcg tagcaaagat gattctccaa gttatcttcc   1719

cactaagctg taagtgaaac attaaaacag aacagaaaac aaaaaaaaaa aa           1771



     <210> 280
     <211> 1109
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (162)..(1064)

     <400> 280
gtttgggccc tttggggtgg tacggaacac aacatcgggg ttgccataca ccggaattcc      60

cgggtcgacg atttcgttgc gcgttccgga actggtttcc cggaaggatt atgtctgcgc     120

cctcgatccg accggaagtt gcacgctgag ccgcggacac c    atg cag tcg gat     173
                                                 Met Gln Ser Asp
                                                   1

gat gtt atc tgg gat aca cta gga aac aag caa ttt tgt tcc ttc aaa       221
Asp Val Ile Trp Asp Thr Leu Gly Asn Lys Gln Phe Cys Ser Phe Lys
  5                  10                  15                  20

ata aga acc aag act cag agc ttc tgc cga aat gaa tat agc ctg act       269
Ile Arg Thr Lys Thr Gln Ser Phe Cys Arg Asn Glu Tyr Ser Leu Thr
                 25                  30                  35

gga ctg tgt aat cgg tca tcc tgt ccc ctg gca aat agt cag tat gcc       317
Gly Leu Cys Asn Arg Ser Ser Cys Pro Leu Ala Asn Ser Gln Tyr Ala
             40                  45                  50

act att aaa gaa gag aaa gga cag tgc tac ttg tat atg aag gtt ata       365
Thr Ile Lys Glu Glu Lys Gly Gln Cys Tyr Leu Tyr Met Lys Val Ile
         55                  60                  65

gaa cga gcg gct ttt cct cgg cgt ctc tgg gaa cgg gtc cgg ctt agt       413
Glu Arg Ala Ala Phe Pro Arg Arg Leu Trp Glu Arg Val Arg Leu Ser
     70                  75                  80
```

```
aaa aac tat gag aaa gca ctg gag caa ata gat gaa aat ctg att tac       461
Lys Asn Tyr Glu Lys Ala Leu Glu Gln Ile Asp Glu Asn Leu Ile Tyr
 85                  90                  95                 100

tgg ccc cgt ttc att cga cac aaa tgt aag cag aga ttc acc aag atc       509
Trp Pro Arg Phe Ile Arg His Lys Cys Lys Gln Arg Phe Thr Lys Ile
                105                 110                 115

acc caa tac cta att cga att aga aaa ctt aca cta aag cga cag agg       557
Thr Gln Tyr Leu Ile Arg Ile Arg Lys Leu Thr Leu Lys Arg Gln Arg
            120                 125                 130

aaa ctt gtt cct ttg agt aag aag gtg gag cgt agg gag aaa aga aga       605
Lys Leu Val Pro Leu Ser Lys Lys Val Glu Arg Arg Glu Lys Arg Arg
        135                 140                 145

gag gaa aag gca tta ata gct gct cag ctg gac aat gcc att gag aag       653
Glu Glu Lys Ala Leu Ile Ala Ala Gln Leu Asp Asn Ala Ile Glu Lys
    150                 155                 160

gaa tta ctg gag aga ctg aaa caa gat acg tat ggc gac atc tac aac       701
Glu Leu Leu Glu Arg Leu Lys Gln Asp Thr Tyr Gly Asp Ile Tyr Asn
165                 170                 175                 180

ttc ccc att cat gcc ttc gac aaa gcc ctg gaa caa cag gag gca gag       749
Phe Pro Ile His Ala Phe Asp Lys Ala Leu Glu Gln Gln Glu Ala Glu
                185                 190                 195

agt gac tct tca gat act gag gaa aaa gat gat gat gat gat gat gag       797
Ser Asp Ser Ser Asp Thr Glu Glu Lys Asp Asp Asp Asp Asp Asp Glu
            200                 205                 210

gaa gat gtg ggg aaa aga gaa ttt gtc gaa gat ggt gag gta gat gag       845
Glu Asp Val Gly Lys Arg Glu Phe Val Glu Asp Gly Glu Val Asp Glu
        215                 220                 225

agt gac ata agt gat ttt gag gat atg gat aaa ctg gat gcc agc agt       893
Ser Asp Ile Ser Asp Phe Glu Asp Met Asp Lys Leu Asp Ala Ser Ser
    230                 235                 240

gat gaa gat cag gat ggt aaa tcc tcc agt gag gag gag gaa gaa aag       941
Asp Glu Asp Gln Asp Gly Lys Ser Ser Ser Glu Glu Glu Glu Glu Lys
245                 250                 255                 260

gcc ctt agt gcg aaa cac aaa ggc aaa atg ccc ttg aga gga cca ctg       989
Ala Leu Ser Ala Lys His Lys Gly Lys Met Pro Leu Arg Gly Pro Leu
                265                 270                 275

cag aga aaa cga gcc tat gtg gaa ata gaa tac gag cag gag aca gag      1037
Gln Arg Lys Arg Ala Tyr Val Glu Ile Glu Tyr Glu Gln Glu Thr Glu
            280                 285                 290

ccc gtg gcc aaa gcc aaa acc acg tga tttcc ctttcagtca tttataccca      1089
Pro Val Ala Lys Ala Lys Thr Thr  *
        295                 300

ggactgaaca tgcagaactg                                                1109
```

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<210> 281
<211> 2018
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (36)..(1520)

<220>
<221> misc_feature
<222> (1)...(2018)
<223> n = a,t,c or g

<400> 281
acagctccca agccacaggc agaagcccca cagag atg gag cag aag gaa ggg       53
                                       Met Glu Gln Lys Glu Gly
                                        1               5

aag ctc tct gag gat ggg acc acc gtc tcc cca gct gcg gac aac cct      101
Lys Leu Ser Glu Asp Gly Thr Thr Val Ser Pro Ala Ala Asp Asn Pro
            10                  15                  20

gag atg tca gga ggt gga gcc cct gca gag gag acc aaa ggc aca gct      149
Glu Met Ser Gly Gly Gly Ala Pro Ala Glu Glu Thr Lys Gly Thr Ala
        25                  30                  35

gga aag gcc atc aat gag ggg cct ccc act gag tca gga aag cag gaa      197
Gly Lys Ala Ile Asn Glu Gly Pro Pro Thr Glu Ser Gly Lys Gln Glu
    40                  45                  50

aag gca cca gcc gag gac ggc atg tca gca gaa ctc cag ggg gaa gca      245
Lys Ala Pro Ala Glu Asp Gly Met Ser Ala Glu Leu Gln Gly Glu Ala
55                  60                  65                  70

aat gga tta gat gag gtc aaa gtg gaa tct cag agg gag gct ggt ggg      293
Asn Gly Leu Asp Glu Val Lys Val Glu Ser Gln Arg Glu Ala Gly Gly
                75                  80                  85

aaa gag gat gct gag gct gaa ctt aaa aag gag gat ggt gag aag gaa      341
Lys Glu Asp Ala Glu Ala Glu Leu Lys Lys Glu Asp Gly Glu Lys Glu
            90                  95                  100

gag acc act gtg ggt tct cag gag atg act ggc agg aaa gaa gag acc      389
Glu Thr Thr Val Gly Ser Gln Glu Met Thr Gly Arg Lys Glu Glu Thr
        105                 110                 115

aaa tct gaa ccc aaa gag gct gag gaa aag gag agc acg ctg gcc tct      437
Lys Ser Glu Pro Lys Glu Ala Glu Glu Lys Glu Ser Thr Leu Ala Ser
    120                 125                 130

gag aag cag aag gct gag gag aaa gag gcc aaa cct gaa tct ggg cag      485
Glu Lys Gln Lys Ala Glu Glu Lys Glu Ala Lys Pro Glu Ser Gly Gln
```

```
135                 140                 145                 150

aaa gcc gat gcc aat gac aga gac aag cct gaa cct aag gca aca gtt        533
Lys Ala Asp Ala Asn Asp Arg Asp Lys Pro Glu Pro Lys Ala Thr Val
                155                 160                 165

gag gag gag gac gcc aag aca gcc tct cag gag gag aca ggc cag agg        581
Glu Glu Glu Asp Ala Lys Thr Ala Ser Gln Glu Glu Thr Gly Gln Arg
            170                 175                 180

aaa gag tgc agc act gaa ccc aag gag aag gct act gat gaa gag gcc        629
Lys Glu Cys Ser Thr Glu Pro Lys Glu Lys Ala Thr Asp Glu Glu Ala
        185                 190                 195

aag gct gaa tcg cag aag gct gtt gtg gag gat gag gct aag gct gaa        677
Lys Ala Glu Ser Gln Lys Ala Val Val Glu Asp Glu Ala Lys Ala Glu
    200                 205                 210

ccc aag gag ccc gat ggg aaa gag gag gcc aaa cat ggt gca aaa gag        725
Pro Lys Glu Pro Asp Gly Lys Glu Glu Ala Lys His Gly Ala Lys Glu
215                 220                 225                 230

gag gct gat gca aaa gag gag gcg gag gat gca gag gag gca gag cca        773
Glu Ala Asp Ala Lys Glu Glu Ala Glu Asp Ala Glu Glu Ala Glu Pro
                235                 240                 245

ggc agt ccc agc gaa gag cag gag cag gac gtg gaa aaa gag cca gag        821
Gly Ser Pro Ser Glu Glu Gln Glu Gln Asp Val Glu Lys Glu Pro Glu
            250                 255                 260

gga ggg gca ggg gtg att ccc agc tcc cca gag gag tgg cct gag agc        869
Gly Gly Ala Gly Val Ile Pro Ser Ser Pro Glu Glu Trp Pro Glu Ser
        265                 270                 275

ccc act ggg gag ggg cac aac ctc agc aca gat ggg ctg ggt cca gac        917
Pro Thr Gly Glu Gly His Asn Leu Ser Thr Asp Gly Leu Gly Pro Asp
    280                 285                 290

tgt gta gct tcc gga cag acc agt cct tca gcc agt gag tct tca ccc        965
Cys Val Ala Ser Gly Gln Thr Ser Pro Ser Ala Ser Glu Ser Ser Pro
295                 300                 305                 310

agc gac gtg ccc cag agt ccc cct gag tcc cct tcc tca ggg gag aag       1013
Ser Asp Val Pro Gln Ser Pro Pro Glu Ser Pro Ser Ser Gly Glu Lys
                315                 320                 325

aag gag aag gca cca gag cgc agg gta tca gcc cct gct cgg ccc cgg       1061
Lys Glu Lys Ala Pro Glu Arg Arg Val Ser Ala Pro Ala Arg Pro Arg
            330                 335                 340

ggg ccc ggg gca cag aac cgc aaa gcc atc gtg gac aag ttt ggc ggg       1109
Gly Pro Gly Ala Gln Asn Arg Lys Ala Ile Val Asp Lys Phe Gly Gly
        345                 350                 355

gca gct tcc ggc ccc acg gcc ttg ttc cgc aac act aag gca gcc ggg       1157
Ala Ala Ser Gly Pro Thr Ala Leu Phe Arg Asn Thr Lys Ala Ala Gly
    360                 365                 370
```

```
gca gcc att ggt ggt gtc aag aac atg ctc ttg gag tgg tgc cga gcc       1205
Ala Ala Ile Gly Gly Val Lys Asn Met Leu Leu Glu Trp Cys Arg Ala
375                 380                 385                 390

atg aca aaa aaa tac gag cat gtg gac atc cag aac ttc tcc tcc agc       1253
Met Thr Lys Lys Tyr Glu His Val Asp Ile Gln Asn Phe Ser Ser Ser
                395                 400                 405

tgg agc agt ggt atg gcc ttc tgt gcc ctc atc cac aag ttc ttc cct       1301
Trp Ser Ser Gly Met Ala Phe Cys Ala Leu Ile His Lys Phe Phe Pro
            410                 415                 420

gac gcc ttt gac tac gca gag ctg gat ccc gca aag cgc cgg cac aac       1349
Asp Ala Phe Asp Tyr Ala Glu Leu Asp Pro Ala Lys Arg Arg His Asn
        425                 430                 435

ttc acc ctg gcc ttc tcc aca gca gag aaa ctg gct gac tgt gct cag       1397
Phe Thr Leu Ala Phe Ser Thr Ala Glu Lys Leu Ala Asp Cys Ala Gln
    440                 445                 450

ctg ctg gac gtg gat gac atg gtg cgg ttg gct gtg ccc gac tcc aag       1445
Leu Leu Asp Val Asp Asp Met Val Arg Leu Ala Val Pro Asp Ser Lys
455                 460                 465                 470

tgc gtc tac aca tac atc cag gaa ctg tac cgc agc ctt gtg cag aaa       1493
Cys Val Tyr Thr Tyr Ile Gln Glu Leu Tyr Arg Ser Leu Val Gln Lys
                475                 480                 485

gga ctg gtg aag acc aag aag aag tga ggagg tgactggctc tgtgggcaga       1545
Gly Leu Val Lys Thr Lys Lys Lys  *
            490                 495

gatgggcagg gtgcccagct cagcagccac ggcccggggg ttcccttctg ctccatggag     1605

gcaccagagc caggggctta ggcaagggtg tgtggcgttg gttttaactg cattaaaagt     1665

acttttgtaa aatcctgtct ggccccctca gtgctctctc ccatacttgg ncccaggaac     1725

ctctgcactc tgggataata aactctggcc catagggggat tcctcacctg ctgaggtctc    1785

aataactgcg caaggtgttt gggaaaggac aatggcctgg tcccaccact aaccagctgt     1845

gtgacacata cagttaacct ctctgggccc cagtttacag tctgaaaggg gataatgaga     1905

gttccaacct tatgaaggtg ttgcaagagt taaacgagat aatgaaatgg gcaaaaagct     1965

ttgcccagtc ctgccactca agtgttcagt aagtggtcgc caaaaataaa aaa            2018


<210> 282
<211> 706
<212> DNA
<213> Homo sapiens
```

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     <220>
     <221> CDS
     <222> (39)..(377)

     <400> 282
cgcctccccg ctgaccccgc gatctgaggc tgtcagag    atg act ctg gtt ctg       53
                                             Met Thr Leu Val Leu
                                              1               5

tcc atg aat aga ttc tgc gag ccc att gtc tcg gaa gga gct gct gaa      101
Ser Met Asn Arg Phe Cys Glu Pro Ile Val Ser Glu Gly Ala Ala Glu
                10                  15                  20

att gct ggg tac caa aca cta tgg gag gct gac agc tac gga ggc cca      149
Ile Ala Gly Tyr Gln Thr Leu Trp Glu Ala Asp Ser Tyr Gly Gly Pro
            25                  30                  35

agc ccc cca ggg cca gca caa gct cct ttg cag gga gac cgg gga gct      197
Ser Pro Pro Gly Pro Ala Gln Ala Pro Leu Gln Gly Asp Arg Gly Ala
        40                  45                  50

ggt ccc cca ctg gca gct cca ctt ggt gac ttc ctt tct gtg tat cag      245
Gly Pro Pro Leu Ala Ala Pro Leu Gly Asp Phe Leu Ser Val Tyr Gln
    55                  60                  65

gag cag agc aga gga caa ctt gta gaa gac atg acc att aag aga cat      293
Glu Gln Ser Arg Gly Gln Leu Val Glu Asp Met Thr Ile Lys Arg His
 70                  75                  80                  85

caa ctt cgc aac aaa tat aag aca agg ata caa gga ttc cta tgt gat      341
Gln Leu Arg Asn Lys Tyr Lys Thr Arg Ile Gln Gly Phe Leu Cys Asp
                90                  95                 100

gca gct agg ttt tta tat cct tct aac aaa tgg tga gcag gagacttttt      391
Ala Ala Arg Phe Leu Tyr Pro Ser Asn Lys Trp  *
            105                 110

tggaaataat tagttgtgaa attccatttt tctgacagcc ccttaaattt gaagttattt    451

catttgtagt taaggttatc acatccctgc caattttact agattttttc agagacaagc    511

attcagcatg gcattagtaa tgatggttta aactaggtgc agaactgtcc catgaagaga    571

agaatgatat cagtatttaa ataataaaag aagagacaat gtatggttta tagtgattca    631

ttttaagatt gctgtatttt gattttgtgg tttaaaataa atgcattaag gatcttttaa    691

gttaaaaaaa aaaaa                                                      706



     <210> 283
     <211> 758
     <212> DNA
     <213> Homo sapiens
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     <220>
     <221> CDS
     <222> (539)..(697)

     <400> 283
agattatgtg tcatcatttc ttgcttctta gacatagtgc gtataagaac agtggaaatc      60

aaagtagaaa atttcacact aggatgaaca tactgtattc tctactaggt agcgaagctg     120

agtagctgac ctgtgatatc attaggagtt gagctgaaac tacttaaaac tgctctagcc     180

ccaacccagc tcaactccta atgatatcac aggtcagcta ctcagcttcg ctacctagta     240

gagaatacag tatgttcatc ctagtgtgaa attttctact ttgatttcca ctgttcttat     300

acgcattatg tctaagaagc aagaaatgat gacacataat ctaaagaaga aacaatcgat     360

agaaaaagac cttatggatc acccaagtgt tggaatttag acaaagactt taaaattcca     420

tgaaaaattt tctttatgtt aaagaaaaac gagaggcaga atgattgaga gaatagaaaa     480

tttgagcaga gaaaaaaagt aacaaaatag aaaatctaga actgaaaata tatccgaa       538
atg aat aaa ttg ttt tat ttg tta ttt att ttt gta gaa aca gga tct       586
Met Asn Lys Leu Phe Tyr Leu Leu Phe Ile Phe Val Glu Thr Gly Ser
 1               5                  10                  15

cat ggt gtt gcc cag gtt ggt ctt gaa ctc ctg agc tca aga gat cct       634
His Gly Val Ala Gln Val Gly Leu Glu Leu Leu Ser Ser Arg Asp Pro
             20                  25                  30

cct gcc tct gcc tcc caa gct gct ggg att aca ggc atg aac cac tgt       682
Pro Ala Ser Ala Ser Gln Ala Ala Gly Ile Thr Gly Met Asn His Cys
         35                  40                  45

gcc cag ctg aaa tga ataaattgga taggcttaac aaaatggata caacaaaatg       737
Ala Gln Leu Lys  *
     50

gatacaacag aaaaaaaaaa a                                               758




     <210> 284
     <211> 1482
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (939)..(1475)

     <400> 284
ccagcctgcc ctcttagtcc ctgacagctg cagtgacagc atctgtgatt gcaaagcatg      60

acaatttata tctctcattt catcacacca tctatcagca gacagtcagg ctttaaaaat     120
```

```
caatcccaca ctgactcagt ccccagcaga gatggcctct gacaacagta tccacactgc    180

aggctggaca agggccctat taattttgag actcagccaa atttccttct gaccctaagc    240

tggtgaatcc ctgctccttt gctttggttg gggttggtgt gagctaaggc tgtgatccca    300

tttgctccta tggcctccag gtggcctggg cctccatgaa tgggccacat ggtcatactg    360

aatgcttgat tacactcaga cctagcagtc gtctgggcgc agctggttta tggatcactt    420

tgtcacaatg ttccatcctt ccaggtcccc atccccgcgg tgggaaaaca ttgctttagg    480

cagtgctaga ggacttcagc aggcattggc agcttctgga ttcaggatta gaacaaagaa    540

ggaggagtca cagcaaagat aggaacagaa ggcagagaga acagacagat gggggtgttt    600

gagaaggagg gcctttgaga cctcagggag tgggagacac tggctcgaga ataataataa    660

tggcaatttc tctcatctgt gttttcaggg catggactgg aactcccaat accccctgaca   720

tgggctgagt caacgtggtc atgaacatgt gacaggaggc agcagaagtt gcagagaaga    780

gtgaggcacg tttgaaaaag gctgaaaaat gtttctgtcc aggcaagggt gtgtgctgaa    840

tgactcaagg atttttttggt gcattgaatg aacagcggga cattggacac ctgctgatcc   900

atcaccccgg gcccgggcag gcccgtggat gaagagag    atg gag aag acc agg     953
                                             Met Glu Lys Thr Arg
                                              1               5

cat gag act gtg gag aag cca cac cac cag aaa ccc ctg ccc cat gcg     1001
His Glu Thr Val Glu Lys Pro His His Gln Lys Pro Leu Pro His Ala
                10                  15                  20

ccg tcc agc cca cac ctg tgg atg cac ggg gga ttg cag gca ggg ctc     1049
Pro Ser Ser Pro His Leu Trp Met His Gly Gly Leu Gln Ala Gly Leu
            25                  30                  35

cca ccg tgg act cag gaa cag gca ggg aag ctg ctg cct cac cag gcg     1097
Pro Pro Trp Thr Gln Glu Gln Ala Gly Lys Leu Leu Pro His Gln Ala
        40                  45                  50

aag ggg cca gga ggg gga ggc gga gag gcc cgt cta gcc cct gcg gct     1145
Lys Gly Pro Gly Gly Gly Gly Gly Glu Ala Arg Leu Ala Pro Ala Ala
    55                  60                  65

gtc acc gtg gtg cct cct cac tgg cca gtg cgg tcg cgc ctc agc ttc     1193
Val Thr Val Val Pro Pro His Trp Pro Val Arg Ser Arg Leu Ser Phe
70                  75                  80                  85

gtt aat agg gga ggg ggc cta aga gtt ttc acg tcc agg ctc ggg cag     1241
Val Asn Arg Gly Gly Gly Leu Arg Val Phe Thr Ser Arg Leu Gly Gln
                90                  95                  100

tgg gga ggc agg cag gag tgg ccg ctg gtt ttt cag acc tcc cag gga     1289
Trp Gly Gly Arg Gln Glu Trp Pro Leu Val Phe Gln Thr Ser Gln Gly
            105                 110                 115
```

```
ggc cga gga aat ggc ccg tcc tgg agt ggg cgt ggt tct gtc ttc aga      1337
Gly Arg Gly Asn Gly Pro Ser Trp Ser Gly Arg Gly Ser Val Phe Arg
        120                 125                 130

tgg atg ctg gag ggt tgg gct gcg tgg gac cct ggg ccc tgc tgc ttc      1385
Trp Met Leu Glu Gly Trp Ala Ala Trp Asp Pro Gly Pro Cys Cys Phe
    135                 140                 145

ccg gag gat gcg ctg tcc ggg gct gca cag gtt ggc tgt gtt ttt tgg      1433
Pro Glu Asp Ala Leu Ser Gly Ala Ala Gln Val Gly Cys Val Phe Trp
150                 155                 160                 165

atg ctt gtt att ttt ttt ttt ctt ctc ttc act ctg tca tga aactggc      1482
Met Leu Val Ile Phe Phe Phe Leu Leu Phe Thr Leu Ser  *
                170                 175
```

```
     <210> 285
     <211> 3504
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (392)..(1120)

     <400> 285
caatgttaag tcattgcctt gtggggatac gcctacagat aggtcagact aaatgttgtt      60

ccttttgact taggagctga agttgccctc ctataaaggc cagtcccctc agttaagtct     120

cagacggtat tttgccgact tgattgccat tgtgagcaat cgcttcacac tctgcccttc     180

tgcccgccat cttgctgtct atttactgga cctgtttatg gaccgctatg acatctctat     240

ccagcagctg catttagttg cgctttcctg cctgcttcta gcaagtaaat ttgaagaaaa     300

agaagacagt gtgcctaagc tggagcagct caacagcctg ggttgtatga ctaatatgaa     360

tctagtatta acaaaacaaa atttgctaca t   atg gaa cta tta tta tta gaa     412
                                     Met Glu Leu Leu Leu Leu Glu
                                      1               5

acc ttt cag tgg aac ctc tgc ctt cca aca gcc gcc cat ttc att gag       460
Thr Phe Gln Trp Asn Leu Cys Leu Pro Thr Ala Ala His Phe Ile Glu
        10                  15                  20

tat tat ctc tct gaa gca gta cac gaa aca gat ctt cat gac ggc tgg       508
Tyr Tyr Leu Ser Glu Ala Val His Glu Thr Asp Leu His Asp Gly Trp
    25                  30                  35

cca atg att tgc ttg gaa aag act aaa ctc tac atg gcc aaa tat gca       556
Pro Met Ile Cys Leu Glu Lys Thr Lys Leu Tyr Met Ala Lys Tyr Ala
```

```
40                  45                  50                  55

gat tac ttc ctg gaa gta tct ttg caa gct gct gca tgt gtg gct tct        604
Asp Tyr Phe Leu Glu Val Ser Leu Gln Ala Ala Ala Cys Val Ala Ser
                60                  65                  70

tcg agg att ata ctt cgt ctt tct cca acg tgg cct aca aga cta cat        652
Ser Arg Ile Ile Leu Arg Leu Ser Pro Thr Trp Pro Thr Arg Leu His
            75                  80                  85

cgt ctt act gcc tac tct tgg gat ttc tta gtg cag tgt att gaa cga        700
Arg Leu Thr Ala Tyr Ser Trp Asp Phe Leu Val Gln Cys Ile Glu Arg
        90                  95                  100

ctg ttg atc gct cat gat aat gat gtg aaa gaa gca aac aaa cag aga        748
Leu Leu Ile Ala His Asp Asn Asp Val Lys Glu Ala Asn Lys Gln Arg
    105                 110                 115

ggg caa gca gga cct cag tca gcg caa cta agt gta ttc cag aca gcc        796
Gly Gln Ala Gly Pro Gln Ser Ala Gln Leu Ser Val Phe Gln Thr Ala
120                 125                 130                 135

tcc cag cca tca cgg cca gtt cac ttt cag caa cct cag tat ctc cat        844
Ser Gln Pro Ser Arg Pro Val His Phe Gln Gln Pro Gln Tyr Leu His
            140                 145                 150

cag aca cat cag acc tca ctg cag tat cgc cat cct acg tca gaa caa        892
Gln Thr His Gln Thr Ser Leu Gln Tyr Arg His Pro Thr Ser Glu Gln
        155                 160                 165

cca agc tgt cag cag att gta tcg acc aca cac acc tca tct tac aca        940
Pro Ser Cys Gln Gln Ile Val Ser Thr Thr His Thr Ser Ser Tyr Thr
        170                 175                 180

cta cag aca tgt cct gct ggc ttc caa act agt gtt cag ggc ctt ggg        988
Leu Gln Thr Cys Pro Ala Gly Phe Gln Thr Ser Val Gln Gly Leu Gly
    185                 190                 195

cac atg cag act ggt gtt ggg atg tca ctg gca ata cca gta gaa gtt       1036
His Met Gln Thr Gly Val Gly Met Ser Leu Ala Ile Pro Val Glu Val
200                 205                 210                 215

aag ccc tgt ctg agt gtt tct tac aac cgg agt tat cag ata aat gaa       1084
Lys Pro Cys Leu Ser Val Ser Tyr Asn Arg Ser Tyr Gln Ile Asn Glu
            220                 225                 230

cat tac cct tgt att act cca tgt ttt gaa agg tga ttat ttgtgaagct       1134
His Tyr Pro Cys Ile Thr Pro Cys Phe Glu Arg  *
            235                 240

gataaccgac ccagactgct ttgtgacatg aagctatggg taagcgtttt gtaaacttct     1194

gttcaaaagg aaagggatct aaatgacatc agaactcttc aggtaccagc accaggaaga     1254

ctgaatatcc tttttaatgc accatgaatc ctgggagact aagcaaatta acagtatgtc     1314

aaattctgtt acaacaaatc cctgtatgac aaaaatgttc aagtcctggc tgatggtcca     1374
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aatatttcaa aaatattcag tacaacagaa aatttggaca gacttcaatt tgccattttg 1434

agatttgacc tgtggtagca tctgggccta atgttggctt ctaagtcaaa gactaaatgt 1494

ttatctcatc tatggacttg ccaaacagtc ttttatgaag gaaagttaca gtattaattt 1554

ttgaaaaggt ttttttatt ctgcaatttt ttatttttgt tctacacatg aatttttgac 1614

taagtttaaa ctcatgaatt gttatgctat accaatctgc agtaaaaaaa atttttttag 1674

atgattctat ataacttcgt ctcacaaata gtgtaggtat ctgggtttat atactaaaat 1734

taagggtgga gaagatctta ttttttaaat catggtcata atttttcttt ttttccctaa 1794

gtgatcaaca tcaaattttt agaattaaaa tacatttaac tcagggaatt tgtactactt 1854

ggaaacactt aactgtaatg caacatgcct tgggaatgtt atagtgtgaa ctacctttat 1914

aacataggtt aaaatacgct tgctagggtg tgttttcaaa tgagaacata atatagctca 1974

gaatgaagtg gtagttcctg tgattcataa tacatatgta ggttttgcat atctcagtgc 2034

aatccatgat ttatactcag aatcgacatt cttaaaaagt tatttcaagg gatggcataa 2094

ctgtaagagg tcagtgctag aataaagtcc tgtaggttta ttttggaagg gactgtggcc 2154

agggtagttc tcaggttgtg ctagagcagc actttgttat gtggaagaca ggttttttaa 2214

gcaacctttg aatccagctc tagtcagtct aagcaggcaa aggtaactga tgactaaatt 2274

tcagtagcta ctttcattgg attgacccta caactgccct gggacatttc actgtaccag 2334

tattaactgc aaacagcaat aattgtcatt acagcaaggg cagtttgggg gtaaagcatt 2394

ttggaggaat aaccttaaaa agttaaaaag tcattgtaat aactgataaa ctgtatacat 2454

tgtgctcctt tctgggggaa gaaagatttg gtggagggaa gctttctggt ttaaaaatta 2514

gtaaggtgtg tctttttgtt tttttaaga tagcacttga atagaaggga aaactgcatg 2574

gcagatacgt gactgccaca atatgcatcg aagacaaact tactataaag atgttgtggg 2634

tatgcagcag gagtctcagt aatcaagcca atggcctttg tcaggaaggg aaggggctca 2694

acacagtgat ggactgatcc agatggctcc cggggatgaa tgtgggtggg tagcttctgt 2754

cagtatcaat gcttagagaa atatcctttc cttaaaaaga aaataacttt tatatttaga 2814

gtacataggg catgatgtgg atttattagt ctggtagata aaatgaaaaa ccactcaggt 2874

aagaacactc actcatggca gtttttaagc atgaaaattg ttttctgaaa gtatcatcac 2934

ttttcctttt taaagaaggc tgctaattgg attttggtag ttcttacctc aagaaaactt 2994

gaattatttg ggggaaagta ggctcaaaag agaatatatc tttcacattc acattcagaa 3054

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cccagcaacc tggagtccaa ttttcagtat tttaactacc tcaataatgc tatgaatgta   3114

agatattggg atagagatcc caacttgaaa caacagccag tgcctgtggt aacttaatgt   3174

cttgtcaaat acttttattg attggtttat atgccattct tgttatagaa gaatatgcct   3234

tttaaaaaag cttattaata acactttccc aatttatatt ttaaaaagct aaagaacact   3294

ggattaataa tcttttggga gggtagaata aaataattga ttactattgc tgcatacccg   3354

gggtgggatg gggtggttgg agaaccagaa ctatttttaa aacattaggt ttcaatataa   3414

atacaactca caactgctag ctttgggggg tgggggaaca ttgtttgggt tttgttttgt   3474

ttaatttatt gattagtctt taaagtaggc                                    3504



<210> 286
<211> 650
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (217)..(510)

<400> 286
ccacaccacc atgcccagtc ataccagcat ctgaagcaac aatataaaaa tcactgtggt     60

ttctgggggt aacaccagca aaactgtgta gaagatgtcc tgaggccacc gcctcccagg    120

gaagagccca ggtccctgcc ccagttctac cacagctctc atgcccacag ccctgtctgt    180

ctggacacat tactaggcac agactgctga caggggg atg tcc tgg gcg gtt gac     234
                                        Met Ser Trp Ala Val Asp
                                        1               5

ctg cct gtg tgt caa agg aca cct cac tgc agg gtc caa gac aga gtg      282
Leu Pro Val Cys Gln Arg Thr Pro His Cys Arg Val Gln Asp Arg Val
            10                  15                  20

ctc cac tgt ggc ttc ctg gga agc ccg ctg gtg gga gct cct ggg agc      330
Leu His Cys Gly Phe Leu Gly Ser Pro Leu Val Gly Ala Pro Gly Ser
        25                  30                  35

agg aga cag ctg tgc tct ccc cac tcc tcc ctc cgg cct cag cac cca      378
Arg Arg Gln Leu Cys Ser Pro His Ser Ser Leu Arg Pro Gln His Pro
    40                  45                  50

cag gtg gcc tct gct ctc ttg gag gcg aag ctg ctc ccc tct cct cca      426
Gln Val Ala Ser Ala Leu Leu Glu Ala Lys Leu Leu Pro Ser Pro Pro
55                  60                  65                  70

acc tca ttc tct gcc tgc ttc atc cgg ccc cac aca cac acc ggt aat      474
Thr Ser Phe Ser Ala Cys Phe Ile Arg Pro His Thr His Thr Gly Asn
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                 75                  80                  85

ctg tgt tcc ttt ctg cca tta atc ctc ctc atg taa atat tcccaatact      524
Leu Cys Ser Phe Leu Pro Leu Ile Leu Leu Met  *
             90                  95

ctttcagtcc ccaaagccat aggcccacat ctgcttgtgg atcagaaaca tgctggcaga    584

gcgcggtggg actgctgccc cctggccctt aggagtgggg tctggggcgc cctcagaaca    644

acgaca                                                               650




     <210> 287
     <211> 1619
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (120)..(1619)

     <400> 287
gcggcctcct tgcccgggct tggggcgccg cgctggggaa agccgggggc ccggacacat     60

tggcgtgaga cctgggagta cgttgtgcca aatcattgcc acttgccaca tgagtgtaa     119
atg atg gcg gat gcc aag tat gtc ctc tgc cga tgg gaa aag cga tta      167
Met Met Ala Asp Ala Lys Tyr Val Leu Cys Arg Trp Glu Lys Arg Leu
  1               5                  10                  15

tgg cct gcg aag gtt ttg gcc cga acc gcg act tca aca aaa aat aag      215
Trp Pro Ala Lys Val Leu Ala Arg Thr Ala Thr Ser Thr Lys Asn Lys
             20                  25                  30

aga aga aag gaa tat ttt cta gct gtg caa atc ctc tcc cta gag gaa      263
Arg Arg Lys Glu Tyr Phe Leu Ala Val Gln Ile Leu Ser Leu Glu Glu
         35                  40                  45

aaa att aag gtg aaa agc act gaa gtt gag atc cta gag aag tct caa      311
Lys Ile Lys Val Lys Ser Thr Glu Val Glu Ile Leu Glu Lys Ser Gln
     50                  55                  60

att gaa gcc att gct tcc tcg tta gcc tca cag aat gag gtt cct gcg      359
Ile Glu Ala Ile Ala Ser Ser Leu Ala Ser Gln Asn Glu Val Pro Ala
 65                  70                  75                  80

gca ccc ctg gaa gaa ctg gcc tac aga cgg tcg ctt cgc gtg gct ctg      407
Ala Pro Leu Glu Glu Leu Ala Tyr Arg Arg Ser Leu Arg Val Ala Leu
                 85                  90                  95

gac gtt ctg agc gag ggc tcg att tgg agt caa gaa agc tct gca ggg      455
Asp Val Leu Ser Glu Gly Ser Ile Trp Ser Gln Glu Ser Ser Ala Gly
            100                 105                 110

aca ggt aga gct gac cgg tct ctg cga ggg aag ccc atg gag cat gtc      503
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Thr Gly Arg Ala Asp Arg Ser Leu Arg Gly Lys Pro Met Glu His Val
        115                 120                 125

tcc tcg ccc tgt gat tcg aac tcc tca tct ctt ccc cgc gga gac gtg      551
Ser Ser Pro Cys Asp Ser Asn Ser Ser Ser Leu Pro Arg Gly Asp Val
    130                 135                 140

ttg ggc agt tcc aga cct cac agg agg agg cca tgt gtg caa caa agc      599
Leu Gly Ser Ser Arg Pro His Arg Arg Arg Pro Cys Val Gln Gln Ser
145                 150                 155                 160

ctg tca agt tcg ttc act tgt gaa aag gac ccc gag tgc aaa gtg gac      647
Leu Ser Ser Ser Phe Thr Cys Glu Lys Asp Pro Glu Cys Lys Val Asp
                165                 170                 175

cac aag aag ggg ctc agg aaa agt gaa aac cca aga ggc ccg ttg gtc      695
His Lys Lys Gly Leu Arg Lys Ser Glu Asn Pro Arg Gly Pro Leu Val
            180                 185                 190

ctc cca gct gga ggt ggt gcc caa gat gag agt ggg tcc aga atc cac      743
Leu Pro Ala Gly Gly Gly Ala Gln Asp Glu Ser Gly Ser Arg Ile His
        195                 200                 205

cac aaa aat tgg act ctt gca agt aag agg gga aga aac tca gcg cag      791
His Lys Asn Trp Thr Leu Ala Ser Lys Arg Gly Arg Asn Ser Ala Gln
    210                 215                 220

aag gct agc ttg tgc ctg aat gga tct tcc ctt tca gag gac gac acg      839
Lys Ala Ser Leu Cys Leu Asn Gly Ser Ser Leu Ser Glu Asp Asp Thr
225                 230                 235                 240

gag aga gac atg ggg agc aaa gga ggc agc tgg gca gcc ccg tcc ttg      887
Glu Arg Asp Met Gly Ser Lys Gly Gly Ser Trp Ala Ala Pro Ser Leu
                245                 250                 255

ccc tcc ggg gtc agg gag gac gat ccc tgt gcc aac gct gag gga cac      935
Pro Ser Gly Val Arg Glu Asp Asp Pro Cys Ala Asn Ala Glu Gly His
            260                 265                 270

gac ccc ggt ctg ccg ttg ggc agc ctc act gcg ccc cca gcc cct gag      983
Asp Pro Gly Leu Pro Leu Gly Ser Leu Thr Ala Pro Pro Ala Pro Glu
        275                 280                 285

ccc tcg gcc tgc tca gag cct gga gaa tgc cct gcg aaa aag agg ccg     1031
Pro Ser Ala Cys Ser Glu Pro Gly Glu Cys Pro Ala Lys Lys Arg Pro
    290                 295                 300

cgc ctg gat ggc agc caa agg ccg cct gcc gtg cag ctg gag ccc atg     1079
Arg Leu Asp Gly Ser Gln Arg Pro Pro Ala Val Gln Leu Glu Pro Met
305                 310                 315                 320

gca gca ggg gcc gca cca tcc ccc ggg ccg ggg cca ggg ccc aga gag     1127
Ala Ala Gly Ala Ala Pro Ser Pro Gly Pro Gly Pro Gly Pro Arg Glu
                325                 330                 335

tct gtg acc ccg cgc agc acc gcc agg ctg ggc ccg cct ccc tcc cac     1175
Ser Val Thr Pro Arg Ser Thr Ala Arg Leu Gly Pro Pro Pro Ser His
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            340                 345                 350

gcc tct gcg gat gca acc aga tgt ctt cct tgc ccg gat tcc cag aag      1223
Ala Ser Ala Asp Ala Thr Arg Cys Leu Pro Cys Pro Asp Ser Gln Lys
        355                 360                 365

ctg gag aaa gag tgc cag tct tcc gaa gag tcc atg ggg tct aat tcc      1271
Leu Glu Lys Glu Cys Gln Ser Ser Glu Glu Ser Met Gly Ser Asn Ser
    370                 375                 380

atg cgt tct atc ctg gag gaa gac gag gaa gac gag gag cca cca aga      1319
Met Arg Ser Ile Leu Glu Glu Asp Glu Glu Asp Glu Glu Pro Pro Arg
385                 390                 395                 400

gtc ctt tta tac cac gaa cca cgt tcg ttt gaa gta gga atg cta gtc      1367
Val Leu Leu Tyr His Glu Pro Arg Ser Phe Glu Val Gly Met Leu Val
                405                 410                 415

tgg cat aaa cat aaa aaa tac ccc ttc tgg cca gca gtg gtc aaa agc      1415
Trp His Lys His Lys Lys Tyr Pro Phe Trp Pro Ala Val Val Lys Ser
            420                 425                 430

gtc agg cag aga gat aag aaa gca agt gtg cta tac atc gaa gga cac      1463
Val Arg Gln Arg Asp Lys Lys Ala Ser Val Leu Tyr Ile Glu Gly His
        435                 440                 445

atg aac ccg aaa atg aaa ggt ttc aca gtg tct ctt aaa agt tta aag      1511
Met Asn Pro Lys Met Lys Gly Phe Thr Val Ser Leu Lys Ser Leu Lys
    450                 455                 460

cac ttt gat tgt aaa gag aaa cag acg ctt ctg aat caa gcc agg gag      1559
His Phe Asp Cys Lys Glu Lys Gln Thr Leu Leu Asn Gln Ala Arg Glu
465                 470                 475                 480

gac ttc aac cag gac atc ggc tgg tgt gct ccc tca tca ccg act aca      1607
Asp Phe Asn Gln Asp Ile Gly Trp Cys Ala Pro Ser Ser Pro Thr Thr
                485                 490                 495

ggg tcc ggt tag                                                      1619
Gly Ser Gly  *
            500



<210> 288
<211> 713
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (202)..(435)

<400> 288
gattatcaga ataatattta ttgatatgct cggtgctacc ttgttaattc tgcatgacat      60
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ggtctccatg gctgaggtat ttagggtggg accagccggg tgccggccgg ggctcccaca 120

ggaagccatg tggcctcagc cgcggcgggg ggcccgggtg ggggacgtgg ttattgcgtt 180

gggccccttc actcctcata c atg ggc cac gcg ctg gcg tgc act cac gca 231
Met Gly His Ala Leu Ala Cys Thr His Ala
1 5 10

ctc gcc cgc ctg ctc aca ctc aca cac tcc cac tca agc tgg cac cac 279
Leu Ala Arg Leu Leu Thr Leu Thr His Ser His Ser Ser Trp His His
15 20 25

acc ctc tgt gca cac gca cac acg tgc aca ctc gta cat aca cac ccg 327
Thr Leu Cys Ala His Ala His Thr Cys Thr Leu Val His Thr His Pro
30 35 40

ctc gct cac gct cac ctc tgc tca tgc ccg ttc aca cac aca cca tcc 375
Leu Ala His Ala His Leu Cys Ser Cys Pro Phe Thr His Thr Pro Ser
45 50 55

tgc ttt aaa ccc atc ctg tct cct gat gat aaa tat gct tgt tcg gta 423
Cys Phe Lys Pro Ile Leu Ser Pro Asp Asp Lys Tyr Ala Cys Ser Val
60 65 70

cag cag tct tag taa aataaaatgt ctgtcaggcg acaaggagaa agtgcacgtt 478
Gln Gln Ser *
75

gacctttgac ccgagggtgg acctcggtcc ctcccacccg agggcatcag gtccctgcag 538

ggggtgaccc ctgagcatgt gaccccatgg gcgtggccac cccactggtg ggactggccc 598

caccttcctc ttccctggct ctgggctggg ggagctgggc tgggggagtt gggctgtctc 658

gccacagccc ggggccagga tgaaacggac taaaaaaata aactcttcac ctcag 713

<210> 289
<211> 975
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (393)..(935)

<400> 289
aaatctcgtg tctttgtctc gctgcagcgg gtgctgcagg tttggccttc acttttctgc 60

gtcctcttac tcctagaggc ccagcctctg tggcgctgtg atctggttat cgggagattc 120

acagctaaga cgccaggatc ccccggaagc ctagaaatgc tctgtgttct cgttttgccc 180

aagacctttg gctagagcag aacataaaag attctttcca aaaagtgaca ctgagcagat 240

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atggaaaata tggacataag aatttacagt taagaaaagg ctgtaaaagt gtggatgagt     300

gtaagggaca ccaaggaggt tataatggac ttaaccaatg tttgaaaatt accacaagca     360

aaatatttca atgtaataaa tatgtaaaag tc  atg cat aaa ttt tca aat tca      413
                                     Met His Lys Phe Ser Asn Ser
                                      1               5

aat aga cac aag ata aga cat act gaa aat aaa cat ttc aga tgt aaa       461
Asn Arg His Lys Ile Arg His Thr Glu Asn Lys His Phe Arg Cys Lys
        10                  15                  20

gaa tgt gac aaa tca ctt tgc atg ctt tca cgc cta act caa cat aaa       509
Glu Cys Asp Lys Ser Leu Cys Met Leu Ser Arg Leu Thr Gln His Lys
    25                  30                  35

aaa att cat act aga gag aat ttc tac aaa tgt gaa gag tgt gga aaa       557
Lys Ile His Thr Arg Glu Asn Phe Tyr Lys Cys Glu Glu Cys Gly Lys
40                  45                  50                  55

acc ttt aac tgg tcc aca aac ctt tct aaa cct aag aaa att cat act       605
Thr Phe Asn Trp Ser Thr Asn Leu Ser Lys Pro Lys Lys Ile His Thr
                60                  65                  70

gga gaa aaa ccc tac aaa tgt gaa gta tgt gga aaa gcc ttt cac caa       653
Gly Glu Lys Pro Tyr Lys Cys Glu Val Cys Gly Lys Ala Phe His Gln
            75                  80                  85

tcc tca atc ctt act aaa cat aag ata att cgt act gga gaa aaa ccc       701
Ser Ser Ile Leu Thr Lys His Lys Ile Ile Arg Thr Gly Glu Lys Pro
        90                  95                  100

tat aaa tgt gca cac tgt ggc aaa gcc ttt aaa cag tcc tca cac ctt       749
Tyr Lys Cys Ala His Cys Gly Lys Ala Phe Lys Gln Ser Ser His Leu
    105                 110                 115

act aga cat aag ata att cat act gaa gag aaa ccc tac aaa tgt gaa       797
Thr Arg His Lys Ile Ile His Thr Glu Glu Lys Pro Tyr Lys Cys Glu
120                 125                 130                 135

caa tgt ggc aag gtc ttt aag cag tcc cca acc ctt act aaa cat cag       845
Gln Cys Gly Lys Val Phe Lys Gln Ser Pro Thr Leu Thr Lys His Gln
                140                 145                 150

ata att tat act gga ggt cga cgc gac cgc gaa ttc gga tcc tcg aga       893
Ile Ile Tyr Thr Gly Gly Arg Arg Asp Arg Glu Phe Gly Ser Ser Arg
            155                 160                 165

gat ctc ttt ttt tgg gtt tgg tgg ggt atc ttc gtc atg taa tagggcg       942
Asp Leu Phe Phe Trp Val Trp Trp Gly Ile Phe Val Met  *
        170                 175                 180

ttctatcatc gccttcaagg ggggggggcg ggg                                  975
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<210> 290
<211> 1336
<212> DNA
<213> Homo sapiens

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<400> 290
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cggcagcagc ctgccagcct gcccgaggag tgctgggacc agcgcgctgc acgccgactg     120

gcacg atg gcc tcg tct cag ggg aaa aac gag ctg aaa tta gcc gac         167
      Met Ala Ser Ser Gln Gly Lys Asn Glu Leu Lys Leu Ala Asp
      1               5                   10

tgg atg gca act ctg ccg gag agc atg cac agc atc ccc ctc acc aat       215
Trp Met Ala Thr Leu Pro Glu Ser Met His Ser Ile Pro Leu Thr Asn
15                  20                  25                  30

tta gcc att cca ggg tct cat gat tcc ttc agc ttc tac att gat gaa       263
Leu Ala Ile Pro Gly Ser His Asp Ser Phe Ser Phe Tyr Ile Asp Glu
                35                  40                  45

gcc tct cca gta ggt cct gag cag cca gaa act gtc cag aat ttt gtc       311
Ala Ser Pro Val Gly Pro Glu Gln Pro Glu Thr Val Gln Asn Phe Val
            50                  55                  60

tct gtg ttt gga act gtg gcc aaa aag ctc atg cgg aaa tgg tta gcc       359
Ser Val Phe Gly Thr Val Ala Lys Lys Leu Met Arg Lys Trp Leu Ala
        65                  70                  75

act cag aca atg aat ttt act ggc cag cta gga gct gga att cgt tat       407
Thr Gln Thr Met Asn Phe Thr Gly Gln Leu Gly Ala Gly Ile Arg Tyr
    80                  85                  90

ttt gat ctt cga att tcc acc aag ccc aga gac ccc gac aat gaa ctc       455
Phe Asp Leu Arg Ile Ser Thr Lys Pro Arg Asp Pro Asp Asn Glu Leu
95                  100                 105                 110

tat ttt gct cat ggt ttg ttc agt gcc aaa gtc aat gaa ggc ctt gag       503
Tyr Phe Ala His Gly Leu Phe Ser Ala Lys Val Asn Glu Gly Leu Glu
                115                 120                 125

gag atc aat gca ttc ctc aca gat cac cat aag gag gta gtg ttc ttg       551
Glu Ile Asn Ala Phe Leu Thr Asp His His Lys Glu Val Val Phe Leu
            130                 135                 140

gac ttc aac cac ttc tat ggg atg cag aaa tat cac cat gaa aaa ctg       599
Asp Phe Asn His Phe Tyr Gly Met Gln Lys Tyr His His Glu Lys Leu
        145                 150                 155

gtc caa atg ctg aaa gac atc tat gga aat aaa atg tgc cca gcg att       647
Val Gln Met Leu Lys Asp Ile Tyr Gly Asn Lys Met Cys Pro Ala Ile
```

```
    160                 165                 170

ttt gcc cag gaa gtt agt tta aag tac ctg tgg gag aag gac tat caa       695
Phe Ala Gln Glu Val Ser Leu Lys Tyr Leu Trp Glu Lys Asp Tyr Gln
175                 180                 185                 190

gtg ctg gtc ttc tac cat agt cca gtg gct ctg gaa gtg ccc ttt ctc       743
Val Leu Val Phe Tyr His Ser Pro Val Ala Leu Glu Val Pro Phe Leu
                195                 200                 205

tgg cct ggg cag atg atg cca gca ccc tgg gcc aac acc aca gac ccc       791
Trp Pro Gly Gln Met Met Pro Ala Pro Trp Ala Asn Thr Thr Asp Pro
            210                 215                 220

gag aaa ctg atc cag ttt ctt caa gca tcc atc act gag aga aga aag       839
Glu Lys Leu Ile Gln Phe Leu Gln Ala Ser Ile Thr Glu Arg Arg Lys
        225                 230                 235

aag gga tcg ttt ttt ata tct cag gtg gtg ctg acc ccc aaa gct agc       887
Lys Gly Ser Phe Phe Ile Ser Gln Val Val Leu Thr Pro Lys Ala Ser
    240                 245                 250

act gtg gtc aaa ggg gtg gca agt ggc ctc aga gaa aca atc aca gaa       935
Thr Val Val Lys Gly Val Ala Ser Gly Leu Arg Glu Thr Ile Thr Glu
255                 260                 265                 270

aga gct ctt cct gcc atg atg cag tgg gtc cgc acg cag aag cca gga       983
Arg Ala Leu Pro Ala Met Met Gln Trp Val Arg Thr Gln Lys Pro Gly
                275                 280                 285

gag agt ggc atc aat att gtc act gcc gat ttt gta gaa ctt ggt gac      1031
Glu Ser Gly Ile Asn Ile Val Thr Ala Asp Phe Val Glu Leu Gly Asp
            290                 295                 300

ttt atc agc act gtc ata aag ctc aac tat gtc ttt gat gaa gga gaa      1079
Phe Ile Ser Thr Val Ile Lys Leu Asn Tyr Val Phe Asp Glu Gly Glu
        305                 310                 315

gcc aac act tga tag cactacttgg agtttccatg aataagatgg agaaagctca      1134
Ala Asn Thr  *
    320

ttgtattagg gcatactatc tgtaaacact ctgatcttcc tattccactg agtctctgaa    1194

gggaataggg ctggtagtgg gtgggaaaag ggaaaaact gtttcttcag tgattacaat     1254

catactcttc attactataa atatttcatt tcccatttga tgagcaaaat ctacttctag    1314

tgttaggaat aaaaaaaaaa aa                                             1336


<210> 291
<211> 3764
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> (148)..(3207)

<400> 291
caagtgttct tcttgagcaa tgaccttgac ctgtatgatg aagagaccga tttatccatt      60

caatgtcgag ccctcaacat cgcagaggac ttgggccaga tccagtacat cttctccgat     120

aagacgggga ccctgacaga gaacaag    atg gtg ttc cga cgt tgc acc atc     171
                                 Met Val Phe Arg Arg Cys Thr Ile
                                  1               5

atg ggc agc gag tat tct cac caa gaa aat gct aag cga ctg gag acc      219
Met Gly Ser Glu Tyr Ser His Gln Glu Asn Ala Lys Arg Leu Glu Thr
    10                  15                  20

cca aag gag ctg gac tca gat ggt gaa gag tgg acc caa tac caa tgc      267
Pro Lys Glu Leu Asp Ser Asp Gly Glu Glu Trp Thr Gln Tyr Gln Cys
25                  30                  35                  40

ctg tcc ttc tcg gct aga tgg gcc cag gat cca gca act atg aga agc      315
Leu Ser Phe Ser Ala Arg Trp Ala Gln Asp Pro Ala Thr Met Arg Ser
                45                  50                  55

caa aaa ggt gct cag cct ctg agg agg agc cag agt gcc cgg gtg ccc      363
Gln Lys Gly Ala Gln Pro Leu Arg Arg Ser Gln Ser Ala Arg Val Pro
            60                  65                  70

atc cag ggc cac tac cgg caa agg tct atg ggg cac cgt gaa agc tca      411
Ile Gln Gly His Tyr Arg Gln Arg Ser Met Gly His Arg Glu Ser Ser
        75                  80                  85

cag cct cct gtg gcc ttc agc agc tcc ata gaa aaa gat gta act cca      459
Gln Pro Pro Val Ala Phe Ser Ser Ser Ile Glu Lys Asp Val Thr Pro
    90                  95                  100

gat aaa aac cta ctg acc aag gtt cga gat gct gcc ctg tgg ttg gag      507
Asp Lys Asn Leu Leu Thr Lys Val Arg Asp Ala Ala Leu Trp Leu Glu
105                 110                 115                 120

acc ttg tca gac agc aga cct gcc aag gct tcc ctc tcc acc acc tcc      555
Thr Leu Ser Asp Ser Arg Pro Ala Lys Ala Ser Leu Ser Thr Thr Ser
                125                 130                 135

tcc att gct gat ttc ttc ctt gcc tta acc atc tgc aac tct gtc atg      603
Ser Ile Ala Asp Phe Phe Leu Ala Leu Thr Ile Cys Asn Ser Val Met
            140                 145                 150

gtg tcc aca acc acc gag ccc agg cag agg gtc acc atc aaa ccc tca      651
Val Ser Thr Thr Thr Glu Pro Arg Gln Arg Val Thr Ile Lys Pro Ser
        155                 160                 165

agc aag gct ctg ggg acg tcc ctg gag aag att cag cag ctc ttc cag      699
Ser Lys Ala Leu Gly Thr Ser Leu Glu Lys Ile Gln Gln Leu Phe Gln
    170                 175                 180
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aag ttg aag cta ttg agc ctc agc cag tca ttc tca tcc act gca ccc       747
Lys Leu Lys Leu Leu Ser Leu Ser Gln Ser Phe Ser Ser Thr Ala Pro
185                 190                 195                 200

tct gac aca gac ctc ggg gag agc tta ggg gcc aac gtg gcc acc aca       795
Ser Asp Thr Asp Leu Gly Glu Ser Leu Gly Ala Asn Val Ala Thr Thr
                205                 210                 215

gac tcg gat gag aga gat gat gca tct gtg tgc agt gga ggt gac tcc       843
Asp Ser Asp Glu Arg Asp Asp Ala Ser Val Cys Ser Gly Gly Asp Ser
            220                 225                 230

act gat gac ggt ggc tac agg agc agc atg tgg gac cag ggc gac atc       891
Thr Asp Asp Gly Gly Tyr Arg Ser Ser Met Trp Asp Gln Gly Asp Ile
        235                 240                 245

ctg gag tct ggg tca ggc act tcc ttg gag gag gca ttg gag gcc cca       939
Leu Glu Ser Gly Ser Gly Thr Ser Leu Glu Glu Ala Leu Glu Ala Pro
    250                 255                 260

gcc aca gac ctg gcc agg cct gag ttc tgt tac gag gct gag agc cct       987
Ala Thr Asp Leu Ala Arg Pro Glu Phe Cys Tyr Glu Ala Glu Ser Pro
265                 270                 275                 280

gat gag gcc gcc ctg gtg cac gct gcc cat gcc tac agc ttc aca cta      1035
Asp Glu Ala Ala Leu Val His Ala Ala His Ala Tyr Ser Phe Thr Leu
                285                 290                 295

gtg tcc cgg aca cct gag cag gtg act gtg cgc ctg ccc cag ggc acc      1083
Val Ser Arg Thr Pro Glu Gln Val Thr Val Arg Leu Pro Gln Gly Thr
            300                 305                 310

tgc ctc acc ttc agc ctc ctc tgc acc ctg ggc ttt gac tct gtc agg      1131
Cys Leu Thr Phe Ser Leu Leu Cys Thr Leu Gly Phe Asp Ser Val Arg
        315                 320                 325

aag aga atg tct gtg gtt gtg agg cac cca ctg act ggc gag att gtt      1179
Lys Arg Met Ser Val Val Val Arg His Pro Leu Thr Gly Glu Ile Val
    330                 335                 340

gtc tac acc aag ggt gct gac tcg gtc atc atg gac ctg ctg gaa gac      1227
Val Tyr Thr Lys Gly Ala Asp Ser Val Ile Met Asp Leu Leu Glu Asp
345                 350                 355                 360

cca gcc tgc gta cct gac att aat atg gaa aag aag ctg aga aaa atc      1275
Pro Ala Cys Val Pro Asp Ile Asn Met Glu Lys Lys Leu Arg Lys Ile
                365                 370                 375

cga gcc cgg acc caa aag cat cta gac ttg tat gca aga gat ggc ctg      1323
Arg Ala Arg Thr Gln Lys His Leu Asp Leu Tyr Ala Arg Asp Gly Leu
            380                 385                 390

cgc aca cta tgc att gcc aag aag gtt gta agc gaa gag gac ttc cgg      1371
Arg Thr Leu Cys Ile Ala Lys Lys Val Val Ser Glu Glu Asp Phe Arg
        395                 400                 405
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aga tgg gcc agt ttc cgg cgt gag gct gag gca tcc ctc gac aac cga      1419
Arg Trp Ala Ser Phe Arg Arg Glu Ala Glu Ala Ser Leu Asp Asn Arg
    410                 415                 420

gat gag ctt ctc atg gaa act gca cag cat ctg gag aat caa ctc acc      1467
Asp Glu Leu Leu Met Glu Thr Ala Gln His Leu Glu Asn Gln Leu Thr
425                 430                 435                 440

tta ctt gga gcc act ggg atc gaa gac cgg ctg cag gaa gga gtt cca      1515
Leu Leu Gly Ala Thr Gly Ile Glu Asp Arg Leu Gln Glu Gly Val Pro
                445                 450                 455

gat acg att gcc act ctg cgg gag gct ggg atc cag ctc tgg gtc ctg      1563
Asp Thr Ile Ala Thr Leu Arg Glu Ala Gly Ile Gln Leu Trp Val Leu
            460                 465                 470

act gga gat aag cag gag aca gcg gtc aac att gcc cat tcc tgc aga      1611
Thr Gly Asp Lys Gln Glu Thr Ala Val Asn Ile Ala His Ser Cys Arg
        475                 480                 485

ctg tta aat cag acc gac act gtt tat acc atc aat aca gag aat cag      1659
Leu Leu Asn Gln Thr Asp Thr Val Tyr Thr Ile Asn Thr Glu Asn Gln
    490                 495                 500

gag acc tgt gaa tcc atc ctc aat tgt gca ttg gaa gag cta aag caa      1707
Glu Thr Cys Glu Ser Ile Leu Asn Cys Ala Leu Glu Glu Leu Lys Gln
505                 510                 515                 520

ttt cgt gaa cta cag aag cca gac cgc aag ctc ttt gga ttc cgc tta      1755
Phe Arg Glu Leu Gln Lys Pro Asp Arg Lys Leu Phe Gly Phe Arg Leu
                525                 530                 535

cct tcc aag aca cca tcc atc acc tca gaa gct gtg gtt cca gaa gct      1803
Pro Ser Lys Thr Pro Ser Ile Thr Ser Glu Ala Val Val Pro Glu Ala
            540                 545                 550

gga ttg gtc atc gat ggg aag aca ttg aat gcc atc ttc cag gga aag      1851
Gly Leu Val Ile Asp Gly Lys Thr Leu Asn Ala Ile Phe Gln Gly Lys
        555                 560                 565

cta gag aag aag ttt ctg gaa ttg acc cag tat tgt cgg tcc gtc ctg      1899
Leu Glu Lys Lys Phe Leu Glu Leu Thr Gln Tyr Cys Arg Ser Val Leu
    570                 575                 580

tgc tgc cgc tcc acg cca ctc cag aag agt atg ata gtc aag ctg gtg      1947
Cys Cys Arg Ser Thr Pro Leu Gln Lys Ser Met Ile Val Lys Leu Val
585                 590                 595                 600

cga gac aag ttg cgc gtc atg acc ctt tcc ata ggt gat gga gca aat      1995
Arg Asp Lys Leu Arg Val Met Thr Leu Ser Ile Gly Asp Gly Ala Asn
                605                 610                 615

gat gta agc atg att caa gct gct gat att gga att gga ata tct gga      2043
Asp Val Ser Met Ile Gln Ala Ala Asp Ile Gly Ile Gly Ile Ser Gly
            620                 625                 630

cag gaa ggc atg cag gct gtc atg tcc agc gac ttt gcc atc acc cgc      2091
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Gln Glu Gly Met Gln Ala Val Met Ser Ser Asp Phe Ala Ile Thr Arg
        635                 640                 645

ttt aag cat ctc aag aag ttg ctg ctc gtg cat ggc cac tgg tgt tac      2139
Phe Lys His Leu Lys Lys Leu Leu Leu Val His Gly His Trp Cys Tyr
    650                 655                 660

tcg cgc ctg gcc agg atg gtg gtg tac tac ctc tac aag aac gtg tgc      2187
Ser Arg Leu Ala Arg Met Val Val Tyr Tyr Leu Tyr Lys Asn Val Cys
665                 670                 675                 680

tac gtc aac ctg ctc ttc tgg tat cag ttc ttc tgt ggt ttc tcc agc      2235
Tyr Val Asn Leu Leu Phe Trp Tyr Gln Phe Phe Cys Gly Phe Ser Ser
                685                 690                 695

tcc acc atg att gat tac tgg cag atg ata ttc ttc aat ctc ttc ttt      2283
Ser Thr Met Ile Asp Tyr Trp Gln Met Ile Phe Phe Asn Leu Phe Phe
            700                 705                 710

acc tcc ttg cct cct ctt gtc ttt gga gtc ctt gac aaa gac atc tct      2331
Thr Ser Leu Pro Pro Leu Val Phe Gly Val Leu Asp Lys Asp Ile Ser
        715                 720                 725

gca gaa aca ctc ctg gca ttg cct gag cta tac aag agt ggc cag aac      2379
Ala Glu Thr Leu Leu Ala Leu Pro Glu Leu Tyr Lys Ser Gly Gln Asn
    730                 735                 740

tct gag tgc tat aac ctg tcg act ttc tgg att tct atg gtg gat gca      2427
Ser Glu Cys Tyr Asn Leu Ser Thr Phe Trp Ile Ser Met Val Asp Ala
745                 750                 755                 760

ttc tac cag agc ctc atc tgt ttc ttt atc cct tac ctg gcc tat aag      2475
Phe Tyr Gln Ser Leu Ile Cys Phe Phe Ile Pro Tyr Leu Ala Tyr Lys
                765                 770                 775

ggc tct gat ata gat gtc ttt acc ttt ggg aca cca atc aac acc atc      2523
Gly Ser Asp Ile Asp Val Phe Thr Phe Gly Thr Pro Ile Asn Thr Ile
            780                 785                 790

tcc ctc acc aca atc ctt ttg cac cag gca atg gaa atg aag aca tgg      2571
Ser Leu Thr Thr Ile Leu Leu His Gln Ala Met Glu Met Lys Thr Trp
        795                 800                 805

acc att ttc cac gga gtc gtg ctc ctc ggc agc ttc ctg atg tac ttt      2619
Thr Ile Phe His Gly Val Val Leu Leu Gly Ser Phe Leu Met Tyr Phe
    810                 815                 820

ctg gta tcc ctc ctg tac aat gcc acc tgc gtc atc tgc aac agc ccc      2667
Leu Val Ser Leu Leu Tyr Asn Ala Thr Cys Val Ile Cys Asn Ser Pro
825                 830                 835                 840

acc aat ccc tat tgg gtg atg gaa ggc cag ctc tca aac ccc act ttc      2715
Thr Asn Pro Tyr Trp Val Met Glu Gly Gln Leu Ser Asn Pro Thr Phe
                845                 850                 855

tac ctc gtc tgc ttt ctc aca cca gtt gtt gct ctt ctc cca aga tac      2763
Tyr Leu Val Cys Phe Leu Thr Pro Val Val Ala Leu Leu Pro Arg Tyr
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            860                 865                 870

ttt ttc ctg tct ctg caa gga act tgt ggg aag tct cta atc tca aaa      2811
Phe Phe Leu Ser Leu Gln Gly Thr Cys Gly Lys Ser Leu Ile Ser Lys
        875                 880                 885

gct cag aaa att gac aaa ctc ccc cca gac aaa aga aac ctg gaa atc      2859
Ala Gln Lys Ile Asp Lys Leu Pro Pro Asp Lys Arg Asn Leu Glu Ile
    890                 895                 900

cag agt tgg aga agc aga cag agg cct gcc cct gtc ccc gaa gtg gct      2907
Gln Ser Trp Arg Ser Arg Gln Arg Pro Ala Pro Val Pro Glu Val Ala
905                 910                 915                 920

cga cca act cac cac cca gtg tca tct atc aca gga cag gac ttc agt      2955
Arg Pro Thr His His Pro Val Ser Ser Ile Thr Gly Gln Asp Phe Ser
                925                 930                 935

gcc agc acc cca aag agc tct aac cct ccc aag agg aag cat gtg gaa      3003
Ala Ser Thr Pro Lys Ser Ser Asn Pro Pro Lys Arg Lys His Val Glu
            940                 945                 950

gag tca gta ctc cac gaa cag aga tgt ggc acg gag tgc atg agg gat      3051
Glu Ser Val Leu His Glu Gln Arg Cys Gly Thr Glu Cys Met Arg Asp
        955                 960                 965

gac tca tgc tca ggg gac tcc tca gct caa ctc tca tcc ggg gag cac      3099
Asp Ser Cys Ser Gly Asp Ser Ser Ala Gln Leu Ser Ser Gly Glu His
    970                 975                 980

ctg ctg gga cct aac agg ata atg gcc tac tca aga gga cag act gat      3147
Leu Leu Gly Pro Asn Arg Ile Met Ala Tyr Ser Arg Gly Gln Thr Asp
985                 990                 995                1000

atg tgc cgg tgc tca aag agg agc agc cat cgc cga tcc cag agt tca      3195
Met Cys Arg Cys Ser Lys Arg Ser Ser His Arg Arg Ser Gln Ser Ser
               1005                1010                1015

ctg acc ata tga gga gctgcagaaa tctgtacaaa ctcaacagag gccacctagt      3250
Leu Thr Ile  *
           1020

cactggtcca cataaccctt gaccccttct tcttcataga ggaaacaatg tgccagtctt    3310

attcttttct tcaacaacct tgacttccat ggaggaagtg ctggccccaa ggggtctgac    3370

acaaagacgg gaaacccagt cggcctctag ttttctgctg ctctcaggca gcacatcttg    3430

caaacagttt ggagaaggag gctgtttttg ttgaatcgag ttctcaaatc ggtttagacc    3490

aaagccattc ttctgaccct ctagataagc gtagcctaca acccagtgcc gtaagtttcc    3550

aagattcaag aagtgtatca acccaggcaa tatctcagga tatggaagtt tctgggttta    3610

tttacccctc agtgcccaga gttaaagttt cagaagagac ttgtgcacat aagggcttca    3670

tctcaagtgt attgcagtaa tggctgaatc ggggttaaca tcccttccag gcacagcgag    3730
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ttggttctgc tttttgcctg taagccaaag aaaa                                3764
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<210> 292
<211> 614
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (361)..(462)

<400> 292

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gccacaagaa tgtatacttc tagcaagttt tgttatccta taaggcccag tccaacatat      60

aagtagtcag aaagacttat atgaccataa gaagtagcat acatttcttt ctttgcagtg     120

gtccaatggc aatttgttca cctctaattt ttataatcat agtttagggt tgtggctaaa     180

agcacaaact ctggaactag actgctagat atataatctt gggtatgctg tttgattgct     240

ctggtactct gtacctcaat tttcaccagt taaatgcaga tttagggtgg gtagttgtga     300

ggattaaaat gtatgggtat accttagaaa ggtgccaaat atggctgggt gtggtggctc     360

atg tct gta atc cca acc cct tgg aag gcc gag gcg ggt ggc tca caa       408
Met Ser Val Ile Pro Thr Pro Trp Lys Ala Glu Ala Gly Gly Ser Gln
 1               5                  10                  15

ggt cag gag atc aag acc act ctg gcc aac acg gtg aaa cac cgt ctc       456
Gly Gln Glu Ile Lys Thr Thr Leu Ala Asn Thr Val Lys His Arg Leu
            20                  25                  30

cac taa aaatacaaaa tacaaaaaat tacaaaaata caaagtacaa aaaatacaaa        512
His  *


aaatacaaaa tactgaaaat actaaaaatt agccgggcat agtggcacgt gcctatagtc     572

ccagctactt gggaatctgc ggacgcgtgg gtcgacccgg gt                        614
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<210> 293
<211> 830
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (219)..(467)

<400> 293

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cgcctgcgaa ccggcccgga attcccgggg cgacccacgc gtccggagcc tgcgagctgc      60

cgaagcaggg ttccgagtcc attcgaactg ccatctgatc cgctcttatc aatgaagcag     120

ccgatcatgg cggatgggcc ccggtgcaag aggcgcaaac aagccaatcc caggaggaaa     180

aacgccttgg agtcagaaat gagcactcgg agcgggag    atg ccc tgc tgc tgc      233
                                             Met Pro Cys Cys Cys
                                              1               5

ttg cca ccg gtg cgg ccc gtt tgt aac ttg caa agt ttg ttg ctt ttg       281
Leu Pro Pro Val Arg Pro Val Cys Asn Leu Gln Ser Leu Leu Leu Leu
                10                  15                  20

ccc ctg att cgg gca gcg ggt cct ggg atg ctc ctg ctt ccc tcc tgc       329
Pro Leu Ile Arg Ala Ala Gly Pro Gly Met Leu Leu Leu Pro Ser Cys
            25                  30                  35

ctc cca cgg agc ccg gga aga ggg tct gcc tcc cca tcc cgc cac ctt       377
Leu Pro Arg Ser Pro Gly Arg Gly Ser Ala Ser Pro Ser Arg His Leu
        40                  45                  50

cca gca tca gcc tct gaa aaa tct cac aga gac atg cac gtt gta gca       425
Pro Ala Ser Ala Ser Glu Lys Ser His Arg Asp Met His Val Val Ala
    55                  60                  65

aaa atc aaa tcc gga aac tgc ttg ttt cag aga aag aaa tga agttgtc       474
Lys Ile Lys Ser Gly Asn Cys Leu Phe Gln Arg Lys Lys  *
 70                  75                  80

ttttaaagaa aaactgaatt aggaggagag aaaagggaaa taggagaaga aaggaaaagt     534

taaatttgat ttttctccag agtttccact aaagggttgg ggacagtgtg aaggagaagg     594

ggagcttttt acaaatacct ttggtctctg aacttcagtg gcaaagaaca gggatcaagt     654

tgaatgttct cagggctttg gatcctagag gagaaacaat cagaagagca gaaatggtta     714

tccctgttta aaataagccc tcactcttta ccacttcctt aaaggagtgg aggtgctggt     774

agtgatggtt agaggcaatg agggacggag aagttgctcc cgtttcagag atgctt         830
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<210> 294
<211> 757
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (493)..(735)

<400> 294
taaaaaaaca actcagactg aacccatgtg aaaaaaccta cctaaaatca gaacatacat      60
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acgaggcaac ctcgaggaaa ccacccttat aatggccaag aacaggattg acgattacaa     120

tctcagctgg cctgtcatat aaaacatact gtcattgagc ttaagctccg cttgttctga     180

ggtttcacct ccatgtgttt cattggtgca aaagtggatc tcttagttgg tcacttaatt     240

ctttcttttt cagaaagata ggatgttcac tggtatattt ggtcactctt agaaccttcc     300

ttcacattgt tttttatggg acccatgaat ggttagcctt tcttttctat tgtagaagga     360

aataaatagg agtaaaaaga ccattgtagt aaataagttc aaggggaact tgggaccaga     420

aaccactgtt atgtacaaaa aaatggcaaa ttcaataaac tcaaatttaa aataattttt     480

aaattaacag tt    atg ata aat ttt ata ttt tat aca aat aga ttg ctt      528
                 Met Ile Asn Phe Ile Phe Tyr Thr Asn Arg Leu Leu
                  1               5                  10

aga atg gtt ctc aag aat tat aag aga aat gaa ctc aca gta caa aaa      576
Arg Met Val Leu Lys Asn Tyr Lys Arg Asn Glu Leu Thr Val Gln Lys
        15                  20                  25

ttt tat aat tac tat act tgt gtt ttg ttt ggg ggc tgg gaa atg tat      624
Phe Tyr Asn Tyr Tyr Thr Cys Val Leu Phe Gly Gly Trp Glu Met Tyr
    30                  35                  40

ttt tac att gta gcc aat cat ttt ata ttt gtc aat tta aat ctt atg      672
Phe Tyr Ile Val Ala Asn His Phe Ile Phe Val Asn Leu Asn Leu Met
45                  50                  55                  60

ggt ctt ttt ttt tta tct ctc ttg atg tca gat ttt ata gtc ttt tta      720
Gly Leu Phe Phe Leu Ser Leu Leu Met Ser Asp Phe Ile Val Phe Leu
                65                  70                  75

aat aaa tcc att taa ttaaaacgtt aaaaaaaaaa aa                         757
Asn Lys Ser Ile  *
            80




     <210> 295
     <211> 2388
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (125)..(1258)

     <400> 295
tgcaggcacc ggtcctgaat tcccgggtcg acccacgcgt ccgaaaggat tggctaaaag      60

caagcaactg gattgaacac cctaagaaga aagattcaca ctgcaccagg agacatcaga    120

aaga atg aaa act ctg ccg ctg ttt gtg tgc atc tgt gca ctg agt gct    169
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```
     Met Lys Thr Leu Pro Leu Phe Val Cys Ile Cys Ala Leu Ser Ala
       1               5                 10                  15

tgc ttc tcg ttc agt gaa ggt cga gaa agg gat cat gaa cta cgt cac       217
Cys Phe Ser Phe Ser Glu Gly Arg Glu Arg Asp His Glu Leu Arg His
                20                  25                  30

aga agg cat cat cac caa tca ccc aaa tct cac ttt gaa tta cca cat       265
Arg Arg His His His Gln Ser Pro Lys Ser His Phe Glu Leu Pro His
            35                  40                  45

tat cct gga ctg cta gct cac cag aag ccg ttc att aga aag tcc tat       313
Tyr Pro Gly Leu Leu Ala His Gln Lys Pro Phe Ile Arg Lys Ser Tyr
        50                  55                  60

aaa tgt ctg cac aaa cgc tgt agg cct aag ctt cca cct tca cct aat       361
Lys Cys Leu His Lys Arg Cys Arg Pro Lys Leu Pro Pro Ser Pro Asn
     65                  70                  75

aac ccc ccc aaa ttc cca aat cct cac cag cca cct aaa cat cca gat       409
Asn Pro Pro Lys Phe Pro Asn Pro His Gln Pro Pro Lys His Pro Asp
 80                  85                  90                  95

aaa aat agc agt gtg gtc aac cct acc tta gtg gct aca acc caa att       457
Lys Asn Ser Ser Val Val Asn Pro Thr Leu Val Ala Thr Thr Gln Ile
               100                 105                 110

cca tct gtg act ttc cca tca gct tcc acc aaa att act acc ctt cca       505
Pro Ser Val Thr Phe Pro Ser Ala Ser Thr Lys Ile Thr Thr Leu Pro
           115                 120                 125

aat gtg act ttt ctt ccc cag aat gcc acc acc ata tct tca aga gaa       553
Asn Val Thr Phe Leu Pro Gln Asn Ala Thr Thr Ile Ser Ser Arg Glu
       130                 135                 140

aat gtt aac aca agc tct tct gta gct aca tta gca cca gtg aat tcc       601
Asn Val Asn Thr Ser Ser Ser Val Ala Thr Leu Ala Pro Val Asn Ser
    145                 150                 155

cca gct cca caa gac acc aca gct gcc cca ccc aca cct tct gca act       649
Pro Ala Pro Gln Asp Thr Thr Ala Ala Pro Pro Thr Pro Ser Ala Thr
160                 165                 170                 175

aca cca gct cca cca tct tcc tca gct cca cca gag acc aca gct gcc       697
Thr Pro Ala Pro Pro Ser Ser Ser Ala Pro Pro Glu Thr Thr Ala Ala
               180                 185                 190

cca ccc aca cct tct gca act aca caa gct cca cca tct tcc tca gct       745
Pro Pro Thr Pro Ser Ala Thr Thr Gln Ala Pro Pro Ser Ser Ser Ala
           195                 200                 205

cca cca gag acc aca gct gcc cca ccc aca cct cct gca act aca caa       793
Pro Pro Glu Thr Thr Ala Ala Pro Pro Thr Pro Pro Ala Thr Thr Gln
       210                 215                 220

gct cca cca tct tcc tca gct cca cca gag acc aca gct gcc cca ccc       841
Ala Pro Pro Ser Ser Ser Ala Pro Pro Glu Thr Thr Ala Ala Pro Pro
```

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    225                 230                 235

aca cct cct gca act aca cca gct cca cca tct tcc tca gct cca cca      889
Thr Pro Pro Ala Thr Thr Pro Ala Pro Pro Ser Ser Ser Ala Pro Pro
240                 245                 250                 255

gag acc aca gct gtc cca ccc aca cct tct gca act acc cta gac cca      937
Glu Thr Thr Ala Val Pro Pro Thr Pro Ser Ala Thr Thr Leu Asp Pro
                260                 265                 270

tca tcc gcc tca gct cca cca gag acc aca gct gcc cca ccc aca cct      985
Ser Ser Ala Ser Ala Pro Pro Glu Thr Thr Ala Ala Pro Pro Thr Pro
            275                 280                 285

tct gca act aca cca gct cca ccg tct tcc cca gct cca caa gag acc     1033
Ser Ala Thr Thr Pro Ala Pro Pro Ser Ser Pro Ala Pro Gln Glu Thr
        290                 295                 300

aca gct gcc cca att acc aca cct aat tct tcc cca act act ctt gca     1081
Thr Ala Ala Pro Ile Thr Thr Pro Asn Ser Ser Pro Thr Thr Leu Ala
    305                 310                 315

cct gac act tct gaa act tca gct gca ccc aca cac cag act act act     1129
Pro Asp Thr Ser Glu Thr Ser Ala Ala Pro Thr His Gln Thr Thr Thr
320                 325                 330                 335

tcg gtc act act caa act act act act aaa caa cca act tca gct cct     1177
Ser Val Thr Thr Gln Thr Thr Thr Thr Lys Gln Pro Thr Ser Ala Pro
                340                 345                 350

ggc caa aat aaa att tct cga ttt ctt tta tat atg aag aat cta cta     1225
Gly Gln Asn Lys Ile Ser Arg Phe Leu Leu Tyr Met Lys Asn Leu Leu
            355                 360                 365

aac aga att att gac gac atg gtg gag caa tag tatattgt atgttgtaaa     1276
Asn Arg Ile Ile Asp Asp Met Val Glu Gln  *
        370                 375

gtgttctgtc atttacaaga tgtgattcat gagtgcagaa ctaccacctt tcttttagca   1336

ccaatcccaa catgaaatta tattactcag atttaaagca ctatcattaa tctttcaatc   1396

taattattca ccaccacaag acctattaac aagacaaaat gcctctatcc cacaagccag   1456

atgcaggtct ggggttcaaa ataactcttt ggatcctaca gagatagcct actgagggca   1516

gagaaagtcc ttagataaag agagaatatt gtatgggcca tcaaccattt acttttccct   1576

gaatgttaga aactacaaaa ccactacctt gtacccccat caaaatccca cctgaaccat   1636

ctaatcctat aaacataaag gggtaaaatt ggaactctcc agatgaacaa agacatctaa   1696

atatctgtag atagaaacat ttatctatct aaatatattg atagacctgt cattgtattg   1756

attaatgaca aaacccttta gataattatc ttccatttta aataaaattt tatttcacaa   1816

atatgagcca agaaagagga aagttgattt gaagtgagga ttagaagtga atgacaataa   1876
```

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agtctggcag ccaagcacga accaagactg gcactatttt tcttagtgta tataattgtt   1936

taaactgcaa ggttgacatt tattgtgttg tgtctaagtt aatttcgatc taatgtacct   1996

gattctagcc tctgtgaaca acaagaatat gtttgtgtat gttcacatgg tgcttataat   2056

atttcactat caattcaatt aattcacata aattccatgt gaaatgtatt caacaatgga   2116

atattttcta aaacatttag tatacatttg aatgtatttt aaaccatgcc aaactactgc   2176

tttaatgtca agtttgcaga attgtctctg aaaataaaaa ccctgacttt agttgtaaaa   2236

caataaaagt tagctacttg gtatacggag atgttaattt gggatatgga ggcattttta   2296

tcttctgtca ctactactta aaactctgat gattatgtta gatttttttg ctaactaata   2356

aagatttcaa atggcaattt aaaaaaaaaa aa                                  2388
```

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<210> 296
<211> 810
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (175)..(444)

<400> 296
ttttatagaa cggcttcaca tgtggccagg cagtcgtgat gtctgtctca atgaatcatc      60

agcttggcct ctgaaatgag gagattatag gggggaccac cacacccagc gcctacaaat     120

aaaattattt cacaagatga agagggtata acggcccatg attcccttgg gaat atg       177
                                                            Met
                                                            1

caa tgg ttt gtt tcc ata act ctg ctg gta ggg atg gaa ttg aaa ccc       225
Gln Trp Phe Val Ser Ile Thr Leu Leu Val Gly Met Glu Leu Lys Pro
              5                  10                  15

acc aca aaa tat aac aac ctg gaa ccc tgc ctt atc acc ttg ata aaa       273
Thr Thr Lys Tyr Asn Asn Leu Glu Pro Cys Leu Ile Thr Leu Ile Lys
         20                  25                  30

cgg gct gtt agg cta gga tac att att caa gag agc aga gtg gga atg       321
Arg Ala Val Arg Leu Gly Tyr Ile Ile Gln Glu Ser Arg Val Gly Met
     35                  40                  45

aga ttt gta ctc aca cct ttt aag gtt gtc cca ctt tca caa gat gtc       369
Arg Phe Val Leu Thr Pro Phe Lys Val Val Pro Leu Ser Gln Asp Val
 50                  55                  60                  65

aaa gtg aca cat cat att ggg cct tca att ctg gcc tta tac caa aat       417
```

```
Lys Val Thr His His Ile Gly Pro Ser Ile Leu Ala Leu Tyr Gln Asn
                70                  75                  80

gtg gat aag cat cca gac tat gct tga caaat acaaatagca tccaatatta      469
Val Asp Lys His Pro Asp Tyr Ala  *
            85                  90

acacagaatt tccatggttt acaatagcag tggtaatccc aaatcatcct gtgaacgtct    529

cctggaatga ctccatagcc acacagaacc acatatggct tcagatagcc atggccctat    589

ttcacttttg tgctgcacca gctgagacct cagctgtagc aaccctcctc tgtccaccta    649

atgccgttta aagcccagcc cctggatttg tgaaccaaat cacatctact atcacagatg    709

agcatatttt tcactgccca tatgcaccag gctgaatgaa actccccatc cactcccaaa    769

gtcatctcaa aatgtttatg aatccagaca gtgataaata g                        810



     <210> 297
     <211> 883
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (495)..(833)

     <400> 297
tttcgtcagg aagctgctgg ggtgggggtt gaggacgctg ggcctccctc cagctcccca     60

cccctcctcc tcaagacacc tgcatgcgca gggctgaggg gtgggagcag ggctctctgc    120

ctccagaacc cccatcctct gggctctttt taggccccta gattggcctg cagctgggag    180

cagagtggca agcatgcagg caggcagttg agaaagagga agtcgaggtg ctattgggtc    240

attctgtggt tatcccaggc tctacccagc cagcggttcc cttgggccag ctcgaaacgc    300

tggccgtagg tcatgggagc tgcaggagct gttagccagg ctaggtgcct gcaggttgaa    360

gaactgagct ctatctggct ctgagcccaa gtcatgtgtc cagccttttg actctggagc    420

tgtggcttca gccaccaaga gcagcagtgg atcctggaaa cctgagaacc cagacttctt    480

ctctgccatg gggg atg atc agg agg atg att ttc cca ggc ggc tca gcg      530
                Met Ile Arg Arg Met Ile Phe Pro Gly Gly Ser Ala
                 1               5                  10

aga gta tgg agg acc tca gcc tgg att tgg ggg ccc ttc agg gca gcg      578
Arg Val Trp Arg Thr Ser Ala Trp Ile Trp Gly Pro Phe Arg Ala Ala
        15                  20                  25

agt atc tgc agg acc tgg gcc ttg ggg ccc ctt ccc aca gcc agc ctg      626
```

```
Ser Ile Cys Arg Thr Trp Ala Leu Gly Pro Leu Pro Thr Ala Ser Leu
     30                  35                  40

ggg aga ccc cag aca gcc gcc cca ccg gtg aag aac cag gaa gag att      674
Gly Arg Pro Gln Thr Ala Ala Pro Pro Val Lys Asn Gln Glu Glu Ile
 45                  50                  55                  60

ctc ttt tct cca gct tgg cag ggt ccc aag acc tgt caa ggc ggc gca      722
Leu Phe Ser Pro Ala Trp Gln Gly Pro Lys Thr Cys Gln Gly Gly Ala
                 65                  70                  75

act ggg aaa ggt cgc gga gct gct cac aga gct ggc gga ggc tca acc      770
Thr Gly Lys Gly Arg Gly Ala Ala His Arg Ala Gly Gly Gly Ser Thr
             80                  85                  90

tcg atg cct cag ctg tgg atg agg aac cct gtc tcc ccc gaa cac tgg      818
Ser Met Pro Gln Leu Trp Met Arg Asn Pro Val Ser Pro Glu His Trp
         95                 100                 105

cca gcc ttg ctt tga acctgccagg aggagggctg aagacctgga ctcaagggtg      873
Pro Ala Leu Leu  *
    110

tctctctggg                                                           883




     <210> 298
     <211> 1920
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (15)..(1664)

     <400> 298
ctcctgagtg ggga  atg tgg ttc gtg gtg ata cct caa gca gaa tat gaa      50
                 Met Trp Phe Val Val Ile Pro Gln Ala Glu Tyr Glu
                   1               5                  10

tgg gac gga aac agc caa gta gga att gga gac tac aga att cct aag       98
Trp Asp Gly Asn Ser Gln Val Gly Ile Gly Asp Tyr Arg Ile Pro Lys
         15                  20                  25

gcg atg ctc aca ttc ttg aat gga agt aga att cct gtc act gag aaa      146
Ala Met Leu Thr Phe Leu Asn Gly Ser Arg Ile Pro Val Thr Glu Lys
     30                  35                  40

gca cct cat aaa gga att att aga gat tca acc tgt aag tac ctt cca      194
Ala Pro His Lys Gly Ile Ile Arg Asp Ser Thr Cys Lys Tyr Leu Pro
 45                  50                  55                  60

gag tgg cag agc tat cag tgc ttt ggg atg gaa tat gca atg atg gtt      242
Glu Trp Gln Ser Tyr Gln Cys Phe Gly Met Glu Tyr Ala Met Met Val
                 65                  70                  75
```

```
att gaa agt ctg gat cct gac aca gaa act cga aga ctt tcc cca gtg       290
Ile Glu Ser Leu Asp Pro Asp Thr Glu Thr Arg Arg Leu Ser Pro Val
             80                  85                  90

gct ata atg ggc aac ggt tat gtt gat ctt att aat ggc cca cag gat       338
Ala Ile Met Gly Asn Gly Tyr Val Asp Leu Ile Asn Gly Pro Gln Asp
         95                 100                 105

cat ggc tgg tgt gct gga tat aca tgc cag aga agg ctg tcc ctg ttt       386
His Gly Trp Cys Ala Gly Tyr Thr Cys Gln Arg Arg Leu Ser Leu Phe
    110                 115                 120

cac agc att gtg gct ctg aac aaa tct tat gaa gtt tac ttc act ggc       434
His Ser Ile Val Ala Leu Asn Lys Ser Tyr Glu Val Tyr Phe Thr Gly
125                 130                 135                 140

acc agt cct cag aat ctt cga ctg atg ttg ctt aat gtt gat cat aac       482
Thr Ser Pro Gln Asn Leu Arg Leu Met Leu Leu Asn Val Asp His Asn
                145                 150                 155

aag gct gtt cta gta gga att ttc ttt tcc aca ctt caa cgt ttg gat       530
Lys Ala Val Leu Val Gly Ile Phe Phe Ser Thr Leu Gln Arg Leu Asp
            160                 165                 170

gtc tat gtg aac aac tta ttg gtc tgt cca aaa act aca ata tgg aat       578
Val Tyr Val Asn Asn Leu Leu Val Cys Pro Lys Thr Thr Ile Trp Asn
        175                 180                 185

gcc cag cag aaa cac tgt gaa ctt aat aac cat ctg tac aaa gac caa       626
Ala Gln Gln Lys His Cys Glu Leu Asn Asn His Leu Tyr Lys Asp Gln
    190                 195                 200

ttc ctt cct aac ctg gat tcc act gtc ctt ggt gaa aac tac ttt gat       674
Phe Leu Pro Asn Leu Asp Ser Thr Val Leu Gly Glu Asn Tyr Phe Asp
205                 210                 215                 220

gga acc tac cag atg ctt tat ctt ttg gtt aaa gga act ata cct gtt       722
Gly Thr Tyr Gln Met Leu Tyr Leu Leu Val Lys Gly Thr Ile Pro Val
                225                 230                 235

gaa att cac act gcc aca gtg ata ttt gtt tct ttc caa tta tct gtt       770
Glu Ile His Thr Ala Thr Val Ile Phe Val Ser Phe Gln Leu Ser Val
            240                 245                 250

gca aca gaa gat gac ttt tat acc tct cac aat ctg gtt aaa aat ctt       818
Ala Thr Glu Asp Asp Phe Tyr Thr Ser His Asn Leu Val Lys Asn Leu
        255                 260                 265

gcc ttg ttc cta aag ata cca agt gac aaa atc cgt atc agc aaa ata       866
Ala Leu Phe Leu Lys Ile Pro Ser Asp Lys Ile Arg Ile Ser Lys Ile
    270                 275                 280

aga ggg aag agt ctg agg agg aag aga tcc atg gga ttc ata att gaa       914
Arg Gly Lys Ser Leu Arg Arg Lys Arg Ser Met Gly Phe Ile Ile Glu
285                 290                 295                 300
```

```
ata gag att gga gac cct cct att cag ttc ata agc aat ggc acc aca       962
Ile Glu Ile Gly Asp Pro Pro Ile Gln Phe Ile Ser Asn Gly Thr Thr
                305                 310                 315

ggt cag atg cag tta tct gaa ctc cag gaa att gct ggt tct ctt gga      1010
Gly Gln Met Gln Leu Ser Glu Leu Gln Glu Ile Ala Gly Ser Leu Gly
            320                 325                 330

caa gct gta att tta gga aac atc agt agt atc ctt gga ttt aac att      1058
Gln Ala Val Ile Leu Gly Asn Ile Ser Ser Ile Leu Gly Phe Asn Ile
        335                 340                 345

tcg tcc atg tct att act aat ccc ctc ccc agc cca agt gac tct ggg      1106
Ser Ser Met Ser Ile Thr Asn Pro Leu Pro Ser Pro Ser Asp Ser Gly
    350                 355                 360

tgg att aat gtg act gcc cag cca gtt gaa agg tct gca ttt cct gtt      1154
Trp Ile Asn Val Thr Ala Gln Pro Val Glu Arg Ser Ala Phe Pro Val
365                 370                 375                 380

cat cac gtg gcc ttc gtg tcc tca ctc tta gtg atc act cag ccg gtg      1202
His His Val Ala Phe Val Ser Ser Leu Leu Val Ile Thr Gln Pro Val
                385                 390                 395

gca gca cag cca gga cag cca ttt cct cag cag cct tcg gta aag gca      1250
Ala Ala Gln Pro Gly Gln Pro Phe Pro Gln Gln Pro Ser Val Lys Ala
            400                 405                 410

aca gat tct gac ggt aac tgt gta tca gtt gga att act gca cta act      1298
Thr Asp Ser Asp Gly Asn Cys Val Ser Val Gly Ile Thr Ala Leu Thr
        415                 420                 425

ttg agg gcc ata ctc aag gac tcc aat aat aac caa gtc aat ggc ctt      1346
Leu Arg Ala Ile Leu Lys Asp Ser Asn Asn Asn Gln Val Asn Gly Leu
    430                 435                 440

agt gga aat aca aca att ccg ttt agc agc tgt tgg gcc aac tac aca      1394
Ser Gly Asn Thr Thr Ile Pro Phe Ser Ser Cys Trp Ala Asn Tyr Thr
445                 450                 455                 460

gac ctt act ccc ctt aga aca gga aaa aat tat aag att gaa ttt ata      1442
Asp Leu Thr Pro Leu Arg Thr Gly Lys Asn Tyr Lys Ile Glu Phe Ile
                465                 470                 475

ctg gat aat gtt gtt ggg gta gaa tcc aga act ttc agc ctg ctg gca      1490
Leu Asp Asn Val Val Gly Val Glu Ser Arg Thr Phe Ser Leu Leu Ala
            480                 485                 490

gag tct gtc tct agc agt ggc agc agc agc agc agc aac agc aaa gca      1538
Glu Ser Val Ser Ser Ser Gly Ser Ser Ser Ser Ser Asn Ser Lys Ala
        495                 500                 505

tca act gtg ggt aca tat gcc cag ata atg act gta gta att agc tgt      1586
Ser Thr Val Gly Thr Tyr Ala Gln Ile Met Thr Val Val Ile Ser Cys
    510                 515                 520

ctg gtt gga aga atg tgg ctc ttg gaa ata ttt atg gct gca gtt tca      1634
```

```
Leu Val Gly Arg Met Trp Leu Leu Glu Ile Phe Met Ala Ala Val Ser
525                 530                 535                 540

act ttg aat ata act tta aga agc tac taa a gtgctgttcc gaagaatagg     1685
Thr Leu Asn Ile Thr Leu Arg Ser Tyr  *
                545                 550

ctgaaacaaa aatataagaa ttattagcta ctttgttggg caataggcaa aagtctatag   1745

cattttcatg aaaatatact aaaaatattt ttatgatata taaaatgtac taattagctt   1805

taaacactaa aatcagattt cttcaaaata taaatttgtt ttgattcttt atatttatat   1865

gtttttattt catttcaata aacttccaga aatttgtcat ttgaaaaaaa aaaaa        1920




    <210> 299
    <211> 573
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (191)..(379)

    <400> 299
tatacgacca ctatagggat ttggccctcg aggcaagaat tcggcacgag ggatactttg     60

cccttttcctc agttgccacc aaggtgcttg gtccttccga ggaagctaag gccacattgg   120

ggtgaggcca tcacttcatc cagtgactag caccacctct ggcaatgtca gcccccacact   180

cgcccgcgcc   atg gcc tcc atc tcc gag ctt gcc tgt gtc tac ttg gcc      229
             Met Ala Ser Ile Ser Glu Leu Ala Cys Val Tyr Leu Ala
              1               5                  10

ctc att ctg cac gat gac gag gtg atc atc atg gag gtt aat atc aat      277
Leu Ile Leu His Asp Asp Glu Val Ile Ile Met Glu Val Asn Ile Asn
     15                  20                  25

acc ctc att aaa gca gcc agt gta aat gtt gaa cct ttt ggc ctg gct      325
Thr Leu Ile Lys Ala Ala Ser Val Asn Val Glu Pro Phe Gly Leu Ala
 30                  35                  40                  45

tgt ttg gaa agg ccc tgg cca acg tca aca ttg gaa gcc tca tct gca      373
Cys Leu Glu Arg Pro Trp Pro Thr Ser Thr Leu Glu Ala Ser Ser Ala
                50                  55                  60

atg tag gggctggtgg acctgctcta gcagctggtg ctgcaccagc aggaggtcct      429
Met  *


gccccctcca ttgctgctgc ttcagctgag gagaagaaaa tggaagcaaa gaaagaagaa   489

tctgaggagt ctgatgatga catgggcttt ggtcttttta ctaaacctgt tttataatgt   549
```

```
gttcaataaa aagctgactt taaa                                           573




     <210> 300
     <211> 1718
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (247)..(1245)

     <400> 300
ccggtcgacg atttcgtgga cgctggcagc tgggttctcc cgtttccctt gggcaggagc     60

agggtcgggt tcaaagcctc cggaacgcgt tgtggcccct tctccggctc gcagccgacc    120

ggtaagcccg cctcctccct cggccggccc tggggccgtg tccgccgggc aactccagcc    180

gaggcctggg cttctgcctg caggtgtctg cggcgaggcc cctagggtac agcccgattt    240

ggcccc   atg gtg ggt ttc ggg gcc aac cgg cgg gct ggc cgc ctg ccc     288
         Met Val Gly Phe Gly Ala Asn Arg Arg Ala Gly Arg Leu Pro
           1               5                  10

tct ctc gtg ctg gtg gtg ctg ctg gtg gtg atc gtc gtc ctc gcc ttc      336
Ser Leu Val Leu Val Val Leu Leu Val Val Ile Val Val Leu Ala Phe
 15                  20                  25                  30

aac tac tgg agc atc tcc tcc cgc cac gtc ctg ctt cag gag gag gtg      384
Asn Tyr Trp Ser Ile Ser Ser Arg His Val Leu Leu Gln Glu Glu Val
                 35                  40                  45

gcc gag ctg cag ggc cag gtc cag cgc acc gaa gtg gcc cgc ggg cgg      432
Ala Glu Leu Gln Gly Gln Val Gln Arg Thr Glu Val Ala Arg Gly Arg
             50                  55                  60

ctg gaa aag cgc aat tcg gac ctc ttg ctg ttg gtg gac acg cac aag      480
Leu Glu Lys Arg Asn Ser Asp Leu Leu Leu Leu Val Asp Thr His Lys
         65                  70                  75

aaa cag atc gac cag aag gag gcc gac tac ggc cgc ctc agc agc cgg      528
Lys Gln Ile Asp Gln Lys Glu Ala Asp Tyr Gly Arg Leu Ser Ser Arg
     80                  85                  90

ctg cag gcc aga gag ggc ctc ggg aag aga tgc gag gat gac aag gtt      576
Leu Gln Ala Arg Glu Gly Leu Gly Lys Arg Cys Glu Asp Asp Lys Val
 95                 100                 105                 110

aaa cta cag aac aac ata tcg tat cag atg gca gac ata cat cat tta      624
Lys Leu Gln Asn Asn Ile Ser Tyr Gln Met Ala Asp Ile His His Leu
                115                 120                 125

aag gag caa ctt gct gag ctt cgt cag gaa ttt ctt cga caa gaa gac      672
```

```
Lys Glu Gln Leu Ala Glu Leu Arg Gln Glu Phe Leu Arg Gln Glu Asp
            130                 135                 140

cag ctt cag gac tat agg aag aac aat act tac ctt gtg aag agg tta      720
Gln Leu Gln Asp Tyr Arg Lys Asn Asn Thr Tyr Leu Val Lys Arg Leu
        145                 150                 155

gaa tat gaa agt ttt cag tgt gga cag cag atg aag gaa ttg aga gca      768
Glu Tyr Glu Ser Phe Gln Cys Gly Gln Gln Met Lys Glu Leu Arg Ala
    160                 165                 170

cag cat gaa gaa aat att aaa aag tta gca gac cag ttt tta gag gaa      816
Gln His Glu Glu Asn Ile Lys Lys Leu Ala Asp Gln Phe Leu Glu Glu
175                 180                 185                 190

caa aag caa gag acc caa aag att caa tca aat gat gga aag gaa ttg      864
Gln Lys Gln Glu Thr Gln Lys Ile Gln Ser Asn Asp Gly Lys Glu Leu
                195                 200                 205

gat ata aac aat caa gta gta cct aaa aat att cca aaa gta gct gag      912
Asp Ile Asn Asn Gln Val Val Pro Lys Asn Ile Pro Lys Val Ala Glu
            210                 215                 220

aat gtt gca gat aag aat gaa gaa ccc tca agc aat cat att cca cat      960
Asn Val Ala Asp Lys Asn Glu Glu Pro Ser Ser Asn His Ile Pro His
        225                 230                 235

ggg aaa gaa caa atc aaa aga ggt ggt gat gca ggg atg cct gga ata     1008
Gly Lys Glu Gln Ile Lys Arg Gly Gly Asp Ala Gly Met Pro Gly Ile
    240                 245                 250

gaa gag aat gac cta gca aaa gtt gat gat ctt ccc cct gct tta agg     1056
Glu Glu Asn Asp Leu Ala Lys Val Asp Asp Leu Pro Pro Ala Leu Arg
255                 260                 265                 270

aag cct cct att tca gtt tct caa cat gaa agt cat caa gca atc tcc     1104
Lys Pro Pro Ile Ser Val Ser Gln His Glu Ser His Gln Ala Ile Ser
                275                 280                 285

cat ctt cca act gga caa gct ctc tcc cca aat atg cct cca gat tca     1152
His Leu Pro Thr Gly Gln Ala Leu Ser Pro Asn Met Pro Pro Asp Ser
            290                 295                 300

cac att aaa cac aat gga aac ccc ggt act tca aaa aca gaa tcc ttc     1200
His Ile Lys His Asn Gly Asn Pro Gly Thr Ser Lys Thr Glu Ser Phe
        305                 310                 315

cag tcc tct tca gcg ttt aat tcc agg ctc aaa ctt gga cag tag aac     1248
Gln Ser Ser Ser Ala Phe Asn Ser Arg Leu Lys Leu Gly Gln  *
    320                 325                 330

ccagaaattc caaacagatt atactaaagg caggttacca aggacagaag ccggggattc   1308

ccataaaatt ggcaccaatg tgaacacaga gagctcgtaa actgggtcct ggaccttggc   1368

agcacgcttc accgacgtcc tcaaaaccca gaggacacac tcgaaaacga aaggggggcg   1428
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aaccgcaaca cccacggccc ccccgacccg gaagggacga aagacagggt acaccaggac   1488

acacaaaatg gcaaaacaaa ggcaacacgc tccaagaaag aacagccata cacaaaagaa   1548

caaaagcgca cacaccaaac aaccccgcac gaaccaacac cacaccaaga catgtcaaca   1608

aacaagacca cataggagac gacaacgcaa agacaccgat cgagtaaccc caaagccacc   1668

aaaccaccaa cggacaccca ctgcccagcc tgtatcattc ctactagaca              1718



      <210> 301
      <211> 423
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (178)..(348)

      <400> 301
tcttttcaca tgattactgg ccatttgtat accttctgtg gaaatgtggt aacacccttt     60

gctgatttta aaatagggtt atttgtttat tattgagttg aaataattcc ttcttttgag    120

tgtcagtgac tgaggttcgc tgtgacacag aggggttctc ctggagagct atggcac       177
atg ctc cat att aaa agg caa cat gat gct cgc tcc acc cag agg ccc      225
Met Leu His Ile Lys Arg Gln His Asp Ala Arg Ser Thr Gln Arg Pro
 1               5                  10                  15

cgg tcc ccg cca ttc att ccg ctc ccg gcc gag agt cgc tct agc caa      273
Arg Ser Pro Pro Phe Ile Pro Leu Pro Ala Glu Ser Arg Ser Ser Gln
            20                  25                  30

tca cct tcc agg ctc agg gcg gcc gag gca ggg cct ctg cct ctt cgg      321
Ser Pro Ser Arg Leu Arg Ala Ala Glu Ala Gly Pro Leu Pro Leu Arg
        35                  40                  45

ggg gcc tct ccc tcc ccc tgc ccc tga ttgtg gctgaactgc caccgcttga      373
Gly Ala Ser Pro Ser Pro Cys Pro  *
    50                  55

tagcaaacca cactcggcac aggaaggaga acagcgcccg cggcacgaaa               423



      <210> 302
      <211> 408
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (44)..(343)
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     <400> 302
agggctcaag gaagccccaa gtccagtctg cccagaaccg agc  atg tca tct ccc      55
                                                 Met Ser Ser Pro
                                                   1

ccg cca aga cgc tcc aac cgc cgc aat cct tgt cca tca ggc atc cag      103
Pro Pro Arg Arg Ser Asn Arg Arg Asn Pro Cys Pro Ser Gly Ile Gln
  5                  10                  15                  20

gcc aga aac tct ggc tgc ccc cac ctc ccc aat ggt ccc cat caa gta      151
Ala Arg Asn Ser Gly Cys Pro His Leu Pro Asn Gly Pro His Gln Val
                 25                  30                  35

ggt aac atc ctg ctg att tta act cct gtg cag ccc tca aat gca caa      199
Gly Asn Ile Leu Leu Ile Leu Thr Pro Val Gln Pro Ser Asn Ala Gln
             40                  45                  50

ctg cct ccc att cct gca cag tgc ccc agt tca ggc ctt cac cac ctt      247
Leu Pro Pro Ile Pro Ala Gln Cys Pro Ser Ser Gly Leu His His Leu
         55                  60                  65

gtt cct ggg cca ctg ccc aag tct ccc ccg act ggt ggc tgg act tct      295
Val Pro Gly Pro Leu Pro Lys Ser Pro Pro Thr Gly Gly Trp Thr Ser
     70                  75                  80

aat act ttt cca act ccc cac tca tta aat cca tcc ccc tct cat taa      343
Asn Thr Phe Pro Thr Pro His Ser Leu Asn Pro Ser Pro Ser His  *
 85                  90                  95                 100

ctggtgggaa ttgaggaaaa ctgagttcca gccttgtcat cctcatactc atgacccttc    403

caggc                                                                408




     <210> 303
     <211> 822
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (69)..(590)

     <400> 303
cagatcaaga cacaggagaa gagtgcaaaa atactgatca ggaagagtct accatttcat     60

ccaaggaa atg cca caa tca ttt tct gca atc aca tta agt aac aca gag     110
         Met Pro Gln Ser Phe Ser Ala Ile Thr Leu Ser Asn Thr Glu
           1               5                  10

atg aat aat att aat act aat gcc ccg aga aac aaa ctt cca ata aag      158
Met Asn Asn Ile Asn Thr Asn Ala Pro Arg Asn Lys Leu Pro Ile Lys
 15                  20                  25                  30
```

```
gaa ctt ggt aaa gtt tct aaa cat aaa att gcc act aaa aga aca cca      206
Glu Leu Gly Lys Val Ser Lys His Lys Ile Ala Thr Lys Arg Thr Pro
                 35                  40                  45

cat aaa gaa gat gag gca atg agc tgt tct gaa aat tgt tcg agt gcc      254
His Lys Glu Asp Glu Ala Met Ser Cys Ser Glu Asn Cys Ser Ser Ala
             50                  55                  60

cag ggc gac tca ctt cag gat gag tct caa ggg tct cat tct gag tcc      302
Gln Gly Asp Ser Leu Gln Asp Glu Ser Gln Gly Ser His Ser Glu Ser
         65                  70                  75

agc tct aat ccc tcc aat cct gaa act ttg cat gca aag gca act gat      350
Ser Ser Asn Pro Ser Asn Pro Glu Thr Leu His Ala Lys Ala Thr Asp
     80                  85                  90

tca gtt cta caa ggt tct gaa gga aac aag gtc aag agg aca tcc tgc      398
Ser Val Leu Gln Gly Ser Glu Gly Asn Lys Val Lys Arg Thr Ser Cys
 95                 100                 105                 110

atg tat ggg gca aac tgc tat agg aag aat cct gtt cat ttt caa cat      446
Met Tyr Gly Ala Asn Cys Tyr Arg Lys Asn Pro Val His Phe Gln His
                115                 120                 125

ttt agc cat cct ggt gat agt gat tat gga ggt gta caa atc gtg ggc      494
Phe Ser His Pro Gly Asp Ser Asp Tyr Gly Gly Val Gln Ile Val Gly
            130                 135                 140

caa gat gag act gat gac cgg cct gaa tgt ccc tat gga cca tcc tgt      542
Gln Asp Glu Thr Asp Asp Arg Pro Glu Cys Pro Tyr Gly Pro Ser Cys
        145                 150                 155

tat agg ttg gaa gtt cag tgt cca gtt gaa aaa cac caa ctc agc tag      590
Tyr Arg Leu Glu Val Gln Cys Pro Val Glu Lys His Gln Leu Ser  *
    160                 165                 170

tttcttctgg tctgcattac agtattttac ctgtcttttt atgaaaagag cacgttctag    650

gaaaggatgg aagattctca aagaaacaac tttccccttc taaggcagat gaaaacctgt    710

acatgtacct aacatttttt cccctttta aaatataaaa tttcacatta cattttctgc    770

tcttcctttt tggaataatt aaatgtaaca cttctttcat aaaaaaaaaa aa            822
```

<210> 304
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (121)..(309)

<400> 304

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tttgaaagct gattgatagc cgtaccgcac cgcaaacccc gggtcgaccc acgcgtccgc      60

ttcacttcac cttcactact tctgtagtct gatcttgtgt aatagagaac ccagccaact     120

atg aag ttc ctt gac ttt gct ttc atc ttg gct ctc aag gtt tcc atg       168
Met Lys Phe Leu Asp Phe Ala Phe Ile Leu Ala Leu Lys Val Ser Met
 1               5                  10                  15

att gga gct gat tcc tct gaa gag aaa ttt ttg cgt ata att gta cga       216
Ile Gly Ala Asp Ser Ser Glu Glu Lys Phe Leu Arg Ile Ile Val Arg
            20                  25                  30

atc ggt tat ggg tat ggc cct tat cat tca gtt tca gaa caa cca cta       264
Ile Gly Tyr Gly Tyr Gly Pro Tyr His Ser Val Ser Glu Gln Pro Leu
        35                  40                  45

tac cca caa cca tac caa cca caa tac caa caa tat acc ttt taa tat       312
Tyr Pro Gln Pro Tyr Gln Pro Gln Tyr Gln Gln Tyr Thr Phe  *
    50                  55                  60

catcagtaac tgcaggacat gattattgag gcttgattgg ctgatacgac ttctacatcc     372

atattctcat gtttcatacc atatcgcact actaccactt tttgaagaat catcatagag     432

ctttgcatat gagaaacact atatg                                           457




     <210> 305
     <211> 1749
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (85)..(873)

     <400> 305
ccgcgccgga attcccgggt cgacccacgc gtccgccgca gcccccagct cgcccccaag      60

atgatgaaga ggcagctgca ccgc   atg cgg cag ctg gcc cag acg ggc agc      111
                             Met Arg Gln Leu Ala Gln Thr Gly Ser
                              1               5

ttg gga cgc acc ccg gag acc gct gag ttc ctg ggt gag gac ctg ctg       159
Leu Gly Arg Thr Pro Glu Thr Ala Glu Phe Leu Gly Glu Asp Leu Leu
 10                  15                  20                  25

cag gta gaa cag cgg ctg gag ccg gcc aag cgg gca gcc cac aac atc       207
Gln Val Glu Gln Arg Leu Glu Pro Ala Lys Arg Ala Ala His Asn Ile
                30                  35                  40

cac aag cgg ctg cag gcc tgt ctg cag ggc cag agc ggg gca gac atg       255
His Lys Arg Leu Gln Ala Cys Leu Gln Gly Gln Ser Gly Ala Asp Met
            45                  50                  55
```

```
gac aag cgg gtg aag aag ctt ccc ctc atg gct ctg tcc acc acg atg        303
Asp Lys Arg Val Lys Lys Leu Pro Leu Met Ala Leu Ser Thr Thr Met
         60                  65                  70

gct gag agc ctc aag gag ctg gac cct gat tcc agc atg ggg aag gcc        351
Ala Glu Ser Leu Lys Glu Leu Asp Pro Asp Ser Ser Met Gly Lys Ala
     75                  80                  85

ttg gag atg agc tgt gcc atc cag aat cag ctg gcc cgc atc ctg gcc        399
Leu Glu Met Ser Cys Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu Ala
 90                  95                 100                 105

gag ttt gag atg acc ctg gag agg gac gtc ctg cag cca ctc agc agg        447
Glu Phe Glu Met Thr Leu Glu Arg Asp Val Leu Gln Pro Leu Ser Arg
                110                 115                 120

ctg agt gag gag gag ctg cca gcc atc ctc aaa cac aag aaa agc ctc        495
Leu Ser Glu Glu Glu Leu Pro Ala Ile Leu Lys His Lys Lys Ser Leu
            125                 130                 135

cag aag ctc gtg tcc gac tgg aac aca ctc aag agc agg ctc agt cag        543
Gln Lys Leu Val Ser Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser Gln
        140                 145                 150

gca acc aag aat tca ggc agc agt caa ggc cta gga ggc agc ccg ggt        591
Ala Thr Lys Asn Ser Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro Gly
    155                 160                 165

agt cac agc cat acg acc atg gcc aac aag gtg gag acg ctg aag gag        639
Ser His Ser His Thr Thr Met Ala Asn Lys Val Glu Thr Leu Lys Glu
170                 175                 180                 185

gag gag gag gag ctg aag agg aaa gtg gag caa tgc agg gac gag tac        687
Glu Glu Glu Glu Leu Lys Arg Lys Val Glu Gln Cys Arg Asp Glu Tyr
                190                 195                 200

ttg gct gac ctg tac cac ttt gtt acc aag gag gac tcc tat gcc aac        735
Leu Ala Asp Leu Tyr His Phe Val Thr Lys Glu Asp Ser Tyr Ala Asn
            205                 210                 215

tac ttc att cgt ctc ctg gag att cag gcc gat tac cat cgc agg tca        783
Tyr Phe Ile Arg Leu Leu Glu Ile Gln Ala Asp Tyr His Arg Arg Ser
        220                 225                 230

ctg agc tcg ctg gac aca gcc ctg gct gag ctg agg gag aac cac ggc        831
Leu Ser Ser Leu Asp Thr Ala Leu Ala Glu Leu Arg Glu Asn His Gly
    235                 240                 245

caa gca ggt ggg gac ata ggc ccg gcg ata cca cac ccc tga ccctgcc        880
Gln Ala Gly Gly Asp Ile Gly Pro Ala Ile Pro His Pro  *
250                 255                 260

ctgctcgggg cttattgaga agctcgcact tcatcctgaa aggtagcagg aagctgtgga      940

tgggttctga gagctaggct caatctgtga tggagaggca gctctggcta ctgtgtggag     1000

ggtggagtga agcgggcagg actagagcca ggcctgtgag gcagaaggag gcaacggtgg     1060
```

```
cctggactag gacagaggca gtggaggcgg gctgattcga gagatgtgac ggatgatttc   1120

agatgtgtgc ctggacagtc agtggcaggt ggtaccacct tgaggacatg aagggggggt   1180

gcccctgcct gactgctcgg ggtgggaagg ccctgggccg ctgatctgtt tcatccctgc   1240

agaccactcc ccttcgatga cagccaccca cttccccagg gtgtatgggg tgtcgctggc   1300

aacccacctg caagagctgg gccgggagat tgccctgccc atcgaggcct gcgtcatgat   1360

gctgctttct gagggcatga aggaagaggg tctcttccgt ctggctgctg ggcctcggt    1420

gctgaagcgt gtcaagcaga caatggcctc ggaccccgac agcctggagg agttctgctc   1480

cgacccgcac gctgtggcag gtgccctcaa gtcctatctg cgggagctgc cagagcctct   1540

gatgaccttc gacctctatg atgactggat gagggcagcc agcctgaagg agccaggggc   1600

ccggctgcag gccctccaag aggtgtgcag ccgcctaccc cccgagaacc tcagcaacct   1660

caggtacctg atgaagttcc tggcacggct ggccgaggag caggaggtga acaagacgaa   1720

atctcgacag cgaagtcgac ccgggaatt                                     1749



<210> 306
<211> 496
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (55)..(372)

<400> 306
aaggatcctt aattaaatta atcccccccc ccgaaccgtt cgctaactga aatg atg      57
                                                            Met
                                                             1

gcg act gga acg cca gag tct caa gcg cgg ttc ggt cag tcc gtg aag     105
Ala Thr Gly Thr Pro Glu Ser Gln Ala Arg Phe Gly Gln Ser Val Lys
            5                   10                  15

ggg ctt ctc acg gag aag gtg acc acc tgt ggt act gac gta atc gcg     153
Gly Leu Leu Thr Glu Lys Val Thr Thr Cys Gly Thr Asp Val Ile Ala
        20                  25                  30

ctc acc aag cag gtg ctg aaa ggc tcc cgg agc tcc gag ctg cta ggt     201
Leu Thr Lys Gln Val Leu Lys Gly Ser Arg Ser Ser Glu Leu Leu Gly
    35                  40                  45

cag gca gct cga aac atg gta ctc cag gaa gat gcc atc ttg cac tca     249
Gln Ala Ala Arg Asn Met Val Leu Gln Glu Asp Ala Ile Leu His Ser
50                  55                  60                  65
```

```
gaa gat agt tta agg aag atg gca ata ata aca aca cat ctt caa tac       297
Glu Asp Ser Leu Arg Lys Met Ala Ile Ile Thr Thr His Leu Gln Tyr
                 70                  75                  80

cag caa gaa gct att cag aag aat gtt gaa cag tca tcg gat cta cag       345
Gln Gln Glu Ala Ile Gln Lys Asn Val Glu Gln Ser Ser Asp Leu Gln
         85                  90                  95

gac cag ttg aat cat ctg ttg aaa tag aatga catgtaagag tgctgtagga       397
Asp Gln Leu Asn His Leu Leu Lys  *
    100                 105

ctcctttgcc taatgctgag gagtaaatac cttacacagc tgtcctctgg gtttggtttt    457

ctattttctt ctccaaaagt taagttagaa aagttcttg                           496



     <210> 307
     <211> 1438
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (88)..(840)

     <400> 307
catggaggag gaaggagatg gcatggctta ccataaagaa gcactggacg ccgggtgcac     60

gttccaggat ccaggtgccc aggggtc    atg aag ctg gga ctc ctc tgt gct     111
                                 Met Lys Leu Gly Leu Leu Cys Ala
                                   1               5

ctg ctc tct ctg ctg gca ggg cat ggc tgg gca gac acc cgt gcc atc       159
Leu Leu Ser Leu Leu Ala Gly His Gly Trp Ala Asp Thr Arg Ala Ile
     10                  15                  20

ggg gcc gag gaa tgt cgc ccc aac tcc cag cct tgg cag gcc ggc ctc       207
Gly Ala Glu Glu Cys Arg Pro Asn Ser Gln Pro Trp Gln Ala Gly Leu
 25                  30                  35                  40

ttc cac ctt act cgg ctc ttc tgt ggg gcg acc ctc atc agt gac cgc       255
Phe His Leu Thr Arg Leu Phe Cys Gly Ala Thr Leu Ile Ser Asp Arg
                 45                  50                  55

tgg ctg ctc aca gct gcc cac tgc cgc aag ccg tat ctg tgg gtc cgc       303
Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro Tyr Leu Trp Val Arg
         60                  65                  70

ctt gga gag cac cac ctc tgg aaa tgg gag ggt ccg gag cag ctg ttc       351
Leu Gly Glu His His Leu Trp Lys Trp Glu Gly Pro Glu Gln Leu Phe
     75                  80                  85

cgg gtt acg gac ttc ttc ccc cac cct ggc ttc aac aag gac ctc agc       399
```

```
Arg Val Thr Asp Phe Phe Pro His Pro Gly Phe Asn Lys Asp Leu Ser
     90                  95                 100

gcc aat gac cac aat gat gac atc atg ctg atc cgc ctg ccc agg cag       447
Ala Asn Asp His Asn Asp Asp Ile Met Leu Ile Arg Leu Pro Arg Gln
105                 110                 115                 120

gca cgt ctg agt cct gct gtg cag ccc ctc aac ctc agc cag acc tgt       495
Ala Arg Leu Ser Pro Ala Val Gln Pro Leu Asn Leu Ser Gln Thr Cys
                125                 130                 135

gtc tcc cca ggc atg cag tgt ctc atc tca ggc tgg ggg gcc gtg tcc       543
Val Ser Pro Gly Met Gln Cys Leu Ile Ser Gly Trp Gly Ala Val Ser
            140                 145                 150

agc ccc aag gcg ctg ttt cca gtc aca ctg cag tgt gcc aac atc agc       591
Ser Pro Lys Ala Leu Phe Pro Val Thr Leu Gln Cys Ala Asn Ile Ser
        155                 160                 165

atc ctg gag aac aaa ctc tgt cac tgg gca tac cct gga cac atc tcg       639
Ile Leu Glu Asn Lys Leu Cys His Trp Ala Tyr Pro Gly His Ile Ser
    170                 175                 180

gac agc atg ctc tgt gcg ggc ctg tgg gag ggg ggc cga ggt tcc tgc       687
Asp Ser Met Leu Cys Ala Gly Leu Trp Glu Gly Gly Arg Gly Ser Cys
185                 190                 195                 200

cag ggt gac tct ggg ggc ccc ctg gtt tgc aat gga acc ttg gca ggc       735
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Thr Leu Ala Gly
                205                 210                 215

gtg gtg tct ggg ggt gct gag ccc tgc tcc aga ccc cgg cgc ccc gca       783
Val Val Ser Gly Gly Ala Glu Pro Cys Ser Arg Pro Arg Arg Pro Ala
            220                 225                 230

gtc tac acc agc gta tgc cac tac ctt gac tgg atc caa gaa atc atg       831
Val Tyr Thr Ser Val Cys His Tyr Leu Asp Trp Ile Gln Glu Ile Met
        235                 240                 245

gag aac tga gcccgcg cgccacgggg gcaccttgga agaccaagag aggccgaagg       887
Glu Asn  *
    250

gcacggggta gggggttctc gtagggtccc agcctcaatg gttcccgccc tggacctcca     947

gctgccctga ctcccctctg gacactaaga ctccgcccct gaggctccgc cccctcacga    1007

ggtcaagcaa gacacagtcg cgccccctcg gaacggagca gggacacgcc cttcagagcc    1067

cgtctctatg acgtcaccga cagccatcac ctccttcttg gaacagcaca gcctgtggct    1127

ccgccccaag gaaccactta cacaaaatag ctccgcccct cggaactttg cccagtggga    1187

cttcccctcg ggactccacc ccttgtggcc ccgcctcctt caccagagat ctcgcccctc    1247

gtgatgtcag ggcgcagta gctccgccca cgtggagctc gggcggtgta gagctcagcc     1307
```

```
ccttgtggcc ccgtcctggg cgtgtgctgg gtttgaatcc tggcggagac ctggggggaa   1367

attgagggag ggtctggata cctttagagc caatgcaacg gatgattttt cagtaaacgc   1427

gggaaacctc a                                                        1438




     <210> 308
     <211> 675
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (110)..(613)

     <400> 308
taggagatcc ttagcggact gggatcttaa tggtctcact gtgtttatct ctttgtaaag     60

gccagccctc acctgacttg tctggttccc tcctggggct aggggatgg   atg aga      115
                                                        Met Arg
                                                          1

agg gct agg ctg gag ctg tca gca gct tct tgg tgc ctg ctg ttt ctc      163
Arg Ala Arg Leu Glu Leu Ser Ala Ala Ser Trp Cys Leu Leu Phe Leu
        5                  10                  15

ttg tct tgt ctg tct tcg gtg tat tgc aat cct gtc ctc tta gca ggc      211
Leu Ser Cys Leu Ser Ser Val Tyr Cys Asn Pro Val Leu Leu Ala Gly
    20                  25                  30

ccc gca gag tca tac ttt ttc tcc ctg gcc ttc cag ctc cct ctc ttc      259
Pro Ala Glu Ser Tyr Phe Phe Ser Leu Ala Phe Gln Leu Pro Leu Phe
 35                  40                  45                  50

cac cca gta tgc cca cct ccc tct ccc ttg act acc cca gcc tct gcc      307
His Pro Val Cys Pro Pro Pro Ser Pro Leu Thr Thr Pro Ala Ser Ala
                55                  60                  65

caa tca cgc cct gcc ctc tac cct tca gag gac acc ttg ccg tct gtg      355
Gln Ser Arg Pro Ala Leu Tyr Pro Ser Glu Asp Thr Leu Pro Ser Val
            70                  75                  80

gag ctg gag cta ttc cta tgg tct ctc tgg gtc cac atg acc tta cat      403
Glu Leu Glu Leu Phe Leu Trp Ser Leu Trp Val His Met Thr Leu His
        85                  90                  95

ggc act cct ctc acc ttc tgt cca tcc aac aaa att ctc tgt tcc ttt      451
Gly Thr Pro Leu Thr Phe Cys Pro Ser Asn Lys Ile Leu Cys Ser Phe
    100                 105                 110

gaa gct ctc ttt tca gta agg cct tcc ttg gcc cct aac agg atg gat      499
Glu Ala Leu Phe Ser Val Arg Pro Ser Leu Ala Pro Asn Arg Met Asp
115                 120                 125                 130
```

```
cac cct ccc ctg agc cct ggt cat tgc ctc tct gtt atg gcc tct cca      547
His Pro Pro Leu Ser Pro Gly His Cys Leu Ser Val Met Ala Ser Pro
                135                 140                 145

ttg gta aac gct ctg ccg atg tgt ttc atc ttc cca cta gat cct tgc      595
Leu Val Asn Ala Leu Pro Met Cys Phe Ile Phe Pro Leu Asp Pro Cys
            150                 155                 160

gcc cac gca cgc ggc tga atcatc tttacatccc cagaggccct ggtatgtggt      649
Ala His Ala Arg Gly  *
        165

ggacaggctt gtttctgccg ggccct                                         675




     <210> 309
     <211> 1042
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (779)..(952)

     <400> 309
gtcccctact actactaaat tcgcggccgc gtcgacgttt aggggaggca tcaccagatt     60

aagagtggag atattagagt tgtgtgatcc cagctctgtc gttaatcacc tgtgtctatg    120

cagtcactta ttcccttcat acctgtcagc cgagagcact gactgcgtga tttccagggt    180

cctttacagc tttagagtat aggggctctg tttttgctgc tcccgaattt ccacctccca    240

tcatccacgc atttcacaga tgcatctgaa tgctcacagt gctctatttg tgctcttctg    300

tttgtccctg ttttttatgt ggatgcgtat cgaccgccat gatagactgc acactccctg    360

tgggcaggag ccatgttcat ttcatttttg tgtcccaggc ataatgtagg tgcgctcacc    420

tcatctctcc catatcttga acctgtgaat ctcagtggac tcttttcagc agatgaacct    480

gtataagtct ttcctgtctt gaaaggacag atgggtggcc cccatcctcc actgagcttc    540

ctgttgaact ccctttgcag gtgacgtcaa aatagaagaa gccctcattc accatatcta    600

ctgttaccct cctcctttcc cctctacttc ccatgaccag ttgttcactg cccctccaca    660

gaacctactt ctgataaatc ccgtgaagaa ttttttattg ccagatccaa attctttggc    720

ctctcacagt gtttgctgtg gcctgattct ccctcattct ggaaactcct ctcctctc      778
atg gct ccc atg gga cca gtt gct cct gca gct cct cct gcc cct cac      826
Met Ala Pro Met Gly Pro Val Ala Pro Ala Ala Pro Pro Ala Pro His
 1               5                  10                  15

tct gct ctc ctt gga ctc ctc ttt cct ggt att ctc tgc agt tct gtc      874
```

```
Ser Ala Leu Leu Gly Leu Leu Phe Pro Gly Ile Leu Cys Ser Ser Val
            20                  25                  30

ctt cgc tct cag ctc ttt gca ccc ttc ttt ccc tcg ctg aca gct tcg      922
Leu Arg Ser Gln Leu Phe Ala Pro Phe Phe Pro Ser Leu Thr Ala Ser
        35                  40                  45

cgc ata cct gtg gct tca ctg tca cgc taa g gaacattctc tgtggccctg      973
Arg Ile Pro Val Ala Ser Leu Ser Arg  *
    50                  55

gcccgtctct cgagcctgag ccccatgatt acaacttctg tctgtacccc acagtacata   1033

accttagcc                                                           1042




     <210> 310
     <211> 1333
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (43)..(555)

     <400> 310
accggtccgg aattcccggg tcgacgattt cgtccttcta cc   atg agg ctc cct       54
                                                 Met Arg Leu Pro
                                                  1

gct cag ctc ctg ggg ctg cta atg ctc tgg gtc cct gga tcc agt gag      102
Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Glu
 5                  10                  15                  20

gat att gtg atg acc cag act cca ctc tcc ctg ccc gtc acc cct gga      150
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Thr Pro Gly
                25                  30                  35

gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ttg gat agt      198
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
            40                  45                  50

gat gat gga aac acc tat ttg gac tgg tac ctg cag aag cca ggg cag      246
Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
        55                  60                  65

tct cca cag ctc ctg atc tat acg ctt tcc tat cgg gcc tct gga gtc      294
Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
    70                  75                  80

cca gac agg ttc agt ggc agt ggg tca ggc act gat ttc aca ctg aaa      342
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
85                  90                  95                  100

atc agc agg gtg gag gct gag gat gtt gga gtt tat tac tgc atg caa      390
```

```
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
                105                 110                 115

cgt ata gag ttt cct tgg act ttt ggc cag ggg acc aag ctg gag atc      438
Arg Ile Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            120                 125                 130

aaa cga act gtt gct gca cca tct gtc ttc atc ttc ccg cca tct gat      486
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        135                 140                 145

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac      534
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    150                 155                 160

ttc tat ccc aga gag gcc taa gt acagtggaaa gtggtaaacg gcctccaaac      587
Phe Tyr Pro Arg Glu Ala  *
165                 170

tggttaaatc cagtaaagtg tcacagagca agacagtaag gacagcacct acgtactcag    647

cagcaaccag aagctgagca aagttgactt atgagatacc acaagtctag gcctgacgaa    707

gtcaaccatt atggacttgg gctgtgtcca atctgaatat agttatacct gggcagagtg    767

gttaaaaggt atagtgtgtc ccctaaattg tatcctaggt ttcaagctcg tagtcacttg    827

cccaggcttt ttgtcccttg taggtccttt tttcccaatg gggacctaa gacactaagt     887

gacgggactc tccaaagtta atgatttaaa acttaaaatc actctctaag ggatcatcag    947

gagttatgaa gtcgatgact aattgttttt gatacgagta tatctgaaaa tgattgaaag   1007

tgtgaattcc tcatggtagg tgagataaac tagtcgttat agtatctagt agatgaccgg   1067

agcatttata gagtagaagt ccgcatactc ccggataatc taccacgaca catgattaga   1127

ctctcgcgat ggtaaacaga tggatgtaaa ctcaatcgtg ggagtaccga aagaggtggc   1187

tatgatgttg acatgatagg gtctaggatg cgtgatcgtg tgacggaatt gtcaaatacg   1247

tgtgaataca catttattgg caatttctgt atgacgtgat atgagattag cagaggttta   1307

tgaatgagtg acatcttgcg tgtggt                                        1333
```

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<210> 311
<211> 803
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (77)..(433)
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     <400> 311
cgcctgcagg taccggtccg gaattcccgg gtcgacgatt tcgtgcttca ttcctgtatg      60

gggtggtatt cctgcc    atg ggt cct ggg ctt ctc cac tgg atg gcc ctt      109
                     Met Gly Pro Gly Leu Leu His Trp Met Ala Leu
                      1               5                  10

tgt ctc ctt gga aca ggt cat ggg gat gcc atg gtc atc cag aac cca      157
Cys Leu Leu Gly Thr Gly His Gly Asp Ala Met Val Ile Gln Asn Pro
            15                  20                  25

aga tac cag gtt acc cag ttt gga aag cca gtg acc ctg agt tgt tct      205
Arg Tyr Gln Val Thr Gln Phe Gly Lys Pro Val Thr Leu Ser Cys Ser
        30                  35                  40

cag act ttg aac cat aac gtc atg tac tgg tac cag cag aag tca agt      253
Gln Thr Leu Asn His Asn Val Met Tyr Trp Tyr Gln Gln Lys Ser Ser
    45                  50                  55

cag gcc cca aag ctg ctg ttc cac tac tat gac aaa gat ttt aac aat      301
Gln Ala Pro Lys Leu Leu Phe His Tyr Tyr Asp Lys Asp Phe Asn Asn
 60                  65                  70                  75

gaa gca gac acc cct gat aac ttc caa tcc agg agg ccg aac act tct      349
Glu Ala Asp Thr Pro Asp Asn Phe Gln Ser Arg Arg Pro Asn Thr Ser
                80                  85                  90

ttc tgc ttt ctt gac atc cgc tca cca ggc ctg ggg gac gca gcc atg      397
Phe Cys Phe Leu Asp Ile Arg Ser Pro Gly Leu Gly Asp Ala Ala Met
            95                  100                 105

tac ctg tgt gcc acc agc gtc cac cgg gac cca tga acac tgaagctttc      447
Tyr Leu Cys Ala Thr Ser Val His Arg Asp Pro  *
        110                 115

tttggacaag gcaccagact cacagttgta gcatgtgaaa aggtccagag ctctgcagtg     507

tgagctttct actgaaatgg cccttggact ttgtggttca ttcatactca gtggtctagc     567

ttgtactact tttgagaatg caaagcttaa ctgtggacgg attccaatcc tggccaggca     627

gggttgctgg acactctgag agaagaaagg gttaatccca tgaccatcaa cttccatggg     687

atttcagcca tcctggacaa gctaccacac cctcctgccc caaggggagg aggaaatgtg     747

gaccatccca tcagaaattg accaaaggac ctgaacaagt ggtccccccc cccccc         803


     <210> 312
     <211> 687
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
```

```
<222>  (6)..(605)

<400>  312
agctg    atg ctc tgc aga caa caa ctc agg aat ttg act gaa aac aag       47
         Met Leu Cys Arg Gln Gln Leu Arg Asn Leu Thr Glu Asn Lys
           1               5                  10

gaa tct gag ttg cag tgt ctc ttt caa cag ata gaa agg cag gag cag       95
Glu Ser Glu Leu Gln Cys Leu Phe Gln Gln Ile Glu Arg Gln Glu Gln
 15                  20                  25                  30

ctt ctg gat gaa ata cat cgt gag aag aga gat cta ctg gaa gag acc      143
Leu Leu Asp Glu Ile His Arg Glu Lys Arg Asp Leu Leu Glu Glu Thr
                 35                  40                  45

caa aga aaa gat gaa gaa atg gga tct ctg cag gac cgt gta att gca      191
Gln Arg Lys Asp Glu Glu Met Gly Ser Leu Gln Asp Arg Val Ile Ala
             50                  55                  60

tta gaa acg agt acc caa gtg gcc ttg gac cat ctg gag tct gtg cct      239
Leu Glu Thr Ser Thr Gln Val Ala Leu Asp His Leu Glu Ser Val Pro
         65                  70                  75

gag aaa ctg agc cta cta gaa gat ttc aaa gac ttc aga gat tcc tgc      287
Glu Lys Leu Ser Leu Leu Glu Asp Phe Lys Asp Phe Arg Asp Ser Cys
     80                  85                  90

agt tca tct gag aga act gat gga aga tat tcc aaa tac agg gtt cgc      335
Ser Ser Ser Glu Arg Thr Asp Gly Arg Tyr Ser Lys Tyr Arg Val Arg
 95                 100                 105                 110

aga aat tct ctt cag cat cac caa gat gac acc aag tac aga acc aaa      383
Arg Asn Ser Leu Gln His His Gln Asp Asp Thr Lys Tyr Arg Thr Lys
                115                 120                 125

agt ttc aaa ggt gac aga acc ttt ctg gaa ggt tcc cac act cgt ggg      431
Ser Phe Lys Gly Asp Arg Thr Phe Leu Glu Gly Ser His Thr Arg Gly
            130                 135                 140

tta gat cac tca tcc tct tgg cag gat cac agt cgc ttc ctg tct agt      479
Leu Asp His Ser Ser Ser Trp Gln Asp His Ser Arg Phe Leu Ser Ser
        145                 150                 155

cca aga ttt tca tac gtg aac tca ttt acc aaa aga act gtt gct cca      527
Pro Arg Phe Ser Tyr Val Asn Ser Phe Thr Lys Arg Thr Val Ala Pro
    160                 165                 170

gat tca gct tca aac aag gaa gat gcc aca atg aat gga aca agt tca      575
Asp Ser Ala Ser Asn Lys Glu Asp Ala Thr Met Asn Gly Thr Ser Ser
175                 180                 185                 190

caa ccc aaa aaa gag gaa tat ggg agc taa a aaagcaaatg taatttgtta      626
Gln Pro Lys Lys Glu Glu Tyr Gly Ser  *
                195                 200

ttttacatga gtatgttaca aataataaca tctctattct tacagcaaaa aaaaaaaaaa    686
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a                                                                      687




     <210> 313
     <211> 1157
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (714)..(947)

     <400> 313
atttggccct cgaggccaag aattcggcac gaggatgaat aacaggataa cacgttgtta      60

cattgtcaca actcctgatc caggaattga tggctaagat attcgtaatt cttatccttt     120

tcagttgtaa cttattccta tttgtcagca ttcaggttat tagcggctgc tggcgaagtc     180

cttgagaaat aaactgcaca ctggatggtg ggggtagtgt aggaaaatgg aggggaagga     240

agtaaagttt caaattaagc ctgaacagca aagttcccct gagaaggcca cctggattct     300

atcagaaact cgaatgtcca tcttgcaaaa cttccttgcc caaaccccac ccctggagtc     360

acaacccacc cttgaccaat agattcattt cactgaggga ggcaaagggc tggtcaatag     420

attcatttca ctgggagagg caaagggctg gggccagag aggagaagta aaaagccaca      480

catgaagcag caatgcaggc atgcttctgg ctcatctgtg atcaccagga aactcccaga     540

tctgacactg tagtgcattt cactgctgac aagaaggctg ctgccaccag cctgtgaagc     600

aaggttaagg tgagaaggct ggaggtgaga ttctgggcag tctcctggtt gtctacccat     660

ggacctagag gtactttgaa agttttggat atctgggctc tgactgtgca ata   atg      716
                                                             Met
                                                              1

ggc aac ccc aaa gtc aag gca cat ggc aag aag gtg ctg atc tcc ttc       764
Gly Asn Pro Lys Val Lys Ala His Gly Lys Lys Val Leu Ile Ser Phe
            5                   10                  15

gga aaa gct gtt atg ctc acg gat gac ctc aaa ggc acc ttt gct aca       812
Gly Lys Ala Val Met Leu Thr Asp Asp Leu Lys Gly Thr Phe Ala Thr
        20                  25                  30

ctg agt gac ctg cac tgt aac aag ctg cac gtg gac cct gag aac ttc       860
Leu Ser Asp Leu His Cys Asn Lys Leu His Val Asp Pro Glu Asn Phe
    35                  40                  45

ctg ctc tta ggc aac gtg ata ttg att gtt ttg gca acc cac ttc agc       908
Leu Leu Leu Gly Asn Val Ile Leu Ile Val Leu Ala Thr His Phe Ser
 50                  55                  60                  65
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```
gag gat ttt acc cta cag ata cag gct tct tgg cag taa ctaacaaatg       957
Glu Asp Phe Thr Leu Gln Ile Gln Ala Ser Trp Gln  *
                 70                  75

ctgtggttaa tgctgtagcc cacaagacca ctgagttccc tgtccactat gtttgtacct   1017

atggtccact atgtttgtac ctatgtccca aaatctcatc tcctttagat gggggaggtt   1077

ggggagaaga gcagtatcct gcctgctgat tcagttcctg catgataaaa atagaataaa   1137

gaaatatgct ctctaagaaa                                               1157



     <210> 314
     <211> 583
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (219)..(479)

     <400> 314
ctatgatctc tgaatccttg gatgccaccc caacacacct aacccccaac tctcaggcca     60

agatagtaaa aagagagtca gagaacagga accgcataaa aagttcttca ttttccatca    120

cttggtggtg actttgaagg tagaggctga cagtgagtgg agtatggaca tgtcacccac    180

aaccagatga agagggactc cgagatagcg actcggct    atg cac aca gtc acc     233
                                             Met His Thr Val Thr
                                             1                5

cac aga gga gga gca ggg aag ggg gaa agt agc ctc tct cag cac atg      281
His Arg Gly Gly Ala Gly Lys Gly Glu Ser Ser Leu Ser Gln His Met
                 10                  15                  20

ata aaa aga cct gga tgg gga ggt gga gca gag gcc ttc act cca tca      329
Ile Lys Arg Pro Gly Trp Gly Gly Gly Ala Glu Ala Phe Thr Pro Ser
             25                  30                  35

ttt ttt aaa tcc atc ctt caa tat ttt caa gag gaa ggg aaa cca gac      377
Phe Phe Lys Ser Ile Leu Gln Tyr Phe Gln Glu Glu Gly Lys Pro Asp
         40                  45                  50

agg cca aac cac agc ctt cag tgg ggc ttg act tta gtt cta cgg acc      425
Arg Pro Asn His Ser Leu Gln Trp Gly Leu Thr Leu Val Leu Arg Thr
     55                  60                  65

tca cca gcc att cca gca gct gaa tgc ctg cca gtt ggt gcc cac acg      473
Ser Pro Ala Ile Pro Ala Ala Glu Cys Leu Pro Val Gly Ala His Thr
 70                  75                  80                  85

cta tga gaccccacaa ctgtgtgaga agctgggaac atttcacagg gaaaaagcag       529
Leu  *
```

```
aaatggaggg agtgaaaccc ctacttagtt tctgctgatc ctccctggta gaga          583



      <210> 315
      <211> 931
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (75)..(677)

      <400> 315
ggaattcgtt ttaagaggat cttctgctcc tcttcatctg gtccgtttcc ttccaaggcc      60

cccgagagga aggc atg cgg tgg gcc cta ctg gtg ctt cta gct ttc ctg       110
                Met Arg Trp Ala Leu Leu Val Leu Leu Ala Phe Leu
                1               5                   10

tct cct gcc agt cag aaa tct tcc aac ttg gaa ggg aga acg aag tca       158
Ser Pro Ala Ser Gln Lys Ser Ser Asn Leu Glu Gly Arg Thr Lys Ser
        15                  20                  25

gtc acc agg cag act ggg tca tct gct gaa atc act tgc gat ctt act       206
Val Thr Arg Gln Thr Gly Ser Ser Ala Glu Ile Thr Cys Asp Leu Thr
    30                  35                  40

gta aca aat acc ttc tac atc cac tgg tac cta cac cag gag ggg aag       254
Val Thr Asn Thr Phe Tyr Ile His Trp Tyr Leu His Gln Glu Gly Lys
45                  50                  55                  60

gcc cca cag cgt ctt ctg tac tat gac gtc tcc act gca agg gat gtg       302
Ala Pro Gln Arg Leu Leu Tyr Tyr Asp Val Ser Thr Ala Arg Asp Val
                65                  70                  75

ttg gaa tca gga ctc agt cca gga aag tat tat act cat aca ccc agg       350
Leu Glu Ser Gly Leu Ser Pro Gly Lys Tyr Tyr Thr His Thr Pro Arg
            80                  85                  90

agg tgg agc tgg ata ttg ata cta cga aat cta att gaa aat gat tct       398
Arg Trp Ser Trp Ile Leu Ile Leu Arg Asn Leu Ile Glu Asn Asp Ser
        95                  100                 105

ggg gtc tat tac tgt gcc acc tgg gac agg cac agt gat tca gac ctg       446
Gly Val Tyr Tyr Cys Ala Thr Trp Asp Arg His Ser Asp Ser Asp Leu
    110                 115                 120

tcc tac acc aca ctg aaa atc tgc ctt gtg gct gcc tct ggt tca cag       494
Ser Tyr Thr Thr Leu Lys Ile Cys Leu Val Ala Ala Ser Gly Ser Gln
125                 130                 135                 140

gat aga gcc gcc ccc tct cat ttc ctg tca cca aat tta ctg tat tct       542
Asp Arg Ala Ala Pro Ser His Phe Leu Ser Pro Asn Leu Leu Tyr Ser
```

```
                145                 150                 155

gaa caa gag aaa gac agc tta act cct gat ctc cct cct aat atc aca      590
Glu Gln Glu Lys Asp Ser Leu Thr Pro Asp Leu Pro Pro Asn Ile Thr
            160                 165                 170

ctg tcc tgg cag cag ctg cat cct gtt ccc cac ccc tcc ccc aca act      638
Leu Ser Trp Gln Gln Leu His Pro Val Pro His Pro Ser Pro Thr Thr
        175                 180                 185

ttc ctg aag atc aag ctg cca tct cca ggc ctc agc taa gcagcctggc       687
Phe Leu Lys Ile Lys Leu Pro Ser Pro Gly Leu Ser  *
    190                 195                 200

tgagagcaag gttctctcag ctctcctagg acatgggga ggcccactca ctctgcttcc     747

tatgacacac aggtacaact agggtccagc tgtgaagcga gatattttgg acagcaaatg    807

ggaagggtat ttatactgaa tcatgtatcc actcatggtc cagagatcac agctgagagt    867

ggtgcttatt ccttatgtct ataacaacat aagcaatact ataatgacca ctaaaacact    927

aggc                                                                 931



     <210> 316
     <211> 943
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (228)..(737)

     <400> 316
aatgccctcc acaagccaag cctcccgctc ttaggagctg agcatctgtc agctgcccaa     60

gcccgtggcc tcttgatggg gtgtttgagc aaccatcctg tttttcgccc caggcccttg    120

gaattgaaag tgaggatgac ttgtataaac tggtgaactt cttccttaaa tatcgagctc    180

accgtttatc ttccagcctc cagatcaagc cctgcagtca ggcgagc  atg gag aag     236
                                                     Met Glu Lys
                                                      1

gcg agc atg gag gag aca agc acg agg tca gaa ttg gag ctg gca gag      284
Ala Ser Met Glu Glu Thr Ser Thr Arg Ser Glu Leu Glu Leu Ala Glu
    5                   10                  15

cag acg gag atg gag gga gaa aag gaa gaa agc ctg gtg gaa ggg gag      332
Gln Thr Glu Met Glu Gly Glu Lys Glu Glu Ser Leu Val Glu Gly Glu
 20                  25                  30                  35

aag gag gaa gag gag gag acc cca ccc tcc ccc tgg gtc atc cac ccc      380
Lys Glu Glu Glu Glu Glu Thr Pro Pro Ser Pro Trp Val Ile His Pro
```

```
                40                  45                  50

aat gat gtc ctc aag att ctg gag gcc ttc ttc atg ggt ctg aag aag        428
Asn Asp Val Leu Lys Ile Leu Glu Ala Phe Phe Met Gly Leu Lys Lys
            55                  60                  65

cct agg gac tcg cgg gcc ccg ctg agg gta cag aag aat gtg cgt gac        476
Pro Arg Asp Ser Arg Ala Pro Leu Arg Val Gln Lys Asn Val Arg Asp
        70                  75                  80

aac tcc aag gac tcg gag tac tgg cag gcc ctg acc aca gtg atc cct        524
Asn Ser Lys Asp Ser Glu Tyr Trp Gln Ala Leu Thr Thr Val Ile Pro
    85                  90                  95

tcc tcc aag cag aac ctc tgg gat gcc ctc tac aca gcc ttg gag aag        572
Ser Ser Lys Gln Asn Leu Trp Asp Ala Leu Tyr Thr Ala Leu Glu Lys
100                 105                 110                 115

tac cac ctt gtc ctg acc cag agg gcc aag ctg ctg ctg gaa aac agt        620
Tyr His Leu Val Leu Thr Gln Arg Ala Lys Leu Leu Leu Glu Asn Ser
                120                 125                 130

tct ctg gag cag cag aac aca gag ctg cag gcg cta ctg cag cag tat        668
Ser Leu Glu Gln Gln Asn Thr Glu Leu Gln Ala Leu Leu Gln Gln Tyr
            135                 140                 145

ctg aac tcc aag atc aac tct gaa ctg caa gtt cct ccc act cag gtg        716
Leu Asn Ser Lys Ile Asn Ser Glu Leu Gln Val Pro Pro Thr Gln Val
        150                 155                 160

ttg cgg gta ccc aca aaa tga gc tggaccgcca aaggctgatg tgttagggct        769
Leu Arg Val Pro Thr Lys  *
    165                 170

ggcctgatgc tggtgtctgt gccggagcca gctcatatca cccactgggc cgcacctggg      829

cctgctctct ggattttcca gggctgtctt tatagcctgt cgaaataagg agccagagga      889

gttacctgtg tcctgcatta tgattaaagc cttttaaagt tgaaaaaaaa aaaa            943


<210> 317
<211> 793
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (339)..(623)

<400> 317
ttaatacgac cactataggg aatttggccc tcgagcgacg taattcggca cgagagaacg       60

gactactggt cttttaaaaa cacacctcac caagctcagc caccaactta aaaaggactt      120
```

```
gataatactt ttaccacttg cccttctcag aattcgggcc tgtcttcgga atgcgacagg     180

atacagccca tttgagctcc tgtatagatg ctccttttta ttaggcccca gtctcattcc     240

agacaccaga ccaacttgga ctgtgccccc aaaaacttgt catccctact atcttctctc     300

tagtcatact cctattcacc gttctcaact actcatac    atg ccc tgc tct tgt      353
                                             Met Pro Cys Ser Cys
                                              1               5

tta cac tgc cgg ttt aca ctg ttt ctc caa gcc atc aca gct gat atc       401
Leu His Cys Arg Phe Thr Leu Phe Leu Gln Ala Ile Thr Ala Asp Ile
                10                  15                  20

tcc tgg tgc tat cct caa act acc act ctt aac tcc ctc ttg gat ttg       449
Ser Trp Cys Tyr Pro Gln Thr Thr Thr Leu Asn Ser Leu Leu Asp Leu
            25                  30                  35

tta tat gat ctt tgc cgg cag gca ccc ctc caa tac ttt cac cct gat       497
Leu Tyr Asp Leu Cys Arg Gln Ala Pro Leu Gln Tyr Phe His Pro Asp
        40                  45                  50

gaa gtt cta ttc ttt act ttt ata ctc act ctt att ctc att ccc att       545
Glu Val Leu Phe Phe Thr Phe Ile Leu Thr Leu Ile Leu Ile Pro Ile
    55                  60                  65

ctt atg cca ccc ttt acc tct ccc cag cta tct cca cca cac tat caa       593
Leu Met Pro Pro Phe Thr Ser Pro Gln Leu Ser Pro Pro His Tyr Gln
70                  75                  80                  85

tct cac tgt ctc tct cct agc cat ttc taa t ccttctttaa caaacaattg       644
Ser His Cys Leu Ser Pro Ser His Phe  *
                90                  95

ctggctttgc atttctcttt cctctaaaac cactgaggcc tcaacttact cactgctgaa     704

aaaggaggac ttttcatatt tctaaatgaa gaatgttgtt tttacctaaa tcaatctggc     764

ctagtacctg acaacataaa aaaaaaaaa                                       793




<210> 318
<211> 1024
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (28)..(366)

<400> 318
gtggggcggc ggcctgcagc cagcaag    atg tac cac tgc agc gag tgc ctg       51
                                 Met Tyr His Cys Ser Glu Cys Leu
                                  1               5
```

```
cgc ttc ttc cag cag cgc aag agc ctg ctg ctg cac cag cgc ctg cac        99
Arg Phe Phe Gln Gln Arg Lys Ser Leu Leu Leu His Gln Arg Leu His
     10                  15                  20

acc ggc aat ggc cag ggc tgg ccc gcc tgc ccc tac tgc ggc aag gcc       147
Thr Gly Asn Gly Gln Gly Trp Pro Ala Cys Pro Tyr Cys Gly Lys Ala
 25                  30                  35                  40

ttc cgc cgg ccc tcg gac ctc ttc cgg cac cag cgc atc cac acc ggt       195
Phe Arg Arg Pro Ser Asp Leu Phe Arg His Gln Arg Ile His Thr Gly
                 45                  50                  55

gag cgg ccc tac cag tgc ccc cag tgt ggc cgg acc ttc aac cgc aac       243
Glu Arg Pro Tyr Gln Cys Pro Gln Cys Gly Arg Thr Phe Asn Arg Asn
             60                  65                  70

cac cac ctg gcc gtg cac atg cag acc cac gcc cga ggc cag gtg ggc       291
His His Leu Ala Val His Met Gln Thr His Ala Arg Gly Gln Val Gly
         75                  80                  85

cca cac ttc cct gcc gcc ccc gcc cgc cac ggg agc ctg ccc ctg ccc       339
Pro His Phe Pro Ala Ala Pro Ala Arg His Gly Ser Leu Pro Leu Pro
     90                  95                 100

tgg ccc agc cgg aag gag gag ggc tga cctgg caggagccca cagaggaccc       391
Trp Pro Ser Arg Lys Glu Glu Gly  *
105                 110

ctggcggggt ctctcccctg tgcctgacgc aggttcttcc ttttcctggg atggagagag      451

gtttgttgtt tttacccatt caaatgggaa gctagctgcc cttctggtga cattgtgtgt      511

gaccgggtgc tttctgtttc ctgtttgcac tcttcgctgc cttttctgca ttcctgactt      571

ctaaaagatg ccttaaggct taagggatgc catatttttg ataaggcctc tggtaggtac      631

cacagccaag aggaccagag atcatggccc ttccagtatg gggcgatag agacatcggg       691

gacctgggat ctcagttttg tgcagagatc tcctgcctgc tgtcaccatg agaaacagtg      751

gagtggagtg gatggatggc ctgacttgaa gaaagggccc tggaaagttt tctactttgc      811

tatattgaaa tataaatccc ttcttataga gactttgaaa tacttctgta aatgtgtgta      871

gtagtcaatg gaactttgcc tttagcaaag tcggaaagag tcggcttttc catgtgaggc      931

tcgcagagct gaaaggggag ctacgtccac caagcctgta ggtcataagg gacacaaaca      991

aggacgagga agaggaccct taaagaacgg acc                                 1024
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<210> 319
<211> 2552
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (281)..(2518)

<400> 319
tttaaaggca aagacacgcc ttcccccccc acttcagccg cgcgcctttc cttcccccaa      60

attcctcaaa gatggtttgt ctcacgtgtt gcagggcgta aaagcggctt gcattcaatt     120

agcagcgaag ctcgcgggcg ctggcgggac aggcgcgtga ggccacaaca catgcgtgta     180

tcttgcttgg gctatcttcc ctgctctgcc acgccgggtc tggagaaggg gtttcagccc     240

caggacattt actgagagtc ggcgaatatt gggagccgcg  atg ttc ccc ctt cgg      295
                                             Met Phe Pro Leu Arg
                                             1               5

gcc ctg tgg ttg gtc tgg gcg ctt cta gga gtg gcc gga tca tgc ccg      343
Ala Leu Trp Leu Val Trp Ala Leu Leu Gly Val Ala Gly Ser Cys Pro
                10                  15                  20

gag ccg tgc gcc tgc gtg gac aag tac gct cac cag ttc gcg gac tgc      391
Glu Pro Cys Ala Cys Val Asp Lys Tyr Ala His Gln Phe Ala Asp Cys
            25                  30                  35

gct tac aaa gag ttg cgt gag gtg ccg gaa gga ctg cct gcc aac gtg      439
Ala Tyr Lys Glu Leu Arg Glu Val Pro Glu Gly Leu Pro Ala Asn Val
        40                  45                  50

acg acg ctt agt ctg tcc gcg aac aag atc act gtg ctg cgg cgc ggg      487
Thr Thr Leu Ser Leu Ser Ala Asn Lys Ile Thr Val Leu Arg Arg Gly
    55                  60                  65

gcc ttc gcc gac gtc aca cag gtc acg tcg ctg tgg ctg gcg cac aat      535
Ala Phe Ala Asp Val Thr Gln Val Thr Ser Leu Trp Leu Ala His Asn
70                  75                  80                  85

gag gtg cgc acc gtg gag cca ggc gca ctg gcc gtg ctg agt cag ctc      583
Glu Val Arg Thr Val Glu Pro Gly Ala Leu Ala Val Leu Ser Gln Leu
                90                  95                  100

aag aac ctc gat ctg agc cac aac ttc ata tcc agc ttt ccg tgg agc      631
Lys Asn Leu Asp Leu Ser His Asn Phe Ile Ser Ser Phe Pro Trp Ser
            105                 110                 115

gac ctg cgc aac ctg agc gcg ctg cag ctg ctc aaa atg aac cac aac      679
Asp Leu Arg Asn Leu Ser Ala Leu Gln Leu Leu Lys Met Asn His Asn
        120                 125                 130

cgc ctg ggc tct ctg ccc cgg gac gca ctc ggt gcg cta ccc gac ctg      727
Arg Leu Gly Ser Leu Pro Arg Asp Ala Leu Gly Ala Leu Pro Asp Leu
    135                 140                 145

cgt tcc ctg cgc atc aac aac aac cgg ctg cgt acg ctg gcg cct ggc      775
Arg Ser Leu Arg Ile Asn Asn Asn Arg Leu Arg Thr Leu Ala Pro Gly
150                 155                 160                 165
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acc ttc gac gcg ctt agc gcg ctg tca cac ttg caa ctc tat cac aat        823
Thr Phe Asp Ala Leu Ser Ala Leu Ser His Leu Gln Leu Tyr His Asn
                170                 175                 180

ccc ttc cac tgc ggc tgc ggc ctt gtg tgg ctg cag gcc tgg gcc gcg        871
Pro Phe His Cys Gly Cys Gly Leu Val Trp Leu Gln Ala Trp Ala Ala
            185                 190                 195

agc acc cgg gtg tcc tta ccc gag ccc gac tcc att gct tgt gcc tcg        919
Ser Thr Arg Val Ser Leu Pro Glu Pro Asp Ser Ile Ala Cys Ala Ser
        200                 205                 210

cct ccc gcg ctg cag ggg gtg ccg gtg tac cgc ctg ccc gcc ctg ccc        967
Pro Pro Ala Leu Gln Gly Val Pro Val Tyr Arg Leu Pro Ala Leu Pro
    215                 220                 225

tgt gca ccg ccc agc gtg cat ctg agt gcc gag cca ccg ctt gaa gca       1015
Cys Ala Pro Pro Ser Val His Leu Ser Ala Glu Pro Pro Leu Glu Ala
230                 235                 240                 245

ccc ggc acc cca ctg cgc gca gga ctg gcg ttc gtg tta cac tgc atc       1063
Pro Gly Thr Pro Leu Arg Ala Gly Leu Ala Phe Val Leu His Cys Ile
                250                 255                 260

gcc gac ggc cac cct acg cct cgc ctg caa tgg caa ctt cag atc ccc       1111
Ala Asp Gly His Pro Thr Pro Arg Leu Gln Trp Gln Leu Gln Ile Pro
            265                 270                 275

ggt ggc acc gta gtc tta gag cca ccg gtt ctg agc ggg gag gac gac       1159
Gly Gly Thr Val Val Leu Glu Pro Pro Val Leu Ser Gly Glu Asp Asp
        280                 285                 290

ggg gtt ggg gcg gag gaa gga gag gga gaa gga gat ggg gat ttg ctg       1207
Gly Val Gly Ala Glu Glu Gly Glu Gly Glu Gly Asp Gly Asp Leu Leu
    295                 300                 305

acg cag acc caa gcc caa acg ccg act cca gca ccc gct tgg ccg gcg       1255
Thr Gln Thr Gln Ala Gln Thr Pro Thr Pro Ala Pro Ala Trp Pro Ala
310                 315                 320                 325

ccc cca gcc aca ccg cgc ttc ctg gcc ctc gca aat ggc tcc ctg ttg       1303
Pro Pro Ala Thr Pro Arg Phe Leu Ala Leu Ala Asn Gly Ser Leu Leu
                330                 335                 340

gtg ccc ctc ctg agt gcc aag gag gcg ggc gtc tac act tgc cgt gca       1351
Val Pro Leu Leu Ser Ala Lys Glu Ala Gly Val Tyr Thr Cys Arg Ala
            345                 350                 355

cac aat gag ctg ggc gcc aac tct acg tca ata cgc gtg gcg gtg gca       1399
His Asn Glu Leu Gly Ala Asn Ser Thr Ser Ile Arg Val Ala Val Ala
        360                 365                 370

gca acc ggg ccc cca aaa cac gcg cct ggc gcc ggg gga gaa ccc gac       1447
Ala Thr Gly Pro Pro Lys His Ala Pro Gly Ala Gly Gly Glu Pro Asp
    375                 380                 385
```

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gga cag gcc ccg acc tct gag cgc aag tcc aca gcc aag ggc cgg ggc        1495
Gly Gln Ala Pro Thr Ser Glu Arg Lys Ser Thr Ala Lys Gly Arg Gly
390                 395                 400                 405

aac agc gtc ctg cct tcc aaa ccc gag ggc aaa atc aaa ggc caa ggc        1543
Asn Ser Val Leu Pro Ser Lys Pro Glu Gly Lys Ile Lys Gly Gln Gly
                410                 415                 420

ctg gcc aag gtc agc att ctc ggg gag acc gag acg gag ccg gag gag        1591
Leu Ala Lys Val Ser Ile Leu Gly Glu Thr Glu Thr Glu Pro Glu Glu
            425                 430                 435

gac aca agt gag gga gag gag gcc gaa gac cag atc ctc gcg gac ccg        1639
Asp Thr Ser Glu Gly Glu Glu Ala Glu Asp Gln Ile Leu Ala Asp Pro
        440                 445                 450

gcg gag gag cag cgc tgt ggc aac ggg gac ccc tct cgg tac gtt tct        1687
Ala Glu Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser
    455                 460                 465

aac cac gcg ttc aac cag agc gca gag ctc aag ccg cac gtc ttc gag        1735
Asn His Ala Phe Asn Gln Ser Ala Glu Leu Lys Pro His Val Phe Glu
470                 475                 480                 485

ctg ggc gtc atc gcg ctg gat gtg gcg gag cgc gag gcg cgg gtg cag        1783
Leu Gly Val Ile Ala Leu Asp Val Ala Glu Arg Glu Ala Arg Val Gln
                490                 495                 500

ctg act ccg ctg gct gcg cgc tgg ggc cct ggg ccc ggc ggg gct ggc        1831
Leu Thr Pro Leu Ala Ala Arg Trp Gly Pro Gly Pro Gly Gly Ala Gly
            505                 510                 515

gga gcc ccg cga ccc ggg cgg cga ccc ctg cgc cta ctc tat ctg tgt        1879
Gly Ala Pro Arg Pro Gly Arg Arg Pro Leu Arg Leu Leu Tyr Leu Cys
        520                 525                 530

cca gcg ggg ggc ggc gcg gca gtg cag tgg tcc cgc gta gag gaa ggc        1927
Pro Ala Gly Gly Gly Ala Ala Val Gln Trp Ser Arg Val Glu Glu Gly
    535                 540                 545

gtc aac gcc tac tgg ttc cgc ggc ctg cgg ccg ggt acc aac tac tcc        1975
Val Asn Ala Tyr Trp Phe Arg Gly Leu Arg Pro Gly Thr Asn Tyr Ser
550                 555                 560                 565

gtg tgc ctg gcg ctg gcg ggc gaa gcc tgc cac gtg caa gtg gtg ttt        2023
Val Cys Leu Ala Leu Ala Gly Glu Ala Cys His Val Gln Val Val Phe
                570                 575                 580

tcc acc aag aag gag ctc cca tcg ctg ctg gtc ata gtg gca gtg agc        2071
Ser Thr Lys Lys Glu Leu Pro Ser Leu Leu Val Ile Val Ala Val Ser
            585                 590                 595

gta ttc ctc ctg gtg ctg gcc aca gtg ccc ctt ctg ggc gcc gcc tgc        2119
Val Phe Leu Leu Val Leu Ala Thr Val Pro Leu Leu Gly Ala Ala Cys
        600                 605                 610

tgc cat ctg ctg gct aaa cac ccg ggc aag ccc tac cgt ctg atc ctg        2167
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Cys His Leu Leu Ala Lys His Pro Gly Lys Pro Tyr Arg Leu Ile Leu
    615                 620                 625

cgg cct cag gcc cct gac cct atg gag aag cgc atc gcc gca gac ttc        2215
Arg Pro Gln Ala Pro Asp Pro Met Glu Lys Arg Ile Ala Ala Asp Phe
630                 635                 640                 645

gac ccg cgt gct tcg tac ctc gag tcc gag aaa agc tac ccg gca ggc        2263
Asp Pro Arg Ala Ser Tyr Leu Glu Ser Glu Lys Ser Tyr Pro Ala Gly
                650                 655                 660

ggc gag gcg ggc ggc gag gag cca gag gac gtg cag ggg gag ggc ctt        2311
Gly Glu Ala Gly Gly Glu Glu Pro Glu Asp Val Gln Gly Glu Gly Leu
            665                 670                 675

gat gaa gac gcg ggg cag gga gac cca agt ggg gac ctg cag aga gag        2359
Asp Glu Asp Ala Gly Gln Gly Asp Pro Ser Gly Asp Leu Gln Arg Glu
        680                 685                 690

gag agc ctg gcg gcc tgc tca ctg gtg gag tcc cag tcc aag gcc aac        2407
Glu Ser Leu Ala Ala Cys Ser Leu Val Glu Ser Gln Ser Lys Ala Asn
    695                 700                 705

caa gag gag ttc gag gcg ggc tct gag tac agc gat cgg ctg ccc ctg        2455
Gln Glu Glu Phe Glu Ala Gly Ser Glu Tyr Ser Asp Arg Leu Pro Leu
710                 715                 720                 725

ggc gcc gag gcg gtc aac atc gcc cag gag att aat ggc aac tac agg        2503
Gly Ala Glu Ala Val Asn Ile Ala Gln Glu Ile Asn Gly Asn Tyr Arg
                730                 735                 740

cag acg gca ggc tga acctccgccc gtccggcccg cccattccga cctg              2552
Gln Thr Ala Gly  *
            745




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ctttgtccgg ccagggctgc ccttccggtt ccgttgggtc cccctttggc tcgggttcct       120

tgcccctccc ccttcccgga gccccgaggg gccggagctc ctggcggtgc cggatcctga       180

cggcggcctt cccccgggtc tgtctgccaa a   atg tct gaa aga tca gat ctc       232
                                     Met Ser Glu Arg Ser Asp Leu
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                                             1               5

ctt cac ttc aag ttt gaa aat tat gga gat tca atg tta caa aaa atg       280
Leu His Phe Lys Phe Glu Asn Tyr Gly Asp Ser Met Leu Gln Lys Met
        10                  15                  20

aac aaa tta aga gaa gag aat aaa ttt tgt gat gtt aca gtt ctc ata       328
Asn Lys Leu Arg Glu Glu Asn Lys Phe Cys Asp Val Thr Val Leu Ile
    25                  30                  35

gat gat att gag gta cag gga cat aaa att gtg ttt gct gca ggt tcc       376
Asp Asp Ile Glu Val Gln Gly His Lys Ile Val Phe Ala Ala Gly Ser
40                  45                  50                  55

ccc ttc tta aga gac caa ttt tta ctg aat gat tcc aga gag gtg aaa       424
Pro Phe Leu Arg Asp Gln Phe Leu Leu Asn Asp Ser Arg Glu Val Lys
                60                  65                  70

atc tcc ata tta cag agt tcc gaa gtg ggg aga caa ttg ctc tta tcc       472
Ile Ser Ile Leu Gln Ser Ser Glu Val Gly Arg Gln Leu Leu Leu Ser
            75                  80                  85

tgt tat agt ggt gtg ctg gaa ttc cct gag atg gaa ctg gta aat tac       520
Cys Tyr Ser Gly Val Leu Glu Phe Pro Glu Met Glu Leu Val Asn Tyr
        90                  95                  100

ttg act gct gca agt ttt ctt cag atg agc cac att gta gaa cgg tgc       568
Leu Thr Ala Ala Ser Phe Leu Gln Met Ser His Ile Val Glu Arg Cys
    105                 110                 115

aca cag gcc ctg tgg aag ttt ata aag cca aaa caa cca atg gat agt       616
Thr Gln Ala Leu Trp Lys Phe Ile Lys Pro Lys Gln Pro Met Asp Ser
120                 125                 130                 135

aaa gag gga tgt gaa cca cag agt gct tct ccc cag tca aaa gaa cag       664
Lys Glu Gly Cys Glu Pro Gln Ser Ala Ser Pro Gln Ser Lys Glu Gln
                140                 145                 150

cag gga gat gcc aga ggc tcc cca aag cag gac tca cct tgt att cat       712
Gln Gly Asp Ala Arg Gly Ser Pro Lys Gln Asp Ser Pro Cys Ile His
            155                 160                 165

cca tct gaa gac agt atg gat atg gag gac agt gat att cag att gtt       760
Pro Ser Glu Asp Ser Met Asp Met Glu Asp Ser Asp Ile Gln Ile Val
        170                 175                 180

aag gta gaa tct att ggg gat gta tca gag gtt aga agt aaa aaa gat       808
Lys Val Glu Ser Ile Gly Asp Val Ser Glu Val Arg Ser Lys Lys Asp
    185                 190                 195

cag aac cag ttt att tct tct gaa ccc act gct tta cat tca tca gag       856
Gln Asn Gln Phe Ile Ser Ser Glu Pro Thr Ala Leu His Ser Ser Glu
200                 205                 210                 215

ccc cag cac tcc ctg ata aat tca act gtg gaa aac aga gta agt gaa       904
Pro Gln His Ser Leu Ile Asn Ser Thr Val Glu Asn Arg Val Ser Glu
                220                 225                 230
```

```
ata gaa caa aac cat ctc cac aat tat gcc ctt tct tat aca ggc agt        952
Ile Glu Gln Asn His Leu His Asn Tyr Ala Leu Ser Tyr Thr Gly Ser
            235                 240                 245

gat aac atc atc atg gcc tca aaa gat gtc ttt ggc cct aat att cga       1000
Asp Asn Ile Ile Met Ala Ser Lys Asp Val Phe Gly Pro Asn Ile Arg
        250                 255                 260

ggt gta gac aaa ggc cta cag tgg cat cac cag tgc cca aag tgt acc       1048
Gly Val Asp Lys Gly Leu Gln Trp His His Gln Cys Pro Lys Cys Thr
    265                 270                 275

agg gtg ttt cgt cac ctg gag aac tac gcc aac cat tta aaa atg cac       1096
Arg Val Phe Arg His Leu Glu Asn Tyr Ala Asn His Leu Lys Met His
280                 285                 290                 295

aaa ctc ttt atg tgt cta ctc tgc ggc aag act ttc act cag aaa ggc       1144
Lys Leu Phe Met Cys Leu Leu Cys Gly Lys Thr Phe Thr Gln Lys Gly
                300                 305                 310

aac ctt cat cga cac atg cgt gtg cat gcc gga att aaa cct ttc cag       1192
Asn Leu His Arg His Met Arg Val His Ala Gly Ile Lys Pro Phe Gln
            315                 320                 325

tgt aaa atc tgt ggg aaa acc ttt tct cag aag tgt tcc tta cag gat       1240
Cys Lys Ile Cys Gly Lys Thr Phe Ser Gln Lys Cys Ser Leu Gln Asp
        330                 335                 340

cat ctt aac ctt cac agt gga gat aag ccc cat aaa tgt aac tat tgt       1288
His Leu Asn Leu His Ser Gly Asp Lys Pro His Lys Cys Asn Tyr Cys
    345                 350                 355

gat atg gtt ttt gca cat aaa cca gtt ttg agg aaa cac ctt aaa cag       1336
Asp Met Val Phe Ala His Lys Pro Val Leu Arg Lys His Leu Lys Gln
360                 365                 370                 375

ctg cat ggc aaa aac agc ttt gat aat gcc aat gag aga aat gta caa       1384
Leu His Gly Lys Asn Ser Phe Asp Asn Ala Asn Glu Arg Asn Val Gln
                380                 385                 390

gac ctc aca gtg gat ttt gat tct ttt gca tgt aca aca gtc aca gac       1432
Asp Leu Thr Val Asp Phe Asp Ser Phe Ala Cys Thr Thr Val Thr Asp
            395                 400                 405

tct aaa ggg tgt cag cca caa ccc gat gca aca cag gtc ctg gat gca       1480
Ser Lys Gly Cys Gln Pro Gln Pro Asp Ala Thr Gln Val Leu Asp Ala
        410                 415                 420

ggt aaa ctg gcc caa gct gtc ctg aac tta aga aat gat agt act tgt       1528
Gly Lys Leu Ala Gln Ala Val Leu Asn Leu Arg Asn Asp Ser Thr Cys
    425                 430                 435

gtg aat tga gtagggg cttcatgccc acaactcgaa ctgactgaca atgtggcaat       1584
Val Asn  *
440
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agtcttagtc tttttaggag tgattttgct agtttgactt ctccaaagcc tctgtgtagg   1644

tggtagggag tgagtcaaag cactaataga ccaggcaact taccacttgg agtggatttg   1704

ccttactttt gccctctccc attttctgtt ttgagttatt tatcttgtaa agtctgtttt   1764

cctttcccaa ggaataattc cttttgtcta cctaacattg acttatgtct tagactgaca   1824

ctgttttagg cttttcacta ggcacattcc gaaggtacca acaagttaat aacatcaact   1884

aatctccact aatagaatgc tatgctaaga agaagtgaat aatctttctt aggtagaaaa   1944

taggctggat tttaagggtg aatattggta ttgactggaa atgtgtgttg aattttggtt   2004

gaccaatgga tattcacact ccatgtcgga ttaagtaaac tggggtccat accattggta   2064

ctgtcctagg aagcgcgata taagaaaata tgccgaactg caacggaccc atacacagat   2124

tattgcacaa aacacacaca ttcaatggca catatcacga agacctatat agagcacctc   2184

gtgaacatat ctattgggag atcatagaga aagtaaaaaa gcgcgtaaac ataattataa   2244

acaacaaagc ggaggtatct gaatagacca gaggaagtag tatatctagg aatagtactg   2304

accaaggaga acacacaagt agagttgaac acatacagag agcagtagca cagaacaaca   2364

agacgatgta gtcgcttaac tttaactact agtctt                             2400



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ggactcctcc tgggataact tgtccacaca tcttccacta gggtaaggct acttctggct      60

gaggagacac ttggatgtag ctcaagtgct gcttaggcag tcctgatctc tcctctcgtc     120

tcttcccagg gagctgaaaa gccagattcg acctggtagc caagca   atg tca cag     175
                                                     Met Ser Gln
                                                     1

cag aag cag caa tct tgg aag cct cca aat gtt ccc aaa tgc tcc cct       223
Gln Lys Gln Gln Ser Trp Lys Pro Pro Asn Val Pro Lys Cys Ser Pro
    5                   10                  15

ccc caa aga tca aac ccc tgc cta gct ccc tac tcg act cct tgt ggt       271
Pro Gln Arg Ser Asn Pro Cys Leu Ala Pro Tyr Ser Thr Pro Cys Gly
20                  25                  30                  35
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gct ccc cat tca gaa ggt tgt cat tcc agt tcc caa agg cct gag gtt         319
Ala Pro His Ser Glu Gly Cys His Ser Ser Ser Gln Arg Pro Glu Val
                40                  45                  50

cag aag cct agg agg gct cgt caa aag ctg cgc tgc cta agt agg ggc         367
Gln Lys Pro Arg Arg Ala Arg Gln Lys Leu Arg Cys Leu Ser Arg Gly
            55                  60                  65

aca acc tac cac tgc aaa gag gaa gag tgt gaa ggc gac tga gcccaga         416
Thr Thr Tyr His Cys Lys Glu Glu Glu Cys Glu Gly Asp  *
        70                  75                  80

agagttgagg cacaggtgca gttactctct ccctgcccca cctttgggta ctaattcccc       476

cttggaaagc caggccctca acctctcatt tggactgaga aacacttcct gatccccagc       536

tctagagaag cgagaactag gctgagccac gctgctactg ctctcttcca ttcacccctt       596

cagctcagca acaataaagc tgctttactt ggaaaaaaaa aaaa                        640




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     <213> Homo sapiens

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     <222> (162)..(2906)

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ttttattccc gggtcgacga tttgtgcagc tgtcttttcc ggcccccgtg cactctcttt        60

ccgaggcgga gcccccggc tcgcggggat cgcccccgag cgctgcgtcc tgcgggtggg        120

tcacctaacc catttgtggc ttcctctacc tgtgctcagc c   atg gcc agc gag         173
                                                Met Ala Ser Glu
                                                  1

agc tca cct ctg ctg gcc tac cgg ctc ctg ggg gag gag ggg gtt gcc         221
Ser Ser Pro Leu Leu Ala Tyr Arg Leu Leu Gly Glu Glu Gly Val Ala
 5                  10                  15                  20

ctc cct gcc aat ggg gcc ggg ggt cct gga ggg gcg tct gcc cgg aag         269
Leu Pro Ala Asn Gly Ala Gly Gly Pro Gly Gly Ala Ser Ala Arg Lys
                25                  30                  35

ctg tcc acc ttc ctg ggt gtg gtg gtg ccc act gtc ctg tcc atg ttc         317
Leu Ser Thr Phe Leu Gly Val Val Val Pro Thr Val Leu Ser Met Phe
            40                  45                  50

agc ata gtt gtt ttt ctg agg att ggg ttc gtg gtg ggt cat gct ggg         365
Ser Ile Val Val Phe Leu Arg Ile Gly Phe Val Val Gly His Ala Gly
        55                  60                  65
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cta ctg cag gcc ctg gcc atg ctg ctg gtt gcc tac ttc atc ctg gca      413
Leu Leu Gln Ala Leu Ala Met Leu Leu Val Ala Tyr Phe Ile Leu Ala
     70                  75                  80

ctc acc gtc ctc tct gtc tgt gcc atc gcc acc aat gga gcc gtg cag      461
Leu Thr Val Leu Ser Val Cys Ala Ile Ala Thr Asn Gly Ala Val Gln
 85                  90                  95                 100

ggg ggc gga gcc tac ttc atg atc agc cgc aca ctg ggg ccc gag gtc      509
Gly Gly Gly Ala Tyr Phe Met Ile Ser Arg Thr Leu Gly Pro Glu Val
                105                 110                 115

ggg ggc agc att ggg ctc atg ttc tac ctg gct aac gtc tgt ggc tgt      557
Gly Gly Ser Ile Gly Leu Met Phe Tyr Leu Ala Asn Val Cys Gly Cys
            120                 125                 130

gcc gtc tcc ctc ctg ggg ctg gtg gag tct gtg ctt gat gtc ttc ggg      605
Ala Val Ser Leu Leu Gly Leu Val Glu Ser Val Leu Asp Val Phe Gly
        135                 140                 145

gcc gat gcc aca ggg ccc agt ggg ctc cgg gtc ctg ccc cag ggc tac      653
Ala Asp Ala Thr Gly Pro Ser Gly Leu Arg Val Leu Pro Gln Gly Tyr
    150                 155                 160

ggc tgg aac ctg ctg tat ggc tcc ctg ctg ctg ggc ctt gtg ggt ggg      701
Gly Trp Asn Leu Leu Tyr Gly Ser Leu Leu Leu Gly Leu Val Gly Gly
165                 170                 175                 180

gtc tgc acc ctg gga gcc ggc ctc tat gcc cgg gcc tca ttc ctc aca      749
Val Cys Thr Leu Gly Ala Gly Leu Tyr Ala Arg Ala Ser Phe Leu Thr
                185                 190                 195

ttc ctg ctg gtc tct ggc tcc ctg gcc tct gtg ctc atc agt ttt gtg      797
Phe Leu Leu Val Ser Gly Ser Leu Ala Ser Val Leu Ile Ser Phe Val
            200                 205                 210

gct gtg ggg ccg agg gac atc cgc ttg act cct agg cct ggc ccc aat      845
Ala Val Gly Pro Arg Asp Ile Arg Leu Thr Pro Arg Pro Gly Pro Asn
        215                 220                 225

ggc tcc tcc ctg ccg ccc cgg ttt ggc cac ttc acc ggc ttc aac agc      893
Gly Ser Ser Leu Pro Pro Arg Phe Gly His Phe Thr Gly Phe Asn Ser
    230                 235                 240

agt acc ctg aag gac aac ttg ggc gct ggc tat gct gag gac tac acc      941
Ser Thr Leu Lys Asp Asn Leu Gly Ala Gly Tyr Ala Glu Asp Tyr Thr
245                 250                 255                 260

acg gga gcc gtg atg aat ttt gcc aac gtc ttt gct gtc ctc ttt aac      989
Thr Gly Ala Val Met Asn Phe Ala Asn Val Phe Ala Val Leu Phe Asn
                265                 270                 275

ggc tgt aca ggc atc atg gct ggg gcc aac atg tca ggg gag ctg aag     1037
Gly Cys Thr Gly Ile Met Ala Gly Ala Asn Met Ser Gly Glu Leu Lys
            280                 285                 290

gac ccc agc cgg gcg atc cct ctg ggc acg atc gtc gcc gtc gcc tac     1085
```

```
Asp Pro Ser Arg Ala Ile Pro Leu Gly Thr Ile Val Ala Val Ala Tyr
        295                 300                 305

acc ttc ttc gtc tat gtc ctg ctt ttc ttt ctc tcc agc ttc act tgt       1133
Thr Phe Phe Val Tyr Val Leu Leu Phe Phe Leu Ser Ser Phe Thr Cys
    310                 315                 320

gac agg acc ctg ctg cag gaa gac tat ggg ttc ttc cgc gcc atc agc       1181
Asp Arg Thr Leu Leu Gln Glu Asp Tyr Gly Phe Phe Arg Ala Ile Ser
325                 330                 335                 340

ctg tgg ccc cca ctg gtg ttg atc gga atc tat gcc aca gcg ctc tca       1229
Leu Trp Pro Pro Leu Val Leu Ile Gly Ile Tyr Ala Thr Ala Leu Ser
                345                 350                 355

gcg tcc atg agc tcg ctc att ggt gcc tcc cgc atc ctc cat gcc ctg       1277
Ala Ser Met Ser Ser Leu Ile Gly Ala Ser Arg Ile Leu His Ala Leu
            360                 365                 370

gcc cgg gat gac ctc ttt ggc gtg atc ttg gca ccg gcc aag gtt gtg       1325
Ala Arg Asp Asp Leu Phe Gly Val Ile Leu Ala Pro Ala Lys Val Val
        375                 380                 385

tcc cga ggg gga aac ccc tgg gca gct gta ctt tat tct tgg ggc ctg       1373
Ser Arg Gly Gly Asn Pro Trp Ala Ala Val Leu Tyr Ser Trp Gly Leu
    390                 395                 400

gtg cag ctg gtg ctc ctg gct ggg aag ctg aac aca ctg gcc gct gtg       1421
Val Gln Leu Val Leu Leu Ala Gly Lys Leu Asn Thr Leu Ala Ala Val
405                 410                 415                 420

gtc act gtc ttc tac ctg gtg gcc tat gct gcc gtg gac ctg tcc tgc       1469
Val Thr Val Phe Tyr Leu Val Ala Tyr Ala Ala Val Asp Leu Ser Cys
                425                 430                 435

ctg agc ctg gag tgg gcc tcg gcc ccc aac ttc cgc ccc acc ttc agc       1517
Leu Ser Leu Glu Trp Ala Ser Ala Pro Asn Phe Arg Pro Thr Phe Ser
            440                 445                 450

ctg ttc tcc tgg cac acc tgc ctg ctg ggg gtg gcc tcc tgc ctg ctc       1565
Leu Phe Ser Trp His Thr Cys Leu Leu Gly Val Ala Ser Cys Leu Leu
        455                 460                 465

atg atg ttc ctc atc agt cct ggc gcg gct ggt ggc tcc ctg ctc ctc       1613
Met Met Phe Leu Ile Ser Pro Gly Ala Ala Gly Gly Ser Leu Leu Leu
    470                 475                 480

atg ggt ctg ctg gct gcc ctg ctc acc gcg cga gga ggc ccc agt agc       1661
Met Gly Leu Leu Ala Ala Leu Leu Thr Ala Arg Gly Gly Pro Ser Ser
485                 490                 495                 500

tgg ggc tat gtc agc cag gcc ttg ctt ttc cac cag gtg cgt aag tat       1709
Trp Gly Tyr Val Ser Gln Ala Leu Leu Phe His Gln Val Arg Lys Tyr
                505                 510                 515

ctg ctt cgg ctg gac gtc cgg aag gat cac gtg aag ttc tgg cgg ccc       1757
Leu Leu Arg Leu Asp Val Arg Lys Asp His Val Lys Phe Trp Arg Pro
```

```
          520                       525                       530

cag ctg ctg ctc ctg gtg ggg aac ccc cgg ggc gcc ctg cct ctg ctg        1805
Gln Leu Leu Leu Leu Val Gly Asn Pro Arg Gly Ala Leu Pro Leu Leu
      535                       540                       545

cgg ttg gcc aac cag ctt aag aag ggg ggg ctg tat gtg ctg ggc cac        1853
Arg Leu Ala Asn Gln Leu Lys Lys Gly Gly Leu Tyr Val Leu Gly His
  550                       555                       560

gtc acc ctg gga gac ctc gac tcc ctg ccc tcg gac cct gta cag ccg        1901
Val Thr Leu Gly Asp Leu Asp Ser Leu Pro Ser Asp Pro Val Gln Pro
565                     570                     575                     580

cag tat ggg gca tgg ctc agc ctg gtg gac cgt gcc cag gtg aag gct        1949
Gln Tyr Gly Ala Trp Leu Ser Leu Val Asp Arg Ala Gln Val Lys Ala
                585                     590                     595

ttt gtg gat cta acc ttc tca ccc tcc gtg cgc cag ggg gct cag cat        1997
Phe Val Asp Leu Thr Phe Ser Pro Ser Val Arg Gln Gly Ala Gln His
            600                     605                     610

ctg ctg cga atc tcc ggc ctc ggt ggc atg aag ccc aac acg ttg gtc        2045
Leu Leu Arg Ile Ser Gly Leu Gly Gly Met Lys Pro Asn Thr Leu Val
        615                     620                     625

cta ggt ttc tac gat gac gct cca ccg cag gac cat ttc ctg acg gac        2093
Leu Gly Phe Tyr Asp Asp Ala Pro Pro Gln Asp His Phe Leu Thr Asp
    630                     635                     640

ccg gct ttc tct gag cct gca gac agc acc agg gag ggc agt tcc cca        2141
Pro Ala Phe Ser Glu Pro Ala Asp Ser Thr Arg Glu Gly Ser Ser Pro
645                     650                     655                     660

gct ctg agc acc ctg ttc cct cct ccc cgg gct cct ggg agc ccc cgg        2189
Ala Leu Ser Thr Leu Phe Pro Pro Pro Arg Ala Pro Gly Ser Pro Arg
                665                     670                     675

gcc ctc aat ccc cag gac tat gtg gcc acg gtg gcc gac gcc ctc aag        2237
Ala Leu Asn Pro Gln Asp Tyr Val Ala Thr Val Ala Asp Ala Leu Lys
            680                     685                     690

atg aac aag aat gtg gtg ctg gcc cgg gcc agc ggg gcc ttg ccc cct        2285
Met Asn Lys Asn Val Val Leu Ala Arg Ala Ser Gly Ala Leu Pro Pro
        695                     700                     705

gag cgg ctg agc cgg ggg tct ggg ggc acc tct cag ttg cac cat gtg        2333
Glu Arg Leu Ser Arg Gly Ser Gly Gly Thr Ser Gln Leu His His Val
    710                     715                     720

gac gtg tgg ccc ctc aac ttg ttg cgg ccc cgg ggt ggg ccc ggc tat        2381
Asp Val Trp Pro Leu Asn Leu Leu Arg Pro Arg Gly Gly Pro Gly Tyr
725                     730                     735                     740

gtg gat gtc tgc ggc ctc ttc ctg ctg cag atg gca acc atc ttg ggc        2429
Val Asp Val Cys Gly Leu Phe Leu Leu Gln Met Ala Thr Ile Leu Gly
                745                     750                     755
```

atg gtg ccc gct tgg cat agc gcc cgg ctc cgg atc ttc ctg tgc ctg 2477
Met Val Pro Ala Trp His Ser Ala Arg Leu Arg Ile Phe Leu Cys Leu
760 765 770

ggg cct cgg gag gcg cct ggg gcg gcc gag ggg cgg ctg cgg gca ctg 2525
Gly Pro Arg Glu Ala Pro Gly Ala Ala Glu Gly Arg Leu Arg Ala Leu
775 780 785

ctg agc caa ctg agg atc cgg gct gag gtg cag gag gtg gtg tgg ggc 2573
Leu Ser Gln Leu Arg Ile Arg Ala Glu Val Gln Glu Val Val Trp Gly
790 795 800

gag ggg gcc ggg gct ggg gaa ccc gag gcg gag gag gaa ggg gac ttt 2621
Glu Gly Ala Gly Ala Gly Glu Pro Glu Ala Glu Glu Glu Gly Asp Phe
805 810 815 820

gtg aac agt ggg cgg gga gac gca gag gca gag gcc ctg gca cgc agc 2669
Val Asn Ser Gly Arg Gly Asp Ala Glu Ala Glu Ala Leu Ala Arg Ser
825 830 835

gcc aac gcc ctg gtt cgg gcc cag cag ggg cgc ggc aca gga gga ggg 2717
Ala Asn Ala Leu Val Arg Ala Gln Gln Gly Arg Gly Thr Gly Gly Gly
840 845 850

ccg ggt ggg ccg gag ggt ggg gat gct gag ggc ccc atc aca gcc ctc 2765
Pro Gly Gly Pro Glu Gly Gly Asp Ala Glu Gly Pro Ile Thr Ala Leu
855 860 865

acc ttc ctg tac ttg cct cgg ccg cca gcc gat ccc gcc cga tac ccc 2813
Thr Phe Leu Tyr Leu Pro Arg Pro Pro Ala Asp Pro Ala Arg Tyr Pro
870 875 880

cgc tac ctg gcg cta ctg gag act cta acc cga gac ctg ggc ccc acg 2861
Arg Tyr Leu Ala Leu Leu Glu Thr Leu Thr Arg Asp Leu Gly Pro Thr
885 890 895 900

ctg ctg gtt cat ggg gtc act cca gtc acc tgc act gat ctg tga 2906
Leu Leu Val His Gly Val Thr Pro Val Thr Cys Thr Asp Leu *
905 910 915

<210> 323
<211> 607
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (78)..(416)

<400> 323
actagcgtgg ttccagtgtc gtcatcgctg ctaaaaaagg ggtttcccgg tgacaggccc 60

```
cgacagagga gcaggcc   atg agg cag gca gga gcc acg tat ctg ggc cca     110
                     Met Arg Gln Ala Gly Ala Thr Tyr Leu Gly Pro
                      1               5                  10

gcg cac ccg cca agc tct cta gcc tct cct ggc ctc agt ata ctt ctc      158
Ala His Pro Pro Ser Ser Leu Ala Ser Pro Gly Leu Ser Ile Leu Leu
            15                  20                  25

tgg gag atg gtc cag ctg aaa atc ccc agc atc cac aag aaa ggg tgg      206
Trp Glu Met Val Gln Leu Lys Ile Pro Ser Ile His Lys Lys Gly Trp
        30                  35                  40

aag ccc tgg ggg ccc tgg cct ggc cca ggt gca ggc tgc atg gcc ggg      254
Lys Pro Trp Gly Pro Trp Pro Gly Pro Gly Ala Gly Cys Met Ala Gly
    45                  50                  55

cgg agc ggt gtc tcc ttt cac agc ttc ccc gtc tgt ccg cag cct cca      302
Arg Ser Gly Val Ser Phe His Ser Phe Pro Val Cys Pro Gln Pro Pro
60                  65                  70                  75

gga gcc cca cac agg gct ggg gct ctg tgc ccc caa ctc aca ccc gtc      350
Gly Ala Pro His Arg Ala Gly Ala Leu Cys Pro Gln Leu Thr Pro Val
                80                  85                  90

ggc tcc ccc agg agg agc agg ctg ggc cca gag ccg cag ggt ggg ctg      398
Gly Ser Pro Arg Arg Ser Arg Leu Gly Pro Glu Pro Gln Gly Gly Leu
            95                  100                 105

cag gga ggt ctg act tag ctgggg aaagtgccat ccctgccatt gctagtgaca      452
Gln Gly Gly Leu Thr  *
        110

agctcgggct gctgtggccc cagcacagat tcaacactca ctgcgctacg tgccagctgt    512

tgcacactca cctccacacc caactcacag gaagcaaggc tgggaaggag ggaactggcc    572

ccaggccaca cagatgctgc gagttgggat tatga                               607




     <210> 324
     <211> 505
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (73)..(252)

     <400> 324
ccctgattag tgtataaatt tgaatatctt tcatatttat tggctattgg gatttcctct     60

gccataactt ga   atg tta gga tct act ggt tat ttt tat ttc ctt gcc      108
                Met Leu Gly Ser Thr Gly Tyr Phe Tyr Phe Leu Ala
                 1               5                  10
```

```
gat ttg ctg ata tta aca ata gat ttt aat ctc ttg tta ata ata tac      156
Asp Leu Leu Ile Leu Thr Ile Asp Phe Asn Leu Leu Leu Ile Ile Tyr
        15                  20                  25

ctt gca aac tac ttt tct cag tct gtg gct tat ctt ttc att tct tta      204
Leu Ala Asn Tyr Phe Ser Gln Ser Val Ala Tyr Leu Phe Ile Ser Leu
    30                  35                  40

tgg gtt ttc ttt ggc atg agg gta caa gtt tta ctt tta atg aag taa      252
Trp Val Phe Phe Gly Met Arg Val Gln Val Leu Leu Leu Met Lys  *
45                  50                  55                  60

aatatgtaac tttacattac agtttgtgct tatttgtatt acttatgaaa catttcccta    312

cccagaagtc atgaaggtat tctcctctat ttccttctag aagtttggct cttcagattt    372

ccaatgttcc tgaaattaac ttctatgtag ggtgaggtag caacccaatt ttattttctt    432

ccatataatc acttgaccta gcaaaatata attgcctatt ctttccccaa tgatctacaa    492

tgccatattt agt                                                       505




<210> 325
<211> 670
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (232)..(624)

<400> 325
ccggatactg cccgggtcga cccacgcgtc cggtagacag ggagctgtga cgagagcaag     60

aggtcataac acatccagac tccttaagag aaagcctttc tgttttggaa acttttcaaa    120

gccagggact tgtccagccc aacctcccca ttgctcctag ctcctgaggc tcaggacccc    180

tggcttctgt cctccctgct cagggtcctg cagcgttgcc tctgctcagc c atg ctc     237
                                                         Met Leu
                                                         1

ctg ctg ctc gtc cca gtg ctc gag gtg att ttt act ctg gga gga acc      285
Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly Gly Thr
        5                   10                  15

aga gcc cag tcg gtg acc cag ctt gac agc cac gtc tct gtc tct gaa      333
Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val Ser Glu
    20                  25                  30

gga acc ccg gtg ctg ctg agg tgc aac tac tca tct tct tat tca cca      381
Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr Ser Pro
35                  40                  45                  50
```

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tct ctc ttc tgg tat gtg caa cac ccc aac aaa gga ctc cag ctt ctc      429
Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln Leu Leu
                 55                  60                  65

ctg aag tac aca tca gcg gcc acc ctg gtt aaa ggc atc aac ggt ttt      477
Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn Gly Phe
             70                  75                  80

gag gct gaa ttt aag aag agt gaa acc tcc ttc cac ctg acg aaa ccc      525
Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr Lys Pro
         85                  90                  95

tca gcc cat atg agc gac gcg gct gag tac ttc tgt gtt gtg agt gac      573
Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val Ser Asp
    100                 105                 110

aca gtg ctt gag act gca gga gag ctg aac aca agc ctc ctg aga tgc      621
Thr Val Leu Glu Thr Ala Gly Glu Leu Asn Thr Ser Leu Leu Arg Cys
115                 120                 125                 130

tga gactttctgt gactcaagaa ctcgaccttg aagtctgttt tataat               670
 *
```

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<210> 326
<211> 794
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (200)..(304)

<220>
<221> misc_feature
<222> (1)...(794)
<223> n = a,t,c or g

<400> 326
gtcagcaatg gtctcatgga agagggaagc tttatttaca ccatcaaggg cccatggatg      60

acccacagtc tgtgtgactg ctgtgtgatt ggttttcaga cattagcttt aataggaatc     120

ataggagaag ggacatggtg gctactgcaa ggggtttttt tgtttaggga gaacgcactg     180

tggaactcaa attccgggt atg cac tca acc tcg gca aag gca cct cgc tgt      232
                     Met His Ser Thr Ser Ala Lys Ala Pro Arg Cys
                      1               5                  10

tgg tca cac ccc gtg agt ttt tgt ggt tta cta att gtc ctc tct gga      280
Trp Ser His Pro Val Ser Phe Cys Gly Leu Leu Ile Val Leu Ser Gly
             15                  20                  25
```

```
aag aaa tcc aat ggg acc tgt tga aacacagctg aatttaattg ctatgcttag      334
Lys Lys Ser Asn Gly Thr Cys  *
        30                  35

catgcagttg ttaactatgt ctgatgtgtg agcaagatat gaatacatgt ttccctggag     394

gctggatttg gttatcaggt ctcggggcag tttgataaat tgtactaatg ctgcaatcac     454

tgtttttcaa aggtccacaa agcacgttgt ggctttggga aaggcagaga taagaagcaa     514

agctttgtga tagagacaga aacaaggcca tgaaaaggga agctaccaaa gcaatggcat     574

agccaaggaa gtgtgtcttc acaagataag tggcaaggac cctgttgagt tgatgcttgt     634

gttgtttggt agaattaaaa attaagatga gtgggttggc cccagtggtc catgcctgta     694

attccctcac tttgggaggc tgaggcaggt ggatagctga ggtcaagagt tcaagaccac     754

gaaatcgtcg acagcgannc nttccgggaa ttccggacgg                           794




     <210> 327
     <211> 507
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (44)..(472)

     <400> 327
tttcgtgaaa attttaatcc tcagtgaacc agggcagaaa aga  atg atg ata tcc      55
                                                 Met Met Ile Ser
                                                  1

ttg aga gtt tta ctg gtg atc ctg tgg ctt cag tta agc tgg gtt tgg      103
Leu Arg Val Leu Leu Val Ile Leu Trp Leu Gln Leu Ser Trp Val Trp
 5                  10                  15                  20

agc caa cgg aag gag gtg gag cag gat cct gga ccc ttc aat gtt cca      151
Ser Gln Arg Lys Glu Val Glu Gln Asp Pro Gly Pro Phe Asn Val Pro
                25                  30                  35

gag gga gcc act gtc gct ttc aac tgt act tac agc aac agt gct tct      199
Glu Gly Ala Thr Val Ala Phe Asn Cys Thr Tyr Ser Asn Ser Ala Ser
            40                  45                  50

cag tct ttc ttc tgg tac aga cag gat tgc agg aaa gaa cct aag ttg      247
Gln Ser Phe Phe Trp Tyr Arg Gln Asp Cys Arg Lys Glu Pro Lys Leu
        55                  60                  65

ctg atg tcc gta tac tcc agt ggt aat gaa gat gga agg ttt aca gca      295
Leu Met Ser Val Tyr Ser Ser Gly Asn Glu Asp Gly Arg Phe Thr Ala
    70                  75                  80
```

```
cag ctc aat aga gcc agc cag tat att tcc ctg ctc atc aga gac tcc       343
Gln Leu Asn Arg Ala Ser Gln Tyr Ile Ser Leu Leu Ile Arg Asp Ser
 85                 90                  95                 100

aag ctc agt gat tca gcc acc tac ctc tgt gtg gtg aac att cgc cca       391
Lys Leu Ser Asp Ser Ala Thr Tyr Leu Cys Val Val Asn Ile Arg Pro
                105                 110                 115

gga aac aca cct ttg gga ctg gaa caa gac ttc agg tca cgc tcg ata       439
Gly Asn Thr Pro Leu Gly Leu Glu Gln Asp Phe Arg Ser Arg Ser Ile
            120                 125                 130

tcc aga acc ctg acc ctg ccg tgt acc agc tga gagactct aaatccagtg       490
Ser Arg Thr Leu Thr Leu Pro Cys Thr Ser  *
        135                 140

acaatgctgt cgaccta                                                    507



     <210> 328
     <211> 1043
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (210)..(1043)

     <400> 328
accggtccgg aattcccggg tcgacgattt cgtccggtgt cgggaagcac cagtgccctg      60

aggaagggcc atttccaaaa gccctgtgct gacacagggt tgctggttcc tcttcaagag     120

cccactctct ggggtggggc catatctcca gcagaggtgg gctggaaagg acccccccaa     180

tcccgcccgc cgtgagctta gctggagcc  atg gcc tct gca ccc atc tcg atg      233
                                 Met Ala Ser Ala Pro Ile Ser Met
                                   1               5

ctt gcg atg ctc ttc aca ttg agt ggg ctg aga gct cag tca gtg gct       281
Leu Ala Met Leu Phe Thr Leu Ser Gly Leu Arg Ala Gln Ser Val Ala
     10                  15                  20

cag ccg gaa gat cag gtc aac gtt gct gaa ggg aat cct ctg act gtg       329
Gln Pro Glu Asp Gln Val Asn Val Ala Glu Gly Asn Pro Leu Thr Val
 25                  30                  35                  40

aaa tgc acc tat tca gtc tct gga aac cct tat ctt ttt tgg tat gtt       377
Lys Cys Thr Tyr Ser Val Ser Gly Asn Pro Tyr Leu Phe Trp Tyr Val
                45                  50                  55

caa tac ccc aac cga ggc ctc cag ttc ctt ctg aaa tac atc aca ggg       425
Gln Tyr Pro Asn Arg Gly Leu Gln Phe Leu Leu Lys Tyr Ile Thr Gly
            60                  65                  70
```

```
gat aac ctg gtt aaa ggc agc tat ggc ttt gaa gct gaa ttt aac aag        473
Asp Asn Leu Val Lys Gly Ser Tyr Gly Phe Glu Ala Glu Phe Asn Lys
         75                  80                  85

agc caa acc tcc ttc cac ctg aag aaa cca tct gcc ctt gtg agc gac        521
Ser Gln Thr Ser Phe His Leu Lys Lys Pro Ser Ala Leu Val Ser Asp
     90                  95                 100

tcc gct ttg tac ttc tgt gct gtg aga gag gta ata ctc acg gga gga        569
Ser Ala Leu Tyr Phe Cys Ala Val Arg Glu Val Ile Leu Thr Gly Gly
105                 110                 115                 120

gga aac aaa ctc acc ttt ggg aca ggc act cag cta aaa gtg gaa ctc        617
Gly Asn Lys Leu Thr Phe Gly Thr Gly Thr Gln Leu Lys Val Glu Leu
                125                 130                 135

aat atc cag aac cct gac cct gcc gtg tac cag ctg aga gac tct aaa        665
Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
            140                 145                 150

tcc agt gac aag tct gtc tgc cta ttc acc gat ttt gat tct caa aca        713
Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
        155                 160                 165

aat gtg tca caa agt aag gat tct gat gtg tat atc aca gac aaa act        761
Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr
    170                 175                 180

gtg cta gac atg agg tct atg gac ttc aag agc aac agt gct gtg gcc        809
Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala
185                 190                 195                 200

tgg agc aac aaa tct gac ttt gca tgt gca aac gcc ttc aac aac agc        857
Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser
                205                 210                 215

att att cca gaa gac acc ttc ttc ccc agc cca gaa agt tcc tgt gat        905
Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp
            220                 225                 230

gtc aag ctg gtc gag aaa agc ttt gaa aca gat acg aac cta aac ttt        953
Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe
        235                 240                 245

caa aac ctg tca gtg att ggg ttc cga atc ctc ctc ctg aaa gtg gcc       1001
Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
    250                 255                 260

ggg ttt aat ctg ctc atg acg ctg cgg ctg tgg tcc agc tga               1043
Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser  *
265                 270                 275
```

<210> 329

```
<211> 1037
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(831)

<400> 329
atg agc atc agc ctc ctg tgc tgt gca gcc ttt cct ctc ctg tgg gca      48
Met Ser Ile Ser Leu Leu Cys Cys Ala Ala Phe Pro Leu Leu Trp Ala
1               5                   10                  15

ggt cca gtg aat gct ggt ggt gtc act cag acc cca aaa ttc cgc atc      96
Gly Pro Val Asn Ala Gly Gly Val Thr Gln Thr Pro Lys Phe Arg Ile
            20                  25                  30

ctg aag ata gga cag agc atg aca ctg cag tgt gcc cag gat atg aac     144
Leu Lys Ile Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn
        35                  40                  45

cat aac tac atg tac tgg tat cga caa gac cca ggc atg ggg ctg aag     192
His Asn Tyr Met Tyr Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Lys
    50                  55                  60

ctg att tat tat tca gtt ggt gct ggt atc act gac aaa gga gaa gtc     240
Leu Ile Tyr Tyr Ser Val Gly Ala Gly Ile Thr Asp Lys Gly Glu Val
65                  70                  75                  80

ccg aat ggc tac aac gtc tcc aga tca acc aca gag gat ttc ccg ctc     288
Pro Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu
                85                  90                  95

agg ctg gag ttg gct gct ccc tcc cag aca tct gtg tac ttc tgt gcc     336
Arg Leu Glu Leu Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala
            100                 105                 110

agc agt agg ggt ggg gcc ggg ctc aat gag cag ttc ttc ggg cca ggg     384
Ser Ser Arg Gly Gly Ala Gly Leu Asn Glu Gln Phe Phe Gly Pro Gly
        115                 120                 125

aca cgg ctc acc gtg cta gag gac ctg aaa aac gtg ttc cca ccc gag     432
Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu
    130                 135                 140

gtc gct gtg ttt gag cca tca gaa gca gag atc tcc cac acc caa aag     480
Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
145                 150                 155                 160

gcc aca ctg gta tgc ctg gcc aca ggc ttc tac ccc gac cac gtg gag     528
Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu
                165                 170                 175

ctg agc tgg tgg gtg aat ggg aag gag gtg cac agt ggg gtc agc aca     576
Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
            180                 185                 190
```

gac ccg cag ccc ctc aag gag cag ccc gcc ctc aat gac tcc aga tac 624
Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
195 200 205

tgc ctg agc agc cgc ctg agg gtc tcg gcc acc ttc tgg cag aac ccc 672
Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
210 215 220

cgc aac cac ttc cgc tgt caa gtc cag ttc tac ggg ctc tcg gag aat 720
Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
225 230 235 240

gac gag tgg acc cag gat agg gcc aaa cct gtc acc cag atc gtc agc 768
Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
245 250 255

gcc gag gcc tgg ggt aga gca ggt gag tgg ggc ctg ggg aga tgc ctg 816
Ala Glu Ala Trp Gly Arg Ala Gly Glu Trp Gly Leu Gly Arg Cys Leu
260 265 270

gag gag att agg tga gaccagctac cagggaaaat ggaaagatcc aggtagcgga 871
Glu Glu Ile Arg *
275

caagactata tccagaagaa agccagagtg gacaaggtgg gatgatcaag gttcacaggg 931

tcagcaaagc acggtgtgca cttcccccac caagaagcat ataggctgaa tggagcacct 991

caagctcatt cttccttcag atcctgacac cttagagcta agcttt 1037

<210> 330
<211> 738
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (300)..(608)

<400> 330
tagttcaaag aagaaaagtc agctggatgt gatgcctcat gcctgtaatc ctaccacttt 60

gggaggccaa cacggttgga tctcttgagc ccaggagttc gagactagcc tggccaacat 120

ggcgaaaccc cttctctttt tctttttta aaattttta gttagaaatg aaaaaaagaa 180

agaagtctag gttttctgaa acaagcactg tcttggtgct acctttttc atgtgtggac 240

acatagaaag cgaggatatt tgtacagcac cttgaaacaa ataagcagga ggtgatgtc 299
atg agc ctt agc cct gca ggg acc aga cta ggc ctt ctg aag ctg agg 347
Met Ser Leu Ser Pro Ala Gly Thr Arg Leu Gly Leu Leu Lys Leu Arg
1 5 10 15

tgg tcc ttg tcc cca cac ctt gta acc cat ttc cag ccc atg ggt gtc 395

```
Trp Ser Leu Ser Pro His Leu Val Thr His Phe Gln Pro Met Gly Val
             20                  25                  30

agt tgg gaa att cta cac aag atc cta gta gat gta att aca tat aat        443
Ser Trp Glu Ile Leu His Lys Ile Leu Val Asp Val Ile Thr Tyr Asn
         35                  40                  45

tca atg gtt ttt gat gat ggg gtt tta aaa tca agt tat tca ata ggt        491
Ser Met Val Phe Asp Asp Gly Val Leu Lys Ser Ser Tyr Ser Ile Gly
     50                  55                  60

ggg gtg cag tgg ctc acg cct gta att cca gca ctt tgg gag gcc gag        539
Gly Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Ala Glu
 65                  70                  75                  80

gag ggc aga tca caa ggt cgg gag ttc aag acc agc ctg acc aac atg        587
Glu Gly Arg Ser Gln Gly Arg Glu Phe Lys Thr Ser Leu Thr Asn Met
                 85                  90                  95

gta aaa ctc cgt ctc tac taa aa attcaaaaat tagccggccg tggtggtgga        640
Val Lys Leu Arg Leu Tyr  *
            100

catctgtaat cccagctact tagggggctg aggcaggaga atcgcttgaa cgggggcagg      700

tcggggcagg gcggcaactc cctcttaaaa aaaaaaaa                              738




     <210> 331
     <211> 679
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (243)..(449)

     <220>
     <221> misc_feature
     <222> (1)...(679)
     <223> n = a,t,c or g

     <400> 331
aacaagcagc agtgaggaca ccaaagccaa gccacgccac ccgggcccgc ccccaggaca       60

cggagtttaa ggaccgcgtc tcccgagatg ccagagggac ctgcgtccgc actgccccag      120

tgtgacccgc atacctaccg gccccgaccc cgaaccgcgt ggcgtccgcc cgagccctgg      180

cgctgctggg tctcctgctg ctgccgctgc tcgcagagcc caggaaactc tgcccgcagc      240

tt   atg acg gtc att aac cag ttt ctg acc aag gac aag gac acc tac       287
     Met Thr Val Ile Asn Gln Phe Leu Thr Lys Asp Lys Asp Thr Tyr
       1               5                  10                  15
```

atg gac act gtc aac aga tac cac ctc acg gag ccg gaa aga aac aca 335
Met Asp Thr Val Asn Arg Tyr His Leu Thr Glu Pro Glu Arg Asn Thr
20 25 30

tcc tct aaa ctc aag gac tgc gtg acc gac aca atg acc ccc gag gag 383
Ser Ser Lys Leu Lys Asp Cys Val Thr Asp Thr Met Thr Pro Glu Glu
35 40 45

aca gag gcc gtc gtg cag caa ctg gaa gaa atc aac aac cag tgt gcc 431
Thr Glu Ala Val Val Gln Gln Leu Glu Glu Ile Asn Asn Gln Cys Ala
50 55 60

gac acg ata ctg aag taa caccat ccataggcac ctcgggttcc tgtccaggct 485
Asp Thr Ile Leu Lys *
65

gcctgtccca accatgagaa tctgggccca gggccccacc ctccctagct cccgccctgc 545

tgctgcctct actctctctc ctgctgtgct gattggggca agcctgggaa cggctgcccc 605

ccacctcccc acccaggncc tgtcctgcgg gacaatgctg cctaataaac tcacctgcat 665

ccaaaaaaaa aaaa 679

<210> 332
<211> 445
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (200)..(400)

<400> 332
ctttagtcca gcgtggtgga attcgtagat ccccgcgtgg caccagccct tctgccacag 60

ctgccattgg agagcagcag ccatggctct gtgctaccca ctatggccgt gtgccttgac 120

aagggccaca agatgaccaa gaacatgagc aagcccaggc acagctgccg ccgcgggcgc 180

ctgaccaaac accaaattc atg tgg gac atg atc cga gag gtg tgt ggt ttc 232
Met Trp Asp Met Ile Arg Glu Val Cys Gly Phe
1 5 10

gcc ccg tat gag cgg cac gcc atg gtg tta ctc aag gtc tcc aag gac 280
Ala Pro Tyr Glu Arg His Ala Met Val Leu Leu Lys Val Ser Lys Asp
15 20 25

aaa cgg gcc ctc aag ttc atc aag aaa aga gtg ggg aca cac atc cgc 328
Lys Arg Ala Leu Lys Phe Ile Lys Lys Arg Val Gly Thr His Ile Arg
30 35 40

act aag agg agg cag gag gag ctg agc aat gtc cca gcc atc atg agg 376
Thr Lys Arg Arg Gln Glu Glu Leu Ser Asn Val Pro Ala Ile Met Arg

```
     45                  50                  55

aaa gct gat gcc aag aaa gac tga gccccctgtc ctgccctctc tctgaaataa     430
Lys Ala Asp Ala Lys Lys Asp  *
 60                  65

agaacacctt gacag                                                     445



     <210> 333
     <211> 1716
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (633)..(1433)

     <400> 333
cccgggtcga cgattcgtag gatatccaag ggacctcagg ctgtgggctg ggcttcaggg      60

agggagccag agggtcagtg tccctagagg atcccccaggg aagtgccaag gaggagaagg    120

aatgtcctgg ctgacctaag ggacgacaga agattgggga agagggggta tcaggaagaa    180

atgggtttca gttcagttta acaaacatct attgtgtgtt cactgggcca ggccagtgct    240

aggtgctagg gagacagagg tgaagagcct gccctctagc agctgacagc ctggcaaaaa    300

aataagacag aataaggtag accctgattt tggaacctga agaccaaagt gcaagattag    360

ctctgctact tccatctgtg gaccattggg caggtatctc tgggccttca cttactcttt    420

gtgaaatgag gacaggggca atccctaccc taccaagtca ttgggagtga agacatgatg    480

acacggtgat tgtgaaaaga ttttgtcaat cgcaccagca ttaagggtgc ccatctccag    540

gttcccccag gcctcaaggc tcccaaggcc tgagtgggca ggtagcaccc aggtatagac    600

cttccacgtg cagcacccag gacacagcca gc  atg aac tgg gca ttt ctg cag     653
                                     Met Asn Trp Ala Phe Leu Gln
                                      1               5

ggc ctg ctg agt ggc gtg aac aag tac tcc aca gtg ctg agc cgc atc      701
Gly Leu Leu Ser Gly Val Asn Lys Tyr Ser Thr Val Leu Ser Arg Ile
        10                  15                  20

tgg ctg tct gtg gtg ttc atc ttt cgt gtg ctg gtg tac gtg gtg gca      749
Trp Leu Ser Val Val Phe Ile Phe Arg Val Leu Val Tyr Val Val Ala
     25                  30                  35

gcg gag gag gtg tgg gac gat gag cag aag gac ttt gtc tgc aac acc      797
Ala Glu Glu Val Trp Asp Asp Glu Gln Lys Asp Phe Val Cys Asn Thr
 40                  45                  50                  55
```

```
aag cag ccc ggc tgc ccc aac gtc tgc tat gac gag ttc ttc ccc gtg       845
Lys Gln Pro Gly Cys Pro Asn Val Cys Tyr Asp Glu Phe Phe Pro Val
                 60                  65                  70

tcc cac gtg cgc ctc tgg gcc cta cag ctc atc ctg gtc acg tgc ccc       893
Ser His Val Arg Leu Trp Ala Leu Gln Leu Ile Leu Val Thr Cys Pro
             75                  80                  85

tca ctg ctc gtg gtc atg cac gtg gcc tac cgc gag gaa cgc gag cgc       941
Ser Leu Leu Val Val Met His Val Ala Tyr Arg Glu Glu Arg Glu Arg
         90                  95                 100

aag cac cac ctg aaa cac ggg ccc aat gcc ccg tcc ctg tac gac aac       989
Lys His His Leu Lys His Gly Pro Asn Ala Pro Ser Leu Tyr Asp Asn
    105                 110                 115

ctg agc aag aag cgg ggc gga ctg tgg tgg acg tac ttg ctg agc ctc      1037
Leu Ser Lys Lys Arg Gly Gly Leu Trp Trp Thr Tyr Leu Leu Ser Leu
120                 125                 130                 135

atc ttc aag gcc gcc gtg gat gct ggc ttc ctc tat atc ttc cac cgc      1085
Ile Phe Lys Ala Ala Val Asp Ala Gly Phe Leu Tyr Ile Phe His Arg
                140                 145                 150

ctc tac aag gat tat gac atg ccc cgc gtg gtg gcc tgc tcc gtg gag      1133
Leu Tyr Lys Asp Tyr Asp Met Pro Arg Val Val Ala Cys Ser Val Glu
            155                 160                 165

cct tgc ccc cac act gtg gac tgt tac atc tcc cgg ccc acg gag aag      1181
Pro Cys Pro His Thr Val Asp Cys Tyr Ile Ser Arg Pro Thr Glu Lys
        170                 175                 180

aag gtc ttc acc tac ttc atg gtg acc aca gct gcc atc tgc atc ctg      1229
Lys Val Phe Thr Tyr Phe Met Val Thr Thr Ala Ala Ile Cys Ile Leu
    185                 190                 195

ctc aac ctc agt gaa gtc ttc tac ctg gtg ggc aag agg tgc atg gag      1277
Leu Asn Leu Ser Glu Val Phe Tyr Leu Val Gly Lys Arg Cys Met Glu
200                 205                 210                 215

atc ttc ggc ccc agg cac cgg cgg cct cgg tgc cgg gaa tgc cta ccc      1325
Ile Phe Gly Pro Arg His Arg Arg Pro Arg Cys Arg Glu Cys Leu Pro
                220                 225                 230

gat acg tgc cca cca tat gtc ctc tcc cag gga ggg cac cct gag gat      1373
Asp Thr Cys Pro Pro Tyr Val Leu Ser Gln Gly Gly His Pro Glu Asp
            235                 240                 245

ggg aac tct gtc cta atg aag gct ggg tcg gcc cca gtg gat gca ggt      1421
Gly Asn Ser Val Leu Met Lys Ala Gly Ser Ala Pro Val Asp Ala Gly
        250                 255                 260

ggg tat cca taa cct gcgagatcag cagataagat caacaggtcc cccccacatg      1476
Gly Tyr Pro  *
    265

aggccaccca ggaaaaaagg caggggcagt ggcatccttg ccgtagcagg gtggtgagga    1536
```

```
gggtggctgt gggggctcag gaagctcgcc caggggccaa tgtgggaggt tgggggtagt   1596

ttggtccctg ggtcctgagc ctcaggggag ggaggttgat agctactggg gattatgtat   1656

atggcaacag tatatgtcaa acctcttaat aaatatgatt ttcccagtaa aaaaaaaaaa   1716




    <210> 334
    <211> 407
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (44)..(340)

    <400> 334
aacagacttc tctcaactca acaaaaaccc acctcccatt gcc  atg tat tgc tgt       55
                                                 Met Tyr Cys Cys
                                                  1

gct ctc cgc tcc tgc agc gtc ccc acc ggc cct gcc acc acc ttc tgc      103
Ala Leu Arg Ser Cys Ser Val Pro Thr Gly Pro Ala Thr Thr Phe Cys
  5                  10                  15                  20

tca ttt gat aaa agc tgc cgc tgt gga gtc tgc cta ccc agc acc tgc      151
Ser Phe Asp Lys Ser Cys Arg Cys Gly Val Cys Leu Pro Ser Thr Cys
                 25                  30                  35

cca cat gag atc agc ctc ctt cag ccc atc tgc tgt gac acc tgc ccc      199
Pro His Glu Ile Ser Leu Leu Gln Pro Ile Cys Cys Asp Thr Cys Pro
             40                  45                  50

cca ccc tgc tgc aag cct gat acc tat gtg cca act tgc tgg ctg ctc      247
Pro Pro Cys Cys Lys Pro Asp Thr Tyr Val Pro Thr Cys Trp Leu Leu
         55                  60                  65

aac aac tgt cac ccg act ccc gga ctg agt ggg atc aac ctg acc acc      295
Asn Asn Cys His Pro Thr Pro Gly Leu Ser Gly Ile Asn Leu Thr Thr
     70                  75                  80

tat gtt cag cct ggc tgt gag agt ccc tgt gag ccc cgc tgt taa cca      343
Tyr Val Gln Pro Gly Cys Glu Ser Pro Cys Glu Pro Arg Cys  *
 85                  90                  95

gccgagtctg cacaggttcc gtgaggtggc tgcccaatgt cctctgcacc atctgggctt   403

cagc                                                                 407




    <210> 335
    <211> 2530
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (23)..(1249)

<220>
<221> misc_feature
<222> (1)...(2530)
<223> n = a,t,c or g

<400> 335
gtcgcaacag gaccggtccc tg atg gag ctc tca gaa cgc tac ggg ccg gtg       52
                         Met Glu Leu Ser Glu Arg Tyr Gly Pro Val
                         1               5                   10

ttc acc gtg cac ctg ggg cgc cag aag acg gtg gtg ctg acg ggg ttc       100
Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr Gly Phe
                15                  20                  25

gag gcg gtc aaa gag gcg ctg gcg ggc ccc ggg cag gag ctg gcc gac       148
Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu Ala Asp
            30                  35                  40

cgg cct ccc atc gcc atc ttc cag ctc atc cag cga ggt gga ggc atc       196
Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly Gly Ile
        45                  50                  55

ttc ttc tca tct ggg gcg cgc tgg agg gct gcc cgc cag ttc acg gtg       244
Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe Thr Val
    60                  65                  70

cgt gcc ctg cac agc ctg ggc gtg ggc cgg gag ccg gtg gct gac aag       292
Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala Asp Lys
75                  80                  85                  90

att ctg cag gag ctg aaa tgc ctc tct ggg cag ctg gat ggc tac aga       340
Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly Tyr Arg
                95                  100                 105

ggc cgg ccc ttc ccg ctg gcc cta ctg ggc tgg gct ccc tcc aat atc       388
Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser Asn Ile
            110                 115                 120

acc ttc gcg ctc ctc ttc ggc cgc cga ttt gac tac cgg gac ccc gtg       436
Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp Pro Val
        125                 130                 135

ttt gtg tcc ctg ctg ggt ctc atc gat gag gtc atg gtc ctc ttg ggg       484
Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu Leu Gly
    140                 145                 150

tcc cct ggc ctg cag ctg ttc aac gtc cac cca tgg ctc ggg gcc ctg       532
Ser Pro Gly Leu Gln Leu Phe Asn Val His Pro Trp Leu Gly Ala Leu
155                 160                 165                 170
```

```
ctc cag ctg cac cgg ccc gtc ctg cgc aag atc gag gag gtc cgt gcc          580
Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val Arg Ala
                175                 180                 185

att ctg agg acc ctc ctg gag gcg cgg agg ccc cac gtg tgc ccg ggg          628
Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys Pro Gly
            190                 195                 200

gac ccc gtg tgc agc tat gtg gac gcc ctg atc cag cag gga cag ggg          676
Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly Gln Gly
        205                 210                 215

gat gac ccc gag ggc ctg ttt gct gag gcc aac gcg gtg gcc tgc acc          724
Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala Cys Thr
    220                 225                 230

ctg gac atg gtc atg gcc ggg acg gag acg acc tcg gcc acg ctg cag          772
Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr Leu Gln
235                 240                 245                 250

tgg gcc gca ctt ctg atg ggc cgg cac ccg gac gtg cag ggc cgg gtg          820
Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly Arg Val
                255                 260                 265

cag gag gag cta gac cgc gtg ctg ggc cct ggg cgg act ccc cgg ctg          868
Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro Arg Leu
            270                 275                 280

gag gac cag cag gct ctg ccc tac aca agc gcc gtg ctc cac gag gtg          916
Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His Glu Val
        285                 290                 295

cag cgg ttc atc acg ctc ctg ccg cac gtg ccc cgc tgc acc gcg gcc          964
Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr Ala Ala
    300                 305                 310

gac aca cag ctg ggc ggc ttc ctg ctc ccc aag ggc acg ccc gtg att         1012
Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro Val Ile
315                 320                 325                 330

ccc ctg ctg acc tcg gtg ctc ctg gat gag aca cag tgg cag acc cca         1060
Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln Thr Pro
                335                 340                 345

ggc cag ttc aac ccc ggc cat ttc ctg gac gcg aat ggg cac ttt gtg         1108
Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His Phe Val
            350                 355                 360

aag cgg gag gcc ttc ctg cct ttc tct gca ggt cag cag ccc tcg ggg         1156
Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Gln Gln Pro Ser Gly
        365                 370                 375

ccg ggg tgg ggc ggc acc tcc agg gct cca ggg gtg gga cgg ccc cag         1204
Pro Gly Trp Gly Gly Thr Ser Arg Ala Pro Gly Val Gly Arg Pro Gln
    380                 385                 390

ctc cgc ctg ccg cct ctg cac cca cct cct gat ctc agg ttc tga agg         1252
```

```
Leu Arg Leu Pro Pro Leu His Pro Pro Pro Asp Leu Arg Phe  *
395                 400                 405

cggctgtggt ggctgctcct gtgctcccct ggggaggtcc ccacccctcc cctccaggag   1312

caggcctggt gcagcccact ctgtgcctgg acatcccccg caggccgccg cgtctgtgtt   1372

ggggagcgcc tggccaggac cgagctcttc ctgctgtttg ccggcctcct gcagaggtac   1432

cgcctgctgc ccccgcctgg cgtcagtccg gcctccctgg acaccacgcc cgcccgggct   1492

tttaccatga ggccgagggc ccaggccctg tgtgcggtgc ccaggcccta ggagctcccc   1552

cagcccccag gtcctcctga ccactcccct cccagccctg ggtcctccca ccctctctcc   1612

tcccacccca cagctcggac tgctctggga gggccctgag gactcccacc ctcaccccca   1672

cccccacagg gtcagcaact gcttccggtt acacccagga ctacccctgc ccgaccctgt   1732

gggaccccca cccctctgat gctgtctgca gctcagtccc tgccagcccc caggagcgcc   1792

tccagggccc cgcccactct cccacccctg aagctgcact cccacccacc tagctccccc   1852

cagggccccc cagcacctac agctggggct gcagggagac aacgggtggc tgcaatccag   1912

ccagagacag gcgcaggtgg gtgtcctcag cgtgcgagcc ctgcaccccc caggtcctgg   1972

gactcctgca gaccccactc cattcccgct cctggaacac ttcctgcagc tgtgcctgga   2032

ggcagtcggc ctgcagtgcc agactctgag ccaagccact ggggccatgc gtatgactgg   2092

tgcagggagg caaggcccac attctccttc agagacaggc actggcgcca gaggcttcct   2152

tggggcgggg ggagggcacc tcagcccctg aagacaagca gcactgcagt ggcaaaaatg   2212

gaaacactga cccggtgcgg tggctcatgc ctgtaatccc agcactttgg gaggccaagg   2272

tgggcggatc acgaggtcag gagttcgaga ccagcctgac caacatggtg aaaccctgtc   2332

tctactaaaa atacaaaaat tagnctgggc gtggtggcat gcacccctgc aatcccaagc   2392

tactcggcgg gggggctgag gcaggaagna attgcttgaa cctgggaggt gaaggggttg   2452

cagtgagccg nnagatcatg ccactgcact ccagcctggg ggacagagcg agactccatc   2512

tcacaaaaaa aaaaaaaa                                                 2530


<210> 336
<211> 765
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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     <222> (107)..(322)

     <400> 336
ctcattacaa aagttgatgt tatttctcgt ggtaaattca gaaaaacatc agggagtaaa      60

caatgccaac atctgagcaa acattttggg gtatatctct attttc   atg ttt aca      115
                                                      Met Phe Thr
                                                        1

ttg tcg ttt aaa aaa caa tca aac gac att agc agt ttt aca aca ttt       163
Leu Ser Phe Lys Lys Gln Ser Asn Asp Ile Ser Ser Phe Thr Thr Phe
      5                  10                  15

tcc ttt cca gtt aaa act gta tac cgt tac cat ttt ccc atc ata ctc       211
Ser Phe Pro Val Lys Thr Val Tyr Arg Tyr His Phe Pro Ile Ile Leu
 20                  25                  30                  35

ttc acc tac gat act gtt tta agt ggc tgt ata gat ttc cac ttt cac       259
Phe Thr Tyr Asp Thr Val Leu Ser Gly Cys Ile Asp Phe His Phe His
                 40                  45                  50

aac aga att agc aga ttc cca aaa ctt gaa tat tta att tta aaa aaa       307
Asn Arg Ile Ser Arg Phe Pro Lys Leu Glu Tyr Leu Ile Leu Lys Lys
             55                  60                  65

att ctt aat aac tga tattaaattt atatacgcaa atctgacaca ttacttcctt       362
Ile Leu Asn Asn  *
         70

aggataaatt cctgtacgca cagtctttcc attttaagcc tattatacta tgaaggagtc     422

tgaatcaaca tctaagagct ccgagagttc aacaccagcc tgggccatat tgtgagaaca     482

cgtctctaca gacgatcaaa aaattagctt ggtgtggtgg cgcgcgcctg tgatctcagc     542

tacccaggag gctgaggtgg gaggatcact taagcccggg aggtcgaggc tgctgtgagc     602

cgtgagccac tgatcatacc actgcactcc agtctgggca acagagcgat cctgtttcag     662

agaaaaaaaa gatccaagac ctctgtagac cacactgaca gccctgctac tatttgcaac     722

tggtcgcgcc ctcgtgccga attcttggcc tcgagggcca aat                       765



     <210> 337
     <211> 773
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (528)..(695)

     <400> 337
aatgaaaaaa gtacaattta taatagtatc tcaaaaagga aatatttagg gataatgtaa      60
```

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caatatgtac aagatcaata tattgaatac tacaaaacac ttgagagaaa cttaaaaaga      120

ctcaaataaa tggagaaata tagtgtgttt atggatcaaa ggactcaata ttgttaagat      180

gtcaactctt cctaaatcaa tccatacagt cagtgtaatt ccattcaatg cccaaccagc      240

accccccacc tgccccgcat tttttttggt aagaattaat aagctagtcc tgaaattcaa      300

atagaaatgc aaagggtgac actcctattt ggcagccatt tctcttaaag ctcagtggtt      360

ctggacctgc agtatctgct gagttaggag ggacaggaga gtagcagcta ggtcggtggc      420

aaatagcccg caacattccc tttagttaca atgagtttac ccctcaatct caaatatttc      480

ctcagtggat taacaggaga gccagtgatg gtgaagctta agtggga  atg gag tat      536
                                                     Met Glu Tyr
                                                      1

aag ggc tac ctg gta tct gta gat ggc tat atg aac atg cag ctt gca        584
Lys Gly Tyr Leu Val Ser Val Asp Gly Tyr Met Asn Met Gln Leu Ala
     5                   10                  15

gat aca gaa ttc ata aat gag gca ttg cct gga cat cta ggt gaa gtt        632
Asp Thr Glu Phe Ile Asn Glu Ala Leu Pro Gly His Leu Gly Glu Val
 20                  25                  30                  35

tca ata agg tgt aat aat gtc ctt tat atc aga gat gtg gaa gaa gag        680
Ser Ile Arg Cys Asn Asn Val Leu Tyr Ile Arg Asp Val Glu Glu Glu
                 40                  45                  50

gaa atg ggg aaa tga gtgaatagca tcttttgaag aggatttttt aaatatgtat        735
Glu Met Gly Lys  *
             55

ttctagacaa taaagatttg tttttcaaaa aaaaaaaa                              773
```

<210> 338
<211> 1251
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (84)..(1085)

<400> 338

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atttggccct cgaggccaag aattcggcac gaggagagag ctagcaccat gagcttcaat       60

acccttcaga tacctttcat aca    atg aat act cag caa agt aca ccc tca       110
                             Met Asn Thr Gln Gln Ser Thr Pro Ser
                              1               5

aat aat gtt cat acc tca tta agc cat gtt cag aat gga gca cct ttt        158
```

```
Asn Asn Val His Thr Ser Leu Ser His Val Gln Asn Gly Ala Pro Phe
 10                  15                  20                  25

cca gca gct ttt cca aag gac aat atc cat ttc aag cct ata aat aca        206
Pro Ala Ala Phe Pro Lys Asp Asn Ile His Phe Lys Pro Ile Asn Thr
                 30                  35                  40

aat ctt gat agg gca aat gaa ttg gca aaa aca gac att ttg agt cta        254
Asn Leu Asp Arg Ala Asn Glu Leu Ala Lys Thr Asp Ile Leu Ser Leu
             45                  50                  55

aca agt caa aac aag acc ttt gat ccc aag aaa gaa aat ccc att gtg        302
Thr Ser Gln Asn Lys Thr Phe Asp Pro Lys Lys Glu Asn Pro Ile Val
         60                  65                  70

tta ctt agt gac ttt tac tat gga cag cat aaa gga gaa ggg cag ccg        350
Leu Leu Ser Asp Phe Tyr Tyr Gly Gln His Lys Gly Glu Gly Gln Pro
     75                  80                  85

gaa cag aag act cac acc acc ttt aaa tgc ctc agc tgc gtg aaa gtt        398
Glu Gln Lys Thr His Thr Thr Phe Lys Cys Leu Ser Cys Val Lys Val
 90                  95                 100                 105

cta aaa aat gtt aag ttt atg aat cac gtg aag cat cat ttg gaa ttt        446
Leu Lys Asn Val Lys Phe Met Asn His Val Lys His His Leu Glu Phe
                110                 115                 120

gag aag cag agg aac gac agc tgg gaa aac cac acc acc tgc cag cac        494
Glu Lys Gln Arg Asn Asp Ser Trp Glu Asn His Thr Thr Cys Gln His
            125                 130                 135

tgc cac cgg agt ctt ccc act ccc ttc cag cta cag tgt cac atc gaa        542
Cys His Arg Ser Leu Pro Thr Pro Phe Gln Leu Gln Cys His Ile Glu
        140                 145                 150

aat gtc cac act gcc cag gag ccc tct act gtc tgt aaa atc tgt gaa        590
Asn Val His Thr Ala Gln Glu Pro Ser Thr Val Cys Lys Ile Cys Glu
    155                 160                 165

ttg tca ttt gaa aca gat cag gtc ctc tta caa cac atg aag gac cat        638
Leu Ser Phe Glu Thr Asp Gln Val Leu Leu Gln His Met Lys Asp His
170                 175                 180                 185

cat aag cct ggc gaa atg ccc tat gtg tgc cag gtt tgc cat tat aga        686
His Lys Pro Gly Glu Met Pro Tyr Val Cys Gln Val Cys His Tyr Arg
                190                 195                 200

tcg tcg gtc ttt gct gat gta gaa aca cat ttt aga acg tgc cat gaa        734
Ser Ser Val Phe Ala Asp Val Glu Thr His Phe Arg Thr Cys His Glu
            205                 210                 215

aac aca aag aat ttg ctt tgt ccc ttt tgt ctc aaa att ttc aaa aca        782
Asn Thr Lys Asn Leu Leu Cys Pro Phe Cys Leu Lys Ile Phe Lys Thr
        220                 225                 230

gca aca cca tac atg tgt cat tat agg ggc cac tgg gga aag agt gca        830
Ala Thr Pro Tyr Met Cys His Tyr Arg Gly His Trp Gly Lys Ser Ala
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    235                 240                 245

cac cag tgt tcc aag tgc cgg cta cag ttt tta act ttc aag gag aaa       878
His Gln Cys Ser Lys Cys Arg Leu Gln Phe Leu Thr Phe Lys Glu Lys
250                 255                 260                 265

atg gag cac aag acc cag tgt cat caa atg ttt aag aag cct aag caa       926
Met Glu His Lys Thr Gln Cys His Gln Met Phe Lys Lys Pro Lys Gln
                270                 275                 280

cta gaa gga tta cct cct gaa aca aaa gtt act att caa gtg tca ctg       974
Leu Glu Gly Leu Pro Pro Glu Thr Lys Val Thr Ile Gln Val Ser Leu
            285                 290                 295

gaa cct ctt cag cca gga tca gtg gat gta gca tcc ata act gtg agc      1022
Glu Pro Leu Gln Pro Gly Ser Val Asp Val Ala Ser Ile Thr Val Ser
        300                 305                 310

aca tct gac tct gaa cca tca ctc ccc agg tct aaa agc aaa att tca      1070
Thr Ser Asp Ser Glu Pro Ser Leu Pro Arg Ser Lys Ser Lys Ile Ser
    315                 320                 325

aaa aag tcc cat taa ttctagtttc agtaaatcta aagcaagtat ttcaaaccaa      1125
Lys Lys Ser His  *
330

attaaaaaac ctcataaaac aaaaaataca aaccatacat tattcagtag caccaaaaat   1185

agtgaaacta gtggattata tatgactttt taaacaagat tcaggatata tattaaaaaa   1245

aaaaaa                                                               1251




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aagaggactt tagactaatt gcagataatt aaggtggtag agaat   atg cct tct       114
                                                    Met Pro Ser
                                                     1

gca tcc tgt gat aca cta ctg gat gac atc gaa gat atc gtg tct cag       162
Ala Ser Cys Asp Thr Leu Leu Asp Asp Ile Glu Asp Ile Val Ser Gln
    5                   10                  15

gaa gat tca aaa cca caa gat agg cat ttt gta aga aag gat gtt gtc       210
Glu Asp Ser Lys Pro Gln Asp Arg His Phe Val Arg Lys Asp Val Val
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 20                  25                  30                  35

ccg aag gta cga agg cga aat acc caa aaa tat ttg caa gag gaa gaa       258
Pro Lys Val Arg Arg Arg Asn Thr Gln Lys Tyr Leu Gln Glu Glu Glu
                40                  45                  50

aac agt cca cca agt gac agc act att cca ggc ata cag aaa att tgg       306
Asn Ser Pro Pro Ser Asp Ser Thr Ile Pro Gly Ile Gln Lys Ile Trp
            55                  60                  65

ata cga aca tgg ggt tgt tct cat aat aat tca gat gga gaa tat atg       354
Ile Arg Thr Trp Gly Cys Ser His Asn Asn Ser Asp Gly Glu Tyr Met
        70                  75                  80

gct gga cag cta gct gct tat ggc tat aaa att aca gaa aat gca tcc       402
Ala Gly Gln Leu Ala Ala Tyr Gly Tyr Lys Ile Thr Glu Asn Ala Ser
    85                  90                  95

gat gca gat tta tgg ctc ctg aac agt tgc act gta aaa aac cca gct       450
Asp Ala Asp Leu Trp Leu Leu Asn Ser Cys Thr Val Lys Asn Pro Ala
100                 105                 110                 115

gaa gac cac ttt aga aac tca att aaa aaa gct caa gag gag aac aag       498
Glu Asp His Phe Arg Asn Ser Ile Lys Lys Ala Gln Glu Glu Asn Lys
                120                 125                 130

aaa atc gta ctg gct gga tgc gtt cct caa gcc cag cct cgc cag gac       546
Lys Ile Val Leu Ala Gly Cys Val Pro Gln Ala Gln Pro Arg Gln Asp
            135                 140                 145

tac ctt aag gga ctg agt atc att ggg gtt cag cag ata gat cgt gtg       594
Tyr Leu Lys Gly Leu Ser Ile Ile Gly Val Gln Gln Ile Asp Arg Val
        150                 155                 160

gta gaa gtt gtg gag gag aca att aaa ggt cac tct gtg aga ctg ctg       642
Val Glu Val Val Glu Glu Thr Ile Lys Gly His Ser Val Arg Leu Leu
    165                 170                 175

ggt cag aaa aag gat aat gga agg cgg ctt ggg gga gca cga ttg gat       690
Gly Gln Lys Lys Asp Asn Gly Arg Arg Leu Gly Gly Ala Arg Leu Asp
180                 185                 190                 195

ttg ccg aag att agg aag aat cca ctg ata gaa atc att tcc atc aat       738
Leu Pro Lys Ile Arg Lys Asn Pro Leu Ile Glu Ile Ile Ser Ile Asn
                200                 205                 210

acc ggg tgt ctc aat gct tgt acc tac tgc aaa act aaa cac gcc aga       786
Thr Gly Cys Leu Asn Ala Cys Thr Tyr Cys Lys Thr Lys His Ala Arg
            215                 220                 225

gga aat ttg gcc agt tat cca att gat gaa cta gta gat aga gcc aaa       834
Gly Asn Leu Ala Ser Tyr Pro Ile Asp Glu Leu Val Asp Arg Ala Lys
        230                 235                 240

caa tct ttt caa gag ggt gtt tgt gag ata tgg ttg acc agt gaa gac       882
Gln Ser Phe Gln Glu Gly Val Cys Glu Ile Trp Leu Thr Ser Glu Asp
    245                 250                 255
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acg ggg gct tat ggc aga gat att ggc acc aat ctc ccc aca ctc ctg       930
Thr Gly Ala Tyr Gly Arg Asp Ile Gly Thr Asn Leu Pro Thr Leu Leu
260                 265                 270                 275

tgg aaa ctg gtt gaa gtg att cct gag gga gca atg ctg agg ctt ggc       978
Trp Lys Leu Val Glu Val Ile Pro Glu Gly Ala Met Leu Arg Leu Gly
                280                 285                 290

atg aca aat ccg ccc tat att tta gag cat ctg gag gaa atg gca aaa      1026
Met Thr Asn Pro Pro Tyr Ile Leu Glu His Leu Glu Glu Met Ala Lys
            295                 300                 305

atc ctt aat cac ccc aga gtc tac gct ttt ctg cac ata cca gtc cag      1074
Ile Leu Asn His Pro Arg Val Tyr Ala Phe Leu His Ile Pro Val Gln
        310                 315                 320

tct gcc tcc gac agc gta ctc atg gaa atg aaa aga gaa tac tgt gtg      1122
Ser Ala Ser Asp Ser Val Leu Met Glu Met Lys Arg Glu Tyr Cys Val
    325                 330                 335

gct gac ttc aaa aga gta gtg gat ttt ctg aaa gag aaa gtt cct gga      1170
Ala Asp Phe Lys Arg Val Val Asp Phe Leu Lys Glu Lys Val Pro Gly
340                 345                 350                 355

ata act att gct aca gat att atc tgt ggt ttt cct gga gaa aca gat      1218
Ile Thr Ile Ala Thr Asp Ile Ile Cys Gly Phe Pro Gly Glu Thr Asp
                360                 365                 370

cag gat ttt caa gaa aca gtg aaa ctt gtt gaa gag tac aaa ttc cca      1266
Gln Asp Phe Gln Glu Thr Val Lys Leu Val Glu Glu Tyr Lys Phe Pro
            375                 380                 385

agc ctg ttt att aac caa ttt tac cca aga cca gga act cct gct gca      1314
Ser Leu Phe Ile Asn Gln Phe Tyr Pro Arg Pro Gly Thr Pro Ala Ala
        390                 395                 400

aaa atg gaa caa gtt cca gca caa gtg aaa aag caa agg aca aaa gat      1362
Lys Met Glu Gln Val Pro Ala Gln Val Lys Lys Gln Arg Thr Lys Asp
    405                 410                 415

ctt tct cgg gtg ttt cat tct tac agt cca tat gat cac aag att ggt      1410
Leu Ser Arg Val Phe His Ser Tyr Ser Pro Tyr Asp His Lys Ile Gly
420                 425                 430                 435

gaa aga caa caa gtg tta gta aca gaa gaa tct ttt gat tcc aag ttt      1458
Glu Arg Gln Gln Val Leu Val Thr Glu Glu Ser Phe Asp Ser Lys Phe
                440                 445                 450

tat gtt gca cac aat caa ttc tat gag cag gtt tta gtg cca aag aac      1506
Tyr Val Ala His Asn Gln Phe Tyr Glu Gln Val Leu Val Pro Lys Asn
            455                 460                 465

cct gcg ttc atg ggg aag atg gtt gaa gtg gac atc tat gaa tca ggc      1554
Pro Ala Phe Met Gly Lys Met Val Glu Val Asp Ile Tyr Glu Ser Gly
        470                 475                 480
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aaa cat ttt atg aaa ggg cag cca gta tct gat gcc aaa gtg tac acg      1602
Lys His Phe Met Lys Gly Gln Pro Val Ser Asp Ala Lys Val Tyr Thr
    485                 490                 495

ccc tcc atc agc aaa ccg cta gca aag gga gaa gtc tca ggt ttg aca      1650
Pro Ser Ile Ser Lys Pro Leu Ala Lys Gly Glu Val Ser Gly Leu Thr
500                 505                 510                 515

aag gac ttc aga aat ggg ctt ggg aac cag ctg agt tca gga tcc cac      1698
Lys Asp Phe Arg Asn Gly Leu Gly Asn Gln Leu Ser Ser Gly Ser His
                520                 525                 530

acc tct gct gca tct cag tgt gac tca gcg agt tcc aga atg gtg ctg      1746
Thr Ser Ala Ala Ser Gln Cys Asp Ser Ala Ser Ser Arg Met Val Leu
            535                 540                 545

ccc atg cca agg cta cat caa gac tgt gcg ctg agg atg tcc gtg ggc      1794
Pro Met Pro Arg Leu His Gln Asp Cys Ala Leu Arg Met Ser Val Gly
        550                 555                 560

ttg gct ctg ctg ggt ctt ctt ttt gct ttt ttt gtc aag gtc tat aat      1842
Leu Ala Leu Leu Gly Leu Leu Phe Ala Phe Phe Val Lys Val Tyr Asn
    565                 570                 575

tag aata caactaatgg aaacatctat aaagaagaat acatttctaa ttaaaatctt      1899
 *
580

caatgaacag gaaagcgaca tctccattct ccaagggcaa taatttgtac tggtcatgct    1959

gcctccttct cagccactct tcttaatgag gctccccctg tctcacattg agttgggccc    2019

attggttatt tgacctaaaa cctaatcacc gctaccatag cacatccttc aaattaaact    2079

gcttttggtt tacttttagc aagaaatgca agcggttgca ttttttctgt ttgtttcaat    2139

ctctaatctt taagtcagaa cctaattgta cagtggctct ggccatcttt tcctcatgtg    2199

gaagaatttt ctatctttaa taaacttttt ctttgttttt tttttccaga tggagtttcg    2259

ctcttgtccc ccaggctgga gtggtgcagt ggcacgatct caggtcactg cagccttgac    2319

ctcctgggtt caagcagtcc tcctacctca gcctccctaa tagccagggg ctacaggcat    2379

ataccaccat gcccaactaa ttttttaatt ttttgtagag atgagtgtca ctatgttgcc    2439

caggcttgcc tggaactcct agcctcaagc agtcttcttg cctcagcctc ccaaagtgct    2499

gggattacag gcgtgagcca ctccacccag cccagattaa atgtttttat ttctacctgc    2559

catcattggt ctttactaag tgaagtgact tctttcttta acaataaatg gaattggtat    2619

actaagcaaa aaaaaaaaa                                                 2638
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tctccaggac tctctcaccc ctgtccagcc ttgcccatgg aaatgcagca ctgttctagc     120

tggctggagg ggagggtagt gagatgggcg gccatctgct ggtagacatg cgggaggact     180

ttccggggca gtgggtttcc agcccccaca tgcccctcag tggggccctg tgccctagag     240

tacaccaag  atg aag act gca gat cac ttc tgg acc gat ccc tcg gct        288
           Met Lys Thr Ala Asp His Phe Trp Thr Asp Pro Ser Ala
           1               5                   10

gac gaa ctt gtc cag agg cac cgc atc cac agc tcc cac gtg cgg cag       336
Asp Glu Leu Val Gln Arg His Arg Ile His Ser Ser His Val Arg Gln
    15                  20                  25

gac tcg ccc acc aag cgt cct gcc ctc tgt atc cag aag agg cat tcc       384
Asp Ser Pro Thr Lys Arg Pro Ala Leu Cys Ile Gln Lys Arg His Ser
30                  35                  40                  45

agt ggc agc atg gat gac cgg cca tcc ctc tct gcc cgc gac tac gtg       432
Ser Gly Ser Met Asp Asp Arg Pro Ser Leu Ser Ala Arg Asp Tyr Val
                50                  55                  60

gag tcc ctg cat cag aac tcc cgt gcc acc ctt ctc tat ggc aaa aac       480
Glu Ser Leu His Gln Asn Ser Arg Ala Thr Leu Leu Tyr Gly Lys Asn
            65                  70                  75

aac gtt ctt gtt cag ccg agg gac gac atg gag gct gtg cca ggg tac       528
Asn Val Leu Val Gln Pro Arg Asp Asp Met Glu Ala Val Pro Gly Tyr
        80                  85                  90

ctg tcc ctg cac cag acg gct gac gtc atg acc ttg aag tgg aca ccc       576
Leu Ser Leu His Gln Thr Ala Asp Val Met Thr Leu Lys Trp Thr Pro
    95                  100                 105

aac cag ctg atg aac ggg tct gtg ggg gac ctg gac tat gag aag agc       624
Asn Gln Leu Met Asn Gly Ser Val Gly Asp Leu Asp Tyr Glu Lys Ser
110                 115                 120                 125

gtc tac tgg gac tat gcc atg acc atc cgc ttg gag gag att gtc tac       672
Val Tyr Trp Asp Tyr Ala Met Thr Ile Arg Leu Glu Glu Ile Val Tyr
                130                 135                 140

ctg cac tgc cac cag caa gtt gac agc ggc ggg aca gtg gta ttg gtc       720
Leu His Cys His Gln Gln Val Asp Ser Gly Gly Thr Val Val Leu Val
            145                 150                 155
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agc cag gac ggg atc cag agg ccg ccc ttc cgc ttc ccc aag ggc ggg       768
Ser Gln Asp Gly Ile Gln Arg Pro Pro Phe Arg Phe Pro Lys Gly Gly
        160                 165                 170

cac ctc ctg cag ttc ctc tcg tgc ctg gag aat ggg ctg ctc cca cat       816
His Leu Leu Gln Phe Leu Ser Cys Leu Glu Asn Gly Leu Leu Pro His
    175                 180                 185

ggg cag ttg gac ccg cca ctg tgg tcc cag agg ggt aag ggc aaa gtg       864
Gly Gln Leu Asp Pro Pro Leu Trp Ser Gln Arg Gly Lys Gly Lys Val
190                 195                 200                 205

ttt cct aaa ctg cgc aag cga agc cct cag ggt tct gcc gag tcc aca       912
Phe Pro Lys Leu Arg Lys Arg Ser Pro Gln Gly Ser Ala Glu Ser Thr
                210                 215                 220

tct tca gac aaa gat gat gat gag gcc acg gat tat gtg ttc agg atc       960
Ser Ser Asp Lys Asp Asp Asp Glu Ala Thr Asp Tyr Val Phe Arg Ile
            225                 230                 235

atc tac cct ggc atg cag tcg gaa ttc gtt gcc ccc gac ttc ttg ggc      1008
Ile Tyr Pro Gly Met Gln Ser Glu Phe Val Ala Pro Asp Phe Leu Gly
        240                 245                 250

agc act tcc tcc gtc tct gtg ggc cct gcc tgg atg atg gtt cct gca      1056
Ser Thr Ser Ser Val Ser Val Gly Pro Ala Trp Met Met Val Pro Ala
    255                 260                 265

ggc cgg tcc atg ctg gtg gtg gcc aga ggg agt cag tgg gag cca gcc      1104
Gly Arg Ser Met Leu Val Val Ala Arg Gly Ser Gln Trp Glu Pro Ala
270                 275                 280                 285

aga tgg gac act act ctc ccc acg cca agc ccg aag gag cag ccc ccc      1152
Arg Trp Asp Thr Thr Leu Pro Thr Pro Ser Pro Lys Glu Gln Pro Pro
                290                 295                 300

agt aat gtc tgg gat ctc ccc gtc ccc agg ggc tgg gtg cca gcc acc      1200
Ser Asn Val Trp Asp Leu Pro Val Pro Arg Gly Trp Val Pro Ala Thr
            305                 310                 315

tct gcc atg ttg tca att gag ttc tgg tcc caa ggg aga tgg agg cag      1248
Ser Ala Met Leu Ser Ile Glu Phe Trp Ser Gln Gly Arg Trp Arg Gln
        320                 325                 330

gaa ggg aga tgg agg cag agg gat tga tgccc tcctgctgtc cagcctccac      1300
Glu Gly Arg Trp Arg Gln Arg Asp  *
    335                 340

t                                                                    1301


      <210> 341
      <211> 723
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<213> Homo sapiens

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<400> 341
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aaggagcgtc acacgattaa gtatcgtgtc acataatagg  atg aca aag ttt tta      115
                                             Met Thr Lys Phe Leu
                                             1               5

att gtt tca gat aca cat ggt gat cgt gag atc att gct gat att ttt      163
Ile Val Ser Asp Thr His Gly Asp Arg Glu Ile Ile Ala Asp Ile Phe
                10                  15                  20

gac aaa tgg cgg gat agc gtt gcc ggc att ttt tac aat ggg gat tct      211
Asp Lys Trp Arg Asp Ser Val Ala Gly Ile Phe Tyr Asn Gly Asp Ser
            25                  30                  35

gaa tta gcg gct gat gac aca gta ttt gat ggc gta tcc act gtg att      259
Glu Leu Ala Ala Asp Asp Thr Val Phe Asp Gly Val Ser Thr Val Ile
        40                  45                  50

ggc aat atg gat gat gat cct gat ttc gtg gcc gca agg gcg aca acg      307
Gly Asn Met Asp Asp Asp Pro Asp Phe Val Ala Ala Arg Ala Thr Thr
    55                  60                  65

att gat ggg att act ttt ttc caa acg cac gga cat ctc tat gac gcg      355
Ile Asp Gly Ile Thr Phe Phe Gln Thr His Gly His Leu Tyr Asp Ala
70                  75                  80                  85

acc caa ttt aac gct tgg gcg aac cta aaa tta atg gcc gtg gca gca      403
Thr Gln Phe Asn Ala Trp Ala Asn Leu Lys Leu Met Ala Val Ala Ala
                90                  95                  100

cag gaa gct aac gca cag gtc gcc ctc ttt ggg cat acc cat ctg gaa      451
Gln Glu Ala Asn Ala Gln Val Ala Leu Phe Gly His Thr His Leu Glu
            105                 110                 115

ggg gcg gtt gtg ttt gat gat atc ttg ttt att aat cca ggt tca atc      499
Gly Ala Val Val Phe Asp Asp Ile Leu Phe Ile Asn Pro Gly Ser Ile
        120                 125                 130

cgg ctg cct aaa ggg cca cat gcc aac tta ggt ggt act tat gct gtg      547
Arg Leu Pro Lys Gly Pro His Ala Asn Leu Gly Gly Thr Tyr Ala Val
    135                 140                 145

ttg gat gtg acg gag acg agc tat gac gtg aga ttt tat aat cgt cag      595
Leu Asp Val Thr Glu Thr Ser Tyr Asp Val Arg Phe Tyr Asn Arg Gln
150                 155                 160                 165

cat caa cca ttg cca caa ctc acg gta cag gtc gca cgt taa gtgaccc      644
His Gln Pro Leu Pro Gln Leu Thr Val Gln Val Ala Arg  *
                170                 175
```

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gtactgattt gcaggcaata aatgtggtaa aatggtagtt atggcaaatg aaaaacacca    704

caatttaatc aatggtatg                                                  723




    <210> 342
    <211> 637
    <212> DNA
    <213> Homo sapiens

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    <221> CDS
    <222> (364)..(543)

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tggcgctgcc ctcgatcact ctgcccctct gggtgcctgt cacctcatta gtgcagttac    120

tcctgggacc aagaccagga aatctaacca ataagcaatg gtaacagtga ctcagtgctc    180

agtccgccct cagtggcccg agtccgaggt gggcatcatg gcaccagttt acatctcgga    240

aagggaggct cagagaggtc aagtcacttg cctaaggtca cccagggact gcttagctgg    300

ctaggatgag aaccagcctg ctccaacgcc ccctcgtgga acagttgcga gcctaggaat    360

taa atg ttc cct ccc cca ggc tat gcc aat gag gtg ggc gag gct ttc      408
    Met Phe Pro Pro Pro Gly Tyr Ala Asn Glu Val Gly Glu Ala Phe
    1               5                   10                  15

cgc tct ctt gtg cca gcg gcg gtg gtg tgg ctg agc tat ggc gtg gcc      456
Arg Ser Leu Val Pro Ala Ala Val Val Trp Leu Ser Tyr Gly Val Ala
                20                  25                  30

agc tcc tac gtg ctg gcg gat gcc att gac aaa ggc aag aag gct gga      504
Ser Ser Tyr Val Leu Ala Asp Ala Ile Asp Lys Gly Lys Lys Ala Gly
            35                  40                  45

gag gtg agt gtt agc cta ttt tcc aac ccc caa ccc tag ctctcctctt       553
Glu Val Ser Val Ser Leu Phe Ser Asn Pro Gln Pro  *
        50                  55                  60

gtgtggctca gtccacagcc tggcatgtga taaagtccct gtgggacact ccagtcccta    613

caacttgcct agtgcagtcc ataa                                           637




    <210> 343
    <211> 998
    <212> DNA
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         Met Ser Phe Asn Arg Leu Leu Ser Val Lys Leu Asn Asp Gly
           1               5                  10

aag ttc atg cct att ctg ggg ttt ggc acc tct gtt gct agg aag gtt       96
Lys Phe Met Pro Ile Leu Gly Phe Gly Thr Ser Val Ala Arg Lys Val
 15                  20                  25                  30

gct atg agt aat gta gaa gaa gcc gtc cag gta gca att gat gta ggc      144
Ala Met Ser Asn Val Glu Glu Ala Val Gln Val Ala Ile Asp Val Gly
                 35                  40                  45

tac cgc cat att gac tca gct tat aca cac ctg aat gaa gaa ggc atc      192
Tyr Arg His Ile Asp Ser Ala Tyr Thr His Leu Asn Glu Glu Gly Ile
             50                  55                  60

ggg cag gcc atc cga aag aag att gcc aac ggc act gtg aag aga aaa      240
Gly Gln Ala Ile Arg Lys Lys Ile Ala Asn Gly Thr Val Lys Arg Lys
         65                  70                  75

gat ata ttc tat acc aca aag gtg tgg ggc acc ttt tcc cgc cca gaa      288
Asp Ile Phe Tyr Thr Thr Lys Val Trp Gly Thr Phe Ser Arg Pro Glu
     80                  85                  90

ttg gtc caa aga ggc ctt gaa atg tca ctg aag aaa ctt cag ctg agc      336
Leu Val Gln Arg Gly Leu Glu Met Ser Leu Lys Lys Leu Gln Leu Ser
 95                 100                 105                 110

tac atg gat ctt tac ctt ttt cat ttc cca gta cct ttg cag cct ggg      384
Tyr Met Asp Leu Tyr Leu Phe His Phe Pro Val Pro Leu Gln Pro Gly
                115                 120                 125

agg agc ttt tgc tga cggatgcaca gggaaagatc atgtttgaca cagtgggtct      439
Arg Ser Phe Cys  *
            130

ctgcagcaca tgggagagtt ttactcctgt tgccaaggct ggagtacagt ggcacgatct    499

cggctcactg caacctccgc ctcccaggtt caagcatgta cctctgcctc ccacatagct    559

gggaatacag gtggaatatc acccttacct caaccaaagc aaactcctgg agtactgtaa    619

gtccaaggac attgtcatga ctgcatattc tgccttgggg tctgactcag acaaagactg    679

gtaatcatct tcataaagtt attttgttta ttttttttag gtgggggtct cattctgtca    739

tccaggctgg agtgcagggg cacaatcaca gcttgttgca ggcttgacct tccaggctca    799

agtcaggatc ttccctccta gacctcctaa gtagctggga ctacaggagt gcaccaccat    859

gcctggctaa ttgtttattt tcatttttgt agagacaggg tctcactacg ttacccaagc    919
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cagtcttgaa ttcctgggct caagtgatcc tcccaccttg gcctcccaaa gtgctgggat      979

tagaggtgta agccacggt                                                   998




<210> 344
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (188)..(376)

<400> 344
aaaatgcaag gtgaagtagt atgtaacata tggtacagtt tacttaagag agaaatacag       60

atgtatatac acattaccta aagcaaaatg aggaccctac tgggctgcca tcccagctgg      120

actgctgctg tggagctcag catcaagtac ttccaggaga agcttcagca ggacctagag      180

gcagagc atg gta gag gta gag gat aca gcc ctc ata cca ccg tgc tgt        229
        Met Val Glu Val Glu Asp Thr Ala Leu Ile Pro Pro Cys Cys
        1               5                   10

atg tcc atc ttt caa gtc ctg gtg gtg ccc gca gag ttt gaa ggg aag        277
Met Ser Ile Phe Gln Val Leu Val Val Pro Ala Glu Phe Glu Gly Lys
15                  20                  25                  30

cca ctg ctt cag aga tac cag gtg gta aat gca tgc cta gtg gaa gtg        325
Pro Leu Leu Gln Arg Tyr Gln Val Val Asn Ala Cys Leu Val Glu Val
                35                  40                  45

tgc tcc tct gca tct atg cct ttg agc aga aag cct ttg agt ccc aat        373
Cys Ser Ser Ala Ser Met Pro Leu Ser Arg Lys Pro Leu Ser Pro Asn
            50                  55                  60

tag tggg cccatgagtg gccaaaatga gggactggga cctgtatagc cgttaaacta        430
 *


taaatcaggg ccaaaaagga aagataaatt ataagtttaa agaaaatg                   478




<210> 345
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (201)..(368)
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     <400> 345
cagtagtcta atctgagttc tctggataat gacttcctgt cattaattat caacatgact     60

tttatacaaa ttaagaaatc tatgggcgtg tgctcttggg ctgctctctg gccagcaccc    120

tctcctgtgt cacctctctt gtgtccacag tctaacccat ctcttcattt ccctcaacct    180

caggtggagc ctccaccaaa    atg cag att ttt cca aaa atc ctt aca ggg     230
                         Met Gln Ile Phe Pro Lys Ile Leu Thr Gly
                          1               5                  10

acg atc atc acc cta gag gtt gaa ccc ttg gat aca aca gaa aaa tgt      278
Thr Ile Ile Thr Leu Glu Val Glu Pro Leu Asp Thr Thr Glu Lys Cys
                15                  20                  25

aaa ggc caa tat cag gat aag gaa cga att cct cct gat cag caa aga      326
Lys Gly Gln Tyr Gln Asp Lys Glu Arg Ile Pro Pro Asp Gln Gln Arg
            30                  35                  40

caa gtg act gga agc tgg caa gta act gga aga tgg aca taa ctttctc      375
Gln Val Thr Gly Ser Trp Gln Val Thr Gly Arg Trp Thr  *
        45                  50                  55

tgactacaac attcaaaagg aatttactct ttttatgttg tgttgagact tcatggtagt    435

gctaaaacta ggaagaaatc ttac                                           459




     <210> 346
     <211> 1867
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (9)..(1835)

     <400> 346
atctgcag atg tta aca tac ctt aac att agc cga aat ctt tta tca aca      50
         Met Leu Thr Tyr Leu Asn Ile Ser Arg Asn Leu Leu Ser Thr
          1               5                  10

ttg cca aaa tac cta ttt gat ctt ccc ctt aaa gtt ttg gtc gtc agt       98
Leu Pro Lys Tyr Leu Phe Asp Leu Pro Leu Lys Val Leu Val Val Ser
 15                  20                  25                  30

aat aat aaa ctg gta tcc att cca gaa gaa att ggg aag tta aaa gat      146
Asn Asn Lys Leu Val Ser Ile Pro Glu Glu Ile Gly Lys Leu Lys Asp
                35                  40                  45

tta atg gaa ttg gat att agc tgc aat gag att caa gtc ctt ccc caa      194
Leu Met Glu Leu Asp Ile Ser Cys Asn Glu Ile Gln Val Leu Pro Gln
            50                  55                  60

caa atg gga aaa tta cat tca ctt aga gag cta aat ata aga aga aat      242
```

```
Gln Met Gly Lys Leu His Ser Leu Arg Glu Leu Asn Ile Arg Arg Asn
            65                  70                  75

aat ctt cat gtt ttg cca gat gaa tta gga gac ctt ccc tta gtc aag        290
Asn Leu His Val Leu Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Lys
        80                  85                  90

ctg gat ttc tct tgt aat aaa gtg acc gaa att cca gtt tgt tac aga        338
Leu Asp Phe Ser Cys Asn Lys Val Thr Glu Ile Pro Val Cys Tyr Arg
 95                 100                 105                 110

aag ctg cat cat tta caa gta ata att ttg gat aac aat cca ttg caa        386
Lys Leu His His Leu Gln Val Ile Ile Leu Asp Asn Asn Pro Leu Gln
                115                 120                 125

gta cca cca gca cag ata tgt tta aag ggt aag gtg cac ata ttt aag        434
Val Pro Pro Ala Gln Ile Cys Leu Lys Gly Lys Val His Ile Phe Lys
            130                 135                 140

tac tta aat att caa gca tgt tgc aga atg gat aag aaa cca gat tcc        482
Tyr Leu Asn Ile Gln Ala Cys Cys Arg Met Asp Lys Lys Pro Asp Ser
        145                 150                 155

ctg gat ctt cca tca ttg agt aaa cga atg ccc tca cag cct ctc aca        530
Leu Asp Leu Pro Ser Leu Ser Lys Arg Met Pro Ser Gln Pro Leu Thr
    160                 165                 170

gac agt atg gaa gat ttt tat cca aat aaa aat cat ggc cct gac tct        578
Asp Ser Met Glu Asp Phe Tyr Pro Asn Lys Asn His Gly Pro Asp Ser
175                 180                 185                 190

gga att gga agt gat aat gga gag aaa cga tta tcc aca aca gaa cca        626
Gly Ile Gly Ser Asp Asn Gly Glu Lys Arg Leu Ser Thr Thr Glu Pro
                195                 200                 205

tca gat gat gac aca gtc agc ctt cat tct caa gtc tca gaa tca aat        674
Ser Asp Asp Asp Thr Val Ser Leu His Ser Gln Val Ser Glu Ser Asn
            210                 215                 220

aga gag cag aca tca aga aat gac agt cac ata ata gga agt aag act        722
Arg Glu Gln Thr Ser Arg Asn Asp Ser His Ile Ile Gly Ser Lys Thr
        225                 230                 235

gat tct cag aaa gac cag gag gta tat gat ttt gtt gac ccc aac aca        770
Asp Ser Gln Lys Asp Gln Glu Val Tyr Asp Phe Val Asp Pro Asn Thr
    240                 245                 250

gaa gat gta gca gtt cct gaa cag gga aat gca cat att gga tca ttt        818
Glu Asp Val Ala Val Pro Glu Gln Gly Asn Ala His Ile Gly Ser Phe
255                 260                 265                 270

gta tca ttc ttt aag gga aaa gaa aaa tgt tct gaa aaa tct cgg aaa        866
Val Ser Phe Phe Lys Gly Lys Glu Lys Cys Ser Glu Lys Ser Arg Lys
                275                 280                 285

aat gaa gaa tta gga gat gaa aaa aga ctt gag aaa gaa cag tta ctg        914
Asn Glu Glu Leu Gly Asp Glu Lys Arg Leu Glu Lys Glu Gln Leu Leu
```

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            290                 295                 300

gca gag gaa gag gat gat gat ttg aag gaa gta act gat ttg agg aaa      962
Ala Glu Glu Glu Asp Asp Asp Leu Lys Glu Val Thr Asp Leu Arg Lys
        305                 310                 315

ata gct gct cag tta ttg cag caa gaa cag aag aac agg att ctt aat     1010
Ile Ala Ala Gln Leu Leu Gln Gln Glu Gln Lys Asn Arg Ile Leu Asn
    320                 325                 330

cat tca act tct gtg atg aga aac aag cca aaa caa act gtg gaa tgt     1058
His Ser Thr Ser Val Met Arg Asn Lys Pro Lys Gln Thr Val Glu Cys
335                 340                 345                 350

gaa aag agt gtc tca gca gat gaa gtt aat tca cca tta tca ccc ctc     1106
Glu Lys Ser Val Ser Ala Asp Glu Val Asn Ser Pro Leu Ser Pro Leu
                355                 360                 365

acc tgg cag ccc tta gaa aat cag aag gat caa ata gat gaa caa ccg     1154
Thr Trp Gln Pro Leu Glu Asn Gln Lys Asp Gln Ile Asp Glu Gln Pro
            370                 375                 380

tgg cca gaa tct cac cct ata atc tgg cag agt gaa gaa agg agg cgg     1202
Trp Pro Glu Ser His Pro Ile Ile Trp Gln Ser Glu Glu Arg Arg Arg
        385                 390                 395

agc aaa cag att aga aaa gaa tat ttc aag tat aaa tca atg agg aag     1250
Ser Lys Gln Ile Arg Lys Glu Tyr Phe Lys Tyr Lys Ser Met Arg Lys
    400                 405                 410

agt tca agt ggc aat gaa aat gat gag caa gac agt gat aat gct aat     1298
Ser Ser Ser Gly Asn Glu Asn Asp Glu Gln Asp Ser Asp Asn Ala Asn
415                 420                 425                 430

atg tca aca caa tct cca gta tca tct gag gaa tat gac aga act gat     1346
Met Ser Thr Gln Ser Pro Val Ser Ser Glu Glu Tyr Asp Arg Thr Asp
                435                 440                 445

ggt ttt tca cac agt ccc ttt ggc ttg aag cct aga tca gct ttt agc     1394
Gly Phe Ser His Ser Pro Phe Gly Leu Lys Pro Arg Ser Ala Phe Ser
            450                 455                 460

cgc tca tct cgc caa gaa tat ggg gca gca gat cca gga ttt aca atg     1442
Arg Ser Ser Arg Gln Glu Tyr Gly Ala Ala Asp Pro Gly Phe Thr Met
        465                 470                 475

aga aga aag atg gaa cat tta cgg gaa gag cga gag caa ata cga caa     1490
Arg Arg Lys Met Glu His Leu Arg Glu Glu Arg Glu Gln Ile Arg Gln
    480                 485                 490

ctt cgc aac aat ctt gaa tcc agg tta aaa gta att ttg cct gat gac     1538
Leu Arg Asn Asn Leu Glu Ser Arg Leu Lys Val Ile Leu Pro Asp Asp
495                 500                 505                 510

att gga gct gca ctg atg gat ggg gtt gtt ctt tgc cat tta gcc aat     1586
Ile Gly Ala Ala Leu Met Asp Gly Val Val Leu Cys His Leu Ala Asn
                515                 520                 525
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cat ata agg cca cgt tct gtt gct agt att cat gta cca tca cca gca      1634
His Ile Arg Pro Arg Ser Val Ala Ser Ile His Val Pro Ser Pro Ala
            530                 535                 540

gtg ccc aaa ctg agc atg gca aaa tgt cga aga aat gta gaa aat ttt      1682
Val Pro Lys Leu Ser Met Ala Lys Cys Arg Arg Asn Val Glu Asn Phe
        545                 550                 555

ctt gat gct tgt aaa aag ttg ggt gtc tca cag gaa aga ctt tgt ttg      1730
Leu Asp Ala Cys Lys Lys Leu Gly Val Ser Gln Glu Arg Leu Cys Leu
    560                 565                 570

cct cat cat att ttg gaa gaa cga gga ctt gtg aaa gtt ggt gtc aca      1778
Pro His His Ile Leu Glu Glu Arg Gly Leu Val Lys Val Gly Val Thr
575                 580                 585                 590

gtt cag gcg ctc ctt gaa tta cca aca acc aag gca tct cag ctt tct      1826
Val Gln Ala Leu Leu Glu Leu Pro Thr Thr Lys Ala Ser Gln Leu Ser
                595                 600                 605

gtg gct taa tataacattt taaaattcta aaaaaaaaaa aa                      1867
Val Ala  *
```

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<210> 347
<211> 527
<212> DNA
<213> Homo sapiens

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<222> (133)..(336)

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tacataactc ttttatctgc agttttgggg gagtccaatt ccaccatttt ttatgtctgt     120

tactgtcatt ca    atg tgg att gct tcc tta tgt ttc att att ttg gat      168
                 Met Trp Ile Ala Ser Leu Cys Phe Ile Ile Leu Asp
                 1               5                   10

tgt gag ctc atc ttt tgt agg gtg tta gct aca gaa atc cta tgc tgc      216
Cys Glu Leu Ile Phe Cys Arg Val Leu Ala Thr Glu Ile Leu Cys Cys
        15                  20                  25

agg gtt gag att tgt ccc tat ttg ctt ctg tat tac tgc cta agg acc      264
Arg Val Glu Ile Cys Pro Tyr Leu Leu Leu Tyr Tyr Cys Leu Arg Thr
    30                  35                  40

aac ttt gct cat tta aaa tat att tat ata agc tca aag att aaa gct      312
Asn Phe Ala His Leu Lys Tyr Ile Tyr Ile Ser Ser Lys Ile Lys Ala
```

```
 45                  50                  55                  60

gac tgt ggg gag gtc tat ggc taa aaattttcaa gggagatttc ttccccctaa     366
Asp Cys Gly Glu Val Tyr Gly  *
                65

tctggctaag atgggcagat tcccattgtc ttcctgtgcc agtgtgcaga tatcatctag    426

tatactcttt cactgcaagc atggctcttc gagggtcctg gctctatgac gaagtcttca    486

gttccaaatc ttcatcttgt gccagcctaa cgcctttgtt t                        527




     <210> 348
     <211> 2112
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (410)..(868)

     <400> 348
atgctacggc atactggcac gagggactgg gaaaacaaat gcaaggaggg ctagttcaca     60

gcaaattcac tgcctcctcc catgcacgtg gtagagagta ccagtatcaa catggccctg    120

ttttctgcta aaaccagatt ttgaggaatc agagaccccc aacactactc actcagtagc    180

tagcagcccc ttcctttcaa ctgggagtgt tattagaatg aaaagtaatt agttagaagg    240

gcatacatct cagtggcatg agcattgtgg aatatccttt cctaggcaca tttgtccact    300

aagggaacag cctcagaaac tggtacagca atgggtgaga tgagatcctg gagagagaac    360

acagccatcc cctatagaaa ggcacagctt ttgggcttct ctggcctga    atg cct     415
                                                         Met Pro
                                                          1

tct ggg gta ttt cca tat gca aca gcc cag agt cat agc ctt ggg caa      463
Ser Gly Val Phe Pro Tyr Ala Thr Ala Gln Ser His Ser Leu Gly Gln
        5                  10                  15

cca cac ata gag gtt tcc ttc tca ctt cag aca cat aca tca ctt tca      511
Pro His Ile Glu Val Ser Phe Ser Leu Gln Thr His Thr Ser Leu Ser
    20                  25                  30

cac cac ttg ggg atg gaa ata cct aca aga gtg aag gtc aag ggc cct      559
His His Leu Gly Met Glu Ile Pro Thr Arg Val Lys Val Lys Gly Pro
 35                  40                  45                  50

ccc cag gca tct cat tca tta ctc agc ttc ctt cct gac caa gtc tgc      607
Pro Gln Ala Ser His Ser Leu Leu Ser Phe Leu Pro Asp Gln Val Cys
                55                  60                  65
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caa cca atg gcc agc tat gcg cct cat cct cat tgc ttc tgc ctc cac       655
Gln Pro Met Ala Ser Tyr Ala Pro His Pro His Cys Phe Cys Leu His
            70                  75                  80

gta aat gaa acc aaa ggc ctc agc ata tcc tgg gag gac tgg ggg ctg       703
Val Asn Glu Thr Lys Gly Leu Ser Ile Ser Trp Glu Asp Trp Gly Leu
        85                  90                  95

tta cct aat ggt cct ctc tgt ccc att ata ggt gca agg cac ccc atc       751
Leu Pro Asn Gly Pro Leu Cys Pro Ile Ile Gly Ala Arg His Pro Ile
    100                 105                 110

cac aca ttt gca cca cta ctc caa gat agt att ttt ctt ttc aca caa       799
His Thr Phe Ala Pro Leu Leu Gln Asp Ser Ile Phe Leu Phe Thr Gln
115                 120                 125                 130

tct ctt tac agc aga atc cag agt tgg gtt gta gtt tac ctt cct gga       847
Ser Leu Tyr Ser Arg Ile Gln Ser Trp Val Val Val Tyr Leu Pro Gly
            135                 140                 145

aag ctc att atc ttt gtt tga at taacatttca gcatggaact aactgggcgg       900
Lys Leu Ile Ile Phe Val  *
            150

aggaaggatc gttatacgtc ttcagaaagt tctcattgcc ccagctgcct agtactatac      960

aagaagctct actttgatgg cagatctaag aaggctatag gcctttgttt gtaggaagca     1020

gtgtcattac attcaagctt cacttctctg attggcttcc aaccactggg attcaaagag     1080

aatccaaggt tctgcctatg tctgatgaca taaggaaaac ttggcttcct ctgctcaagg     1140

ttcccctctg ctcatccctc ctcattcaga catcctccac cataccagtg tttagaagca     1200

aaacatgaag ggctagcgcc accaggatag ttagcagaaa tattgtctgt aaagctaggc     1260

aggtgagccc agaagaatgg tcccagagaa agcagactgg ctccaataga tatcaggcag     1320

caatcccaat aaattctgac atgtccttgg caatggaagc ctgggttgga gatcctgagg     1380

cagctgtgcc tactgttccc cacctcagaa gcttcctgcc cagagagcca gcagccttgg     1440

gatactaatg aggatgcaac tggcttattg gtatgaaata gaaggtggct ttgtaggggc     1500

aagcaggcaa agagtactat ccacatggca ggcaggtggc tttgtgtctg gaaagctttg     1560

cctagccagt acagctgtga gcagaggctg gttataaatt tgaactccct cagcccattt     1620

gcaactctgc ctctgttccc ttgcattctg tttggttgcc ctttagtttc ctagtaaatg     1680

ctccttttga aaaactccaa ccttgtctta tttaacttgg gggaagggga ttctccaatg     1740

tcttttccag gataaagaag gaaattaaaa taccatgaaa aaatggacat ggcagtagaa     1800

aggaaacatt ctgatcagac cttgggaaaa gctggtgccg agagagggag aggccaggtg     1860

tccccccacc caactggcac tgattctcag ccccttcctc ttacttctgt tggcttcaag     1920
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gagacctgcc cttgatgtgt gttgctgctg aagcaccctc ccagccagtg agttggacat   1980

atgcagcagg cactttgatg tccaggaagt acactggtac atgacaggag caagggtcag   2040

ggaggggagg ggaaaggttt ctacaatgca gatgttttca aaattctcca acaatcatga   2100

ctctaaatgg ta                                                       2112



      <210> 349
      <211> 1385
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (19)..(984)

      <220>
      <221> misc_feature
      <222> (1)...(1385)
      <223> n = a,t,c or g

      <400> 349
atttagtaat taaaagca  atg agc tgg gcc aag atg gca gtg cag gtg gtg      51
                     Met Ser Trp Ala Lys Met Ala Val Gln Val Val
                       1               5                  10

cag gcg gtg cag gcg gtt cat ctc gag tct gac gct ttc ctc gtt tgt      99
Gln Ala Val Gln Ala Val His Leu Glu Ser Asp Ala Phe Leu Val Cys
            15                  20                  25

ctc aac cac gct ctg agc aca gag aag gag gaa gta atg ggg ctg tgc     147
Leu Asn His Ala Leu Ser Thr Glu Lys Glu Glu Val Met Gly Leu Cys
        30                  35                  40

ata ggg gag ttg aac gat gat aca agg agt gac tcc aaa ttt gca tat     195
Ile Gly Glu Leu Asn Asp Asp Thr Arg Ser Asp Ser Lys Phe Ala Tyr
    45                  50                  55

act gga act gaa atg cgc aca gtt gct gaa aag gtt gat gcc gtc aga     243
Thr Gly Thr Glu Met Arg Thr Val Ala Glu Lys Val Asp Ala Val Arg
60                  65                  70                  75

att gtt cac att cat tct gtc atc atc tta cga cgt tct gat aag agg     291
Ile Val His Ile His Ser Val Ile Ile Leu Arg Arg Ser Asp Lys Arg
                80                  85                  90

aag gac cga gta gaa att tct cca gag cag ctg tct gca gct tca aca     339
Lys Asp Arg Val Glu Ile Ser Pro Glu Gln Leu Ser Ala Ala Ser Thr
            95                  100                 105

gag gca gag agg ttg gct gaa ctg aca ggc cgc ccc atg aga gtt gtg     387
Glu Ala Glu Arg Leu Ala Glu Leu Thr Gly Arg Pro Met Arg Val Val
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        110                 115                 120

ggc tgg tat cat tcc cat cct cat ata act gtt tgg cct tca cat gtt       435
Gly Trp Tyr His Ser His Pro His Ile Thr Val Trp Pro Ser His Val
    125                 130                 135

gat gtt cgc aca caa gcc atg tac cag atg atg gat caa ggc ttt gta       483
Asp Val Arg Thr Gln Ala Met Tyr Gln Met Met Asp Gln Gly Phe Val
140                 145                 150                 155

gga ctt att ttt tcc tgt ttc ata gaa gat aag aac acg aag act ggc       531
Gly Leu Ile Phe Ser Cys Phe Ile Glu Asp Lys Asn Thr Lys Thr Gly
                160                 165                 170

cgg gta ctc tac act tgc ttc caa tcc ata cag gcc caa aag agt tca       579
Arg Val Leu Tyr Thr Cys Phe Gln Ser Ile Gln Ala Gln Lys Ser Ser
            175                 180                 185

gag tcc ctt cat ggt cca cga gac ttc tgg agc tcc agc cag cac atc       627
Glu Ser Leu His Gly Pro Arg Asp Phe Trp Ser Ser Ser Gln His Ile
        190                 195                 200

tcc att gag ggc cag aag gaa gag gaa agg tat gag aga atc gaa atc       675
Ser Ile Glu Gly Gln Lys Glu Glu Glu Arg Tyr Glu Arg Ile Glu Ile
    205                 210                 215

cca atc cat att gta cct cat gtc act atc tgg aaa gtg tgc ctt gaa       723
Pro Ile His Ile Val Pro His Val Thr Ile Trp Lys Val Cys Leu Glu
220                 225                 230                 235

tca gca gta gag ctg ccc aag atc ctg tgc cag gag gag cag gat gcg       771
Ser Ala Val Glu Leu Pro Lys Ile Leu Cys Gln Glu Glu Gln Asp Ala
                240                 245                 250

tat agg agg atc cac agc ctt aca cat ctg gac tca gta acc aag atc       819
Tyr Arg Arg Ile His Ser Leu Thr His Leu Asp Ser Val Thr Lys Ile
            255                 260                 265

cat aat ggc tca gtg ttt acc aag aat ctg tgc agt cag atg tcg gca       867
His Asn Gly Ser Val Phe Thr Lys Asn Leu Cys Ser Gln Met Ser Ala
        270                 275                 280

gtc agc ggg cct ctc cta cag tgg ttg gag gac aga ctg gag caa aac       915
Val Ser Gly Pro Leu Leu Gln Trp Leu Glu Asp Arg Leu Glu Gln Asn
    285                 290                 295

caa cag cat ttg cag gaa tta caa caa gaa aag gaa gag ctt atg caa       963
Gln Gln His Leu Gln Glu Leu Gln Gln Glu Lys Glu Glu Leu Met Gln
300                 305                 310                 315

gaa ctt tct tct cta gaa taa at caggagacaa aatggggaaa gatgaaaata      1016
Glu Leu Ser Ser Leu Glu  *
                320

tccagtgtaa agttacttaa gctaaatcaa tttcaaagaa gaaaaacttg gaggactcat    1076

tttacctgac ttcaagactt actataaagc tatagtaatc aagatagatg gtattggcag    1136
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aggaacagac acatacgtca atggaacaga tgagagaacc cagaaataaa cccatataaa   1196

tatgctcagc tgattttgaa aaagtgaaaa agcaattcaa tggaggaaga atagcctttc   1256

tgacaaatta tgctagagca attagacacc catggcgagg agaaaaaaga acctctactt   1316

anacctcaca tcttatataa aatttaactc aaaatgtata acggacttaa atgtgataca   1376

taaaactag                                                           1385



      <210> 350
      <211> 437
      <212> DNA
      <213> Homo sapiens

      <220>
      <221> CDS
      <222> (146)..(394)

      <400> 350
ctcactatag ggaattgggc cctcgaggcc aagaattcgg cacgaggtta aggacgtact     60

cgtcttggtg agagcgtgag ctgctgagat ttgggagtct gcgctaggcc cgcttggagt    120

tctgagccga tgtaagagtt cactc atg ttt gca ccc gcg gtg atg cgt gct      172
                            Met Phe Ala Pro Ala Val Met Arg Ala
                             1               5

ttt cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg atg gat      220
Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Met Asp
 10                  15                  20                  25

cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct tta gag tcg      268
Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu Ser
                 30                  35                  40

gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg aag aat att      316
Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn Ile
             45                  50                  55

cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa gga aga aat      364
Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg Asn
         60                  65                  70

cca gaa agc ctt aag act aag aca act tga c tctgctgatt ctttttttcct     415
Pro Glu Ser Leu Lys Thr Lys Thr Thr  *
     75                  80

tttttttttt ttaaaaaaaa aa                                             437
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<210> 351
<211> 1415
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (25)..(1239)

<400> 351

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gccaggaccc tggaaggaag cagg    atg gca gcc gga aca gca gtt gga gcc       51
                              Met Ala Ala Gly Thr Ala Val Gly Ala
                               1               5

tgg gtg ctg gtc ctc agt ctg tgg ggg gca gta gta ggt gct caa aac       99
Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn
 10                  15                  20                  25

atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc      147
Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala
                 30                  35                  40

ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg      195
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg
             45                  50                  55

aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac      243
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp
         60                  65                  70

agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc      291
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val
     75                  80                  85

ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat      339
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn
 90                  95                 100                 105

gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct      387
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro
                110                 115                 120

ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt      435
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val
            125                 130                 135

ccc aat aag gtg ggg aca tgt gtg tca gag gga agc tac cct gca ggg      483
Pro Asn Lys Val Gly Thr Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly
        140                 145                 150

act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag      531
Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys
    155                 160                 165

gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc      579
Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu
170                 175                 180                 185
```

```
ttc aca ctg cag tcg gag cta atg gtg acc cca gcc cgg gga gga gat         627
Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp
                190                 195                 200

ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac         675
Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His
            205                 210                 215

cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg         723
Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val
        220                 225                 230

cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta         771
Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val
    235                 240                 245

gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc         819
Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro
250                 255                 260                 265

tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc         867
Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro
                270                 275                 280

ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga         915
Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly
            285                 290                 295

acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc         963
Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser
        300                 305                 310

cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act        1011
Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr
    315                 320                 325

gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg        1059
Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu
330                 335                 340                 345

ggg atc ctg gga ggc ctg ggg aca gcc gcc ctg ctc att ggg gtc atc        1107
Gly Ile Leu Gly Gly Leu Gly Thr Ala Ala Leu Leu Ile Gly Val Ile
                350                 355                 360

ttg tgg caa agg cgg caa cgc cga gga gag gag agg aag gcc cca gaa        1155
Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu
            365                 370                 375

aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa        1203
Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu
        380                 385                 390

cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca        1253
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro  *
    395                 400                 405
```

```
gatcccatcc atcagctccc ttttcttttt cccttgaact gttctggcct cagaccaact   1313

ctctcctgta taatctctct cctgtataac cccaccttgc caagctttct tctacaacca   1373

gagcccccca caatgatgat taaacacctg acacatcttg ca                      1415




<210> 352
<211> 1463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (25)..(1287)

<400> 352
gccaggaccc tggaaggaag cagg   atg gca gcc gga aca gca gtt gga gcc      51
                             Met Ala Ala Gly Thr Ala Val Gly Ala
                              1               5

tgg gtg ctg gtc ctc agt ctg tgg ggg gca gta gta ggt gct caa aac      99
Trp Val Leu Val Leu Ser Leu Trp Gly Ala Val Val Gly Ala Gln Asn
 10                  15                  20                  25

atc aca gcc cgg att ggc gag cca ctg gtg ctg aag tgt aag ggg gcc     147
Ile Thr Ala Arg Ile Gly Glu Pro Leu Val Leu Lys Cys Lys Gly Ala
                 30                  35                  40

ccc aag aaa cca ccc cag cgg ctg gaa tgg aaa ctg aac aca ggc cgg     195
Pro Lys Lys Pro Pro Gln Arg Leu Glu Trp Lys Leu Asn Thr Gly Arg
             45                  50                  55

aca gaa gct tgg aag gtc ctg tct ccc cag gga gga ggc ccc tgg gac     243
Thr Glu Ala Trp Lys Val Leu Ser Pro Gln Gly Gly Gly Pro Trp Asp
         60                  65                  70

agt gtg gct cgt gtc ctt ccc aac ggc tcc ctc ttc ctt ccg gct gtc     291
Ser Val Ala Arg Val Leu Pro Asn Gly Ser Leu Phe Leu Pro Ala Val
     75                  80                  85

ggg atc cag gat gag ggg att ttc cgg tgc cag gca atg aac agg aat     339
Gly Ile Gln Asp Glu Gly Ile Phe Arg Cys Gln Ala Met Asn Arg Asn
 90                  95                 100                 105

gga aag gag acc aag tcc aac tac cga gtc cgt gtc tac cag att cct     387
Gly Lys Glu Thr Lys Ser Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro
                110                 115                 120

ggg aag cca gaa att gta gat tct gcc tct gaa ctc acg gct ggt gtt     435
Gly Lys Pro Glu Ile Val Asp Ser Ala Ser Glu Leu Thr Ala Gly Val
            125                 130                 135

ccc aat aag gta gtg gaa gaa agc agg aga agt aga aaa cgg ccc tgt     483
Pro Asn Lys Val Val Glu Glu Ser Arg Arg Ser Arg Lys Arg Pro Cys
```

```
        140                 145                 150

gaa cag gag gtg ggg aca tgt gtg tca gag gga agc tac cct gca ggg        531
Glu Gln Glu Val Gly Thr Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly
    155                 160                 165

act ctt agc tgg cac ttg gat ggg aag ccc ctg gtg cct aat gag aag        579
Thr Leu Ser Trp His Leu Asp Gly Lys Pro Leu Val Pro Asn Glu Lys
170                 175                 180                 185

gga gta tct gtg aag gaa cag acc agg aga cac cct gag aca ggg ctc        627
Gly Val Ser Val Lys Glu Gln Thr Arg Arg His Pro Glu Thr Gly Leu
                190                 195                 200

ttc aca ctg cag tcg gag cta atg gtg acc cca gcc cgg gga gga gat        675
Phe Thr Leu Gln Ser Glu Leu Met Val Thr Pro Ala Arg Gly Gly Asp
            205                 210                 215

ccc cgt ccc acc ttc tcc tgt agc ttc agc cca ggc ctt ccc cga cac        723
Pro Arg Pro Thr Phe Ser Cys Ser Phe Ser Pro Gly Leu Pro Arg His
        220                 225                 230

cgg gcc ttg cgc aca gcc ccc atc cag ccc cgt gtc tgg gag cct gtg        771
Arg Ala Leu Arg Thr Ala Pro Ile Gln Pro Arg Val Trp Glu Pro Val
    235                 240                 245

cct ctg gag gag gtc caa ttg gtg gtg gag cca gaa ggt gga gca gta        819
Pro Leu Glu Glu Val Gln Leu Val Val Glu Pro Glu Gly Gly Ala Val
250                 255                 260                 265

gct cct ggt gga acc gta acc ctg acc tgt gaa gtc cct gcc cag ccc        867
Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Val Pro Ala Gln Pro
                270                 275                 280

tct cct caa atc cac tgg atg aag gat ggt gtg ccc ttg ccc ctt ccc        915
Ser Pro Gln Ile His Trp Met Lys Asp Gly Val Pro Leu Pro Leu Pro
            285                 290                 295

ccc agc cct gtg ctg atc ctc cct gag ata ggg cct cag gac cag gga        963
Pro Ser Pro Val Leu Ile Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly
        300                 305                 310

acc tac agc tgt gtg gcc acc cat tcc agc cac ggg ccc cag gaa agc       1011
Thr Tyr Ser Cys Val Ala Thr His Ser Ser His Gly Pro Gln Glu Ser
    315                 320                 325

cgt gct gtc agc atc agc atc atc gaa cca ggc gag gag ggg cca act       1059
Arg Ala Val Ser Ile Ser Ile Ile Glu Pro Gly Glu Glu Gly Pro Thr
330                 335                 340                 345

gca ggc tct gtg gga gga tca ggg ctg gga act cta gcc ctg gcc ctg       1107
Ala Gly Ser Val Gly Gly Ser Gly Leu Gly Thr Leu Ala Leu Ala Leu
                350                 355                 360

ggg atc ctg gga ggc ctg ggg aca gcc gcc ctg ctc att ggg gtc atc       1155
Gly Ile Leu Gly Gly Leu Gly Thr Ala Ala Leu Leu Ile Gly Val Ile
            365                 370                 375
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```
ttg tgg caa agg cgg caa cgc cga gga gag gag agg aag gcc cca gaa      1203
Leu Trp Gln Arg Arg Gln Arg Arg Gly Glu Glu Arg Lys Ala Pro Glu
        380                 385                 390

aac cag gag gaa gag gag gag cgt gca gaa ctg aat cag tcg gag gaa      1251
Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu Asn Gln Ser Glu Glu
    395                 400                 405

cct gag gca ggc gag agt agt act gga ggg cct tga gggg cccacagaca      1301
Pro Glu Ala Gly Glu Ser Ser Thr Gly Gly Pro  *
410                 415                 420

gatcccatcc atcagctccc ttttcttttt cccttgaact gttctggcct cagaccaact    1361

ctctcctgta taatctctct cctgtataac cccaccttgc caagctttct tctacaacca    1421

gagcccccca caatgatgat taaacacctg acacatcttg ca                       1463




     <210> 353
     <211> 926
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (10)..(600)

     <400> 353
tttcgtggt    atg gtc ccc ggg tcc gag ggc ccg gcc cgc gcc ggg agc       48
             Met Val Pro Gly Ser Glu Gly Pro Ala Arg Ala Gly Ser
               1               5                  10

gtg gtg gcc gac gtg gtg ttt gtg att gag ggt acg gcc aac ctg gga       96
Val Val Ala Asp Val Val Phe Val Ile Glu Gly Thr Ala Asn Leu Gly
    15                  20                  25

ccc tac ttc gag ggg ctc cgc aag cac tac ctg ctc ccg gcc atc gag      144
Pro Tyr Phe Glu Gly Leu Arg Lys His Tyr Leu Leu Pro Ala Ile Glu
 30                  35                  40                  45

tat ttt aat ggt ggt cct cct gct gag acg gac ttc ggg gga gac tat      192
Tyr Phe Asn Gly Gly Pro Pro Ala Glu Thr Asp Phe Gly Gly Asp Tyr
                50                  55                  60

ggg ggg acc cag tac agc ctc gtg gtg ttc aac aca gtg gac tgc gct      240
Gly Gly Thr Gln Tyr Ser Leu Val Val Phe Asn Thr Val Asp Cys Ala
            65                  70                  75

ccc gag tcc tac gta caa tgt cac gct ccc acc agc agc gcc tat gag      288
Pro Glu Ser Tyr Val Gln Cys His Ala Pro Thr Ser Ser Ala Tyr Glu
        80                  85                  90

ttt gtc acc tgg ctc gat ggc att aag ttc atg ggc ggg ggt ggt gag      336
```

```
Phe Val Thr Trp Leu Asp Gly Ile Lys Phe Met Gly Gly Gly Gly Glu
     95                 100                 105

agc tgc agc ctc atc gcg gaa gga ctc agc aca gcc ttg cag ctg ttt        384
Ser Cys Ser Leu Ile Ala Glu Gly Leu Ser Thr Ala Leu Gln Leu Phe
110                 115                 120                 125

gat gac ttc aag aag atg cgc gag cag att ggc cag acg cac cgg gtc        432
Asp Asp Phe Lys Lys Met Arg Glu Gln Ile Gly Gln Thr His Arg Val
                130                 135                 140

tgc ctc ctc atc tgc aac tca ccc cca tac ttg ttg cct gct gtt gag        480
Cys Leu Leu Ile Cys Asn Ser Pro Pro Tyr Leu Leu Pro Ala Val Glu
            145                 150                 155

agc acc acg tac tct gga tgc aca act gag aat ctt gtg cag cca gat        528
Ser Thr Thr Tyr Ser Gly Cys Thr Thr Glu Asn Leu Val Gln Pro Asp
        160                 165                 170

tgg gga agc ggg gga tcc act tct cca ttg gtg tct ccc cgg aag ctg        576
Trp Gly Ser Gly Gly Ser Thr Ser Pro Leu Val Ser Pro Arg Lys Leu
    175                 180                 185

cct gcg ctt cgg ctt cct ggt tga agaaaggcag ccccccggcc tgggtggagc       630
Pro Ala Leu Arg Leu Pro Gly  *
190                 195

cgctgaggcc tccgacagat gttgaggcac tgaccgaggg acatggtggt ggttcgggga      690

ctcgtgctgc tggggggggt ggtcagccca gggccttcaa taaagaagca gggcctgcca      750

acagagcgag cagagacgga accgcaccac cgcagagaac caaagaaagg cgcaaaaaga      810

aagcaacaga ggcaaaaaag cacacaaacg cacacgacac agccgcgcga caacacgacg      870

agccaacaca aaagacgacg cacaaggcac gccagaaaag aggcgagaga acacaa          926


     <210> 354
     <211> 510
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (149)..(493)

     <400> 354
gataccagct tccttcagca gcgcaggcgg tggtccctga ggcccgtgga aggagtcaaa       60

cttgcgggaa ttttgcagaa gtcattgtat tcaaagaaga ataagcaaga aagaaaagaa      120

ggaaggaaga gaggtagaca gatacaag   atg aaa tcc tgt caa aaa atg gaa       172
                                 Met Lys Ser Cys Gln Lys Met Glu
                                  1               5
```

```
gga aaa cca gaa aat gag agt gaa cca aag cat gag gaa gag cca aag       220
Gly Lys Pro Glu Asn Glu Ser Glu Pro Lys His Glu Glu Glu Pro Lys
    10                  15                  20

cct gag gaa aag cca gaa gag gag gag aag cta gag gag gag gcc aaa       268
Pro Glu Glu Lys Pro Glu Glu Glu Glu Lys Leu Glu Glu Glu Ala Lys
25                  30                  35                  40

gca aaa gga act ttt aga gaa agg ctg att caa tct ctc cag gag ttt       316
Ala Lys Gly Thr Phe Arg Glu Arg Leu Ile Gln Ser Leu Gln Glu Phe
                45                  50                  55

aaa gaa gat ata cac aac agg cat tta agc aat gaa gat atg ttt aga       364
Lys Glu Asp Ile His Asn Arg His Leu Ser Asn Glu Asp Met Phe Arg
            60                  65                  70

gaa gtg gat gaa ata gat gag ata agg aga gtc aga aac aaa ctt ata       412
Glu Val Asp Glu Ile Asp Glu Ile Arg Arg Val Arg Asn Lys Leu Ile
        75                  80                  85

gtg atg cgt tgg aag gta acg aac cct cct acc cca ttt aaa tta gag       460
Val Met Arg Trp Lys Val Thr Asn Pro Pro Thr Pro Phe Lys Leu Glu
    90                  95                  100

tac ccg gat ttc tct cat att aca tac cca tag cgctcttata gcagcac        510
Tyr Pro Asp Phe Ser His Ile Thr Tyr Pro  *
105                 110                 115




     <210> 355
     <211> 1045
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (95)..(1045)

     <400> 355
tagaggagta gattaccgag aaaaatatcc catcagtgag gagattttcg gtatcaccag      60

aaagaccaaa gatcagggct gcttaattgc tgac    atg atg gga ctc acc gag      112
                                         Met Met Gly Leu Thr Glu
                                          1               5

ggg gtg ttc ctg att ctg tct ggc act cag ttc aca ctg gga att ctg       160
Gly Val Phe Leu Ile Leu Ser Gly Thr Gln Phe Thr Leu Gly Ile Leu
            10                  15                  20

gtc aat tgt ttc att gag ttg gtc aat ggt agc agc tgg ttc aag acc       208
Val Asn Cys Phe Ile Glu Leu Val Asn Gly Ser Ser Trp Phe Lys Thr
        25                  30                  35
```

```
aag aga atg tct ttg tct gac ttc atc atc acc acc ctg gca ctc ttg      256
Lys Arg Met Ser Leu Ser Asp Phe Ile Ile Thr Thr Leu Ala Leu Leu
     40                  45                  50

agg atc att ctg ctg tgt att atc ttg act gat agt ttt tta ata gaa      304
Arg Ile Ile Leu Leu Cys Ile Ile Leu Thr Asp Ser Phe Leu Ile Glu
 55                  60                  65                  70

ttc tct ccc aac aca cat gat tca ggg ata ata atg caa att att gat      352
Phe Ser Pro Asn Thr His Asp Ser Gly Ile Ile Met Gln Ile Ile Asp
                 75                  80                  85

gtt tcc tgg aca ttt aca aac cat ctg agc att tgg ctt gcc acc tgt      400
Val Ser Trp Thr Phe Thr Asn His Leu Ser Ile Trp Leu Ala Thr Cys
             90                  95                 100

ctt ggt gtc ctc tac tgc ctg aaa atc gcc agt ttc tct cac ccc aca      448
Leu Gly Val Leu Tyr Cys Leu Lys Ile Ala Ser Phe Ser His Pro Thr
        105                 110                 115

ttc ctc tgg ctc aag tgg aga gtt tct agg gtg atg gta tgg atg ctg      496
Phe Leu Trp Leu Lys Trp Arg Val Ser Arg Val Met Val Trp Met Leu
    120                 125                 130

ttg ggt gca ctg ctc tta tcc tgt ggt agt acc gca tct ctg atc aat      544
Leu Gly Ala Leu Leu Leu Ser Cys Gly Ser Thr Ala Ser Leu Ile Asn
135                 140                 145                 150

gag ttt aag ctc tat tct gtc ttt agg gga att gag gcc acc agg aat      592
Glu Phe Lys Leu Tyr Ser Val Phe Arg Gly Ile Glu Ala Thr Arg Asn
                155                 160                 165

gtg act gaa cac ttc aga aag aag agg agt gag tat tat ctg atc cat      640
Val Thr Glu His Phe Arg Lys Lys Arg Ser Glu Tyr Tyr Leu Ile His
            170                 175                 180

gtt ctt ggg act ctg tgg tac ctg cct ccc tta att gtg tcc ctg gcc      688
Val Leu Gly Thr Leu Trp Tyr Leu Pro Pro Leu Ile Val Ser Leu Ala
        185                 190                 195

tcc tac tct ttg ctc atc ttc tcc ctg ggg agg cac aca cgg cag atg      736
Ser Tyr Ser Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met
    200                 205                 210

ctg caa aat ggg aca agc tcc aga gat cca acc act gag gcc cac aag      784
Leu Gln Asn Gly Thr Ser Ser Arg Asp Pro Thr Thr Glu Ala His Lys
215                 220                 225                 230

agg gcc atc aga atc atc ctt tcc ttc ttc ttt ctc ttc tta ctt tac      832
Arg Ala Ile Arg Ile Ile Leu Ser Phe Phe Phe Leu Phe Leu Leu Tyr
                235                 240                 245

ttt ctt gct ttc tta att gca tca ttt ggt aat ttc cta cca aaa acc      880
Phe Leu Ala Phe Leu Ile Ala Ser Phe Gly Asn Phe Leu Pro Lys Thr
            250                 255                 260

aag atg gct aag atg att ggc gaa gta atg aca atg ttt tat cct gct      928
```

```
Lys Met Ala Lys Met Ile Gly Glu Val Met Thr Met Phe Tyr Pro Ala
        265                 270                 275

ggc cac tca ttt att ctc att ctg ggg aac agt aag ctg aag cag aca      976
Gly His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr
    280                 285                 290

ttt gta gtg atg ctc cgg tgt gag tct ggt cat ctg aag cct gga tcc     1024
Phe Val Val Met Leu Arg Cys Glu Ser Gly His Leu Lys Pro Gly Ser
295                 300                 305                 310

aag gga ccc att ttc tct tag                                         1045
Lys Gly Pro Ile Phe Ser  *
                315
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<210> 356
<211> 790
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (86)..(310)

<220>
<221> misc_feature
<222> (1)...(790)
<223> n = a,t,c or g

<400> 356
agacaaacct catctgccct gttgtttttt gttctcacct tcttattcag tatgagtgtc      60

gtttggtgct tctaatggtc ttcta atg gtc ctc ctg gaa ccc aag ccc tgg      112
                            Met Val Leu Leu Glu Pro Lys Pro Trp
                             1               5

ctg gaa ctg atg ctg ctg tgg tgg tca ggg ttc agt gag cag gag gaa      160
Leu Glu Leu Met Leu Leu Trp Trp Ser Gly Phe Ser Glu Gln Glu Glu
 10                  15                  20                  25

gga ctt ggt gtt tac ccc ttg ttt acc cct ttc ctt ggc ttc ctt cca      208
Gly Leu Gly Val Tyr Pro Leu Phe Thr Pro Phe Leu Gly Phe Leu Pro
                 30                  35                  40

tgc agg cca ccc tgt gac ccc gtg gtg gcc ccc tct gga acc aag agc      256
Cys Arg Pro Pro Cys Asp Pro Val Val Ala Pro Ser Gly Thr Lys Ser
             45                  50                  55

tgc cga ctt cca gca gca cac aca gga tca gtg ctg ggg cca tct gtg      304
Cys Arg Leu Pro Ala Ala His Thr Gly Ser Val Leu Gly Pro Ser Val
         60                  65                  70

cac tga ccaaagcctc tgctggcctc accagaccaa ggccagtgag tgcttcaggg      360
```

```
His  *
    75

agccttggat cctccaggct gccaacagaa acaccggccc tctcggcagc agccccatcc    420

ttccacccct gcactgggtc ctgaaaagcc cattttgggg ccgttgctat ttagccaacc    480

tgccctccct tgctctcctg tgatttctca ctattccggc tgcagctcgc tgggagaaac    540

acttgagagt cttttgtgct ccacacccat gtacttaaaa taccaggcct ataggtcatt    600

tcaatgaggg aatttggctc ataacacgtg tgccccgagg cnagnatcct acttctgcag    660

atgctggcca agaagggctg tgtcccagcc gccatggggt ggggccacag agagggcagg    720

gccacgtgga gggcagagca tgtggctcct gtcaggtgcg cccattgctt nacttcagcc    780

cagtatcaag                                                            790
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     <210> 357
     <211> 433
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (67)..(246)

     <400> 357
ggcatatttc aggtttcagt gacatagatc aagtaatttt aaaccaattt ggttattcta     60

tctaag   atg agg gac atg gct att aag gtc aag cca aac tat act aaa      108
         Met Arg Asp Met Ala Ile Lys Val Lys Pro Asn Tyr Thr Lys
           1               5                  10

agt agt ata ggg cag cag tta aaa tta tct ttt gaa aat caa gta tta      156
Ser Ser Ile Gly Gln Gln Leu Lys Leu Ser Phe Glu Asn Gln Val Leu
 15                  20                  25                  30

cct ggt ttc ttc tgt cac aac aga ata gct ggt tac cta gtc agt cac      204
Pro Gly Phe Phe Cys His Asn Arg Ile Ala Gly Tyr Leu Val Ser His
                 35                  40                  45

agt tgc cct tgc ctt ccc ttg tta gtc cct gga ggt act tga gtggaac      253
Ser Cys Pro Cys Leu Pro Leu Leu Val Pro Gly Gly Thr  *
             50                  55                  60

agaaggtaga attagcaaca gctcaatcac tttaggtagc atttctcctg aattctgctg    313

ccaaatcctc agggtctatg gattggttga aatagtaaaa tcacacatag tgatttcttg    373

cacagcgtaa aggcgtttaa ttttagtgta tagtgaacaa agaaggaaaa ctgggtcata    433
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<210> 358
<211> 1483
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (117)..(911)

<400> 358
agttgattgc aggtcctcct ggggccagaa gggtgcctgg gaggccaggt tctggggatc      60

ccctccatcc agaagaacca cctgctcact ctgtcccttc gcctgctgct gggacc         116
atg ggg gct ggg gcc agt gct gag gag aag cac tcc agg gag ctg gaa       164
Met Gly Ala Gly Ala Ser Ala Glu Glu Lys His Ser Arg Glu Leu Glu
1               5                   10                  15

aag aag ctg aaa gag gac gct gag aag gat gct cga acc gtg aag ctg       212
Lys Lys Leu Lys Glu Asp Ala Glu Lys Asp Ala Arg Thr Val Lys Leu
            20                  25                  30

ctg ctt ctg ggt gcc ggt gag tcc ggg aag agc acc atc gtc aag cag       260
Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln
        35                  40                  45

atg aag att atc cac cag gac ggg tac tcg ctg gaa gag tgc ctc gag       308
Met Lys Ile Ile His Gln Asp Gly Tyr Ser Leu Glu Glu Cys Leu Glu
    50                  55                  60

ttt atc gcc atc atc tac ggc aac acg ttg cag tcc atc ctg gcc atc       356
Phe Ile Ala Ile Ile Tyr Gly Asn Thr Leu Gln Ser Ile Leu Ala Ile
65                  70                  75                  80

gta cgc gcc atg acc aca ctc aac atc cag tac gga gac tct gca cgc       404
Val Arg Ala Met Thr Thr Leu Asn Ile Gln Tyr Gly Asp Ser Ala Arg
                85                  90                  95

cag gac gac gcc cgg aag ctg atg cac atg gca gac act atc gag gag       452
Gln Asp Asp Ala Arg Lys Leu Met His Met Ala Asp Thr Ile Glu Glu
            100                 105                 110

ggc acg atg ccc aag gag atg tcg gac atc atc cag cgg ctg tgg aag       500
Gly Thr Met Pro Lys Glu Met Ser Asp Ile Ile Gln Arg Leu Trp Lys
        115                 120                 125

gac tcc ggt atc cag gcc tgt ttt gag cgc gcc tcg gag tac cag ctc       548
Asp Ser Gly Ile Gln Ala Cys Phe Glu Arg Ala Ser Glu Tyr Gln Leu
    130                 135                 140

aac gac tcg gcg ggc tac tac ctc tcc gac ctg gag cgc ctg gta acc       596
Asn Asp Ser Ala Gly Tyr Tyr Leu Ser Asp Leu Glu Arg Leu Val Thr
145                 150                 155                 160

ccg ggc tac gtg ccc acc gag cag gac gtg ctg cgc tcg cga gtc aag       644
Pro Gly Tyr Val Pro Thr Glu Gln Asp Val Leu Arg Ser Arg Val Lys
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                165                 170                 175

acc act ggc atc atc gag acg cag ttc tcc ttc aag gat ctc aac ttc       692
Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp Leu Asn Phe
            180                 185                 190

cgg atg ttc gat gtg ggc ggg cag cgc tcg gag cgc aag aag tgg atc       740
Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys Lys Trp Ile
        195                 200                 205

cac tgc ttc gag ggc gtg acc tgc atc atc ttc atc gcg gcg ctg agc       788
His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Ile Ala Ala Leu Ser
    210                 215                 220

gcc cta cga cat ggt gct agt gga gga cga cga agt gaa ccg cat gca       836
Ala Leu Arg His Gly Ala Ser Gly Gly Arg Arg Ser Glu Pro His Ala
225                 230                 235                 240

cga gag cct gca cct gtt caa cag cat ctg caa cca ccg cta ctt cgc       884
Arg Glu Pro Ala Pro Val Gln Gln His Leu Gln Pro Pro Leu Leu Arg
                245                 250                 255

cac gac gtc cat cgt gct ctt cct taa caaga aggacgtctt cttcgagaag       936
His Asp Val His Arg Ala Leu Pro  *
            260                 265

atcaagaagg cgcacctcag catctgtttc ccggactacg atggacccaa cacctacgag     996

gacgccggca actacatcaa ggtgcagttc ctcgagctca acatgcggcg cgacgtgaag    1056

gagatctatt cccacatgac gtgcgccacc gacacgcaga acgtcaaatt tgtcttcgac    1116

gctgtcaccg acatcatcat caaggagaac ctcaaagact gtggcctctt ctgagcacca    1176

aatctttgct tatagatcca cagccagggc ctgtgctgca gtcggggaca aggagcttcc    1236

gtctggcaag ggaagctgag agccatggct gaactatcag ggacaaaggc ccatgtcccc    1296

acatccctgc tccctccttc ctcatccagc accaaatctt tgcttatgct ccacagccag    1356

ggcctgtgct gcagtcgggg acaaggagct tccgtactgg caaggccggg gcacaatttg    1416

cactcccctc agctagacgc acagactcag caataaacct ttgcatcagg caaaaaaaaa    1476

aaaaaaa                                                              1483


       <210> 359
       <211> 714
       <212> DNA
       <213> Homo sapiens

       <220>
       <221> CDS
       <222> (1)..(441)
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<400> 359
atg aag ccc acc ctc atc tca gtg ctt gtg ata ata ttt ata ctc aga        48
Met Lys Pro Thr Leu Ile Ser Val Leu Val Ile Ile Phe Ile Leu Arg
 1               5                  10                  15

gga aca aga gcc cag aga gtg act cag ccc gag aag ctc ctc tct gtc        96
Gly Thr Arg Ala Gln Arg Val Thr Gln Pro Glu Lys Leu Leu Ser Val
             20                  25                  30

ttt aaa ggg gcc cca gtg gag ctg aag tgc aac tat tcc tat tct ggg       144
Phe Lys Gly Ala Pro Val Glu Leu Lys Cys Asn Tyr Ser Tyr Ser Gly
         35                  40                  45

agt cct gaa ctc ttc tgg tat gtc cag tac tcc aga caa cgc ctc cag       192
Ser Pro Glu Leu Phe Trp Tyr Val Gln Tyr Ser Arg Gln Arg Leu Gln
     50                  55                  60

tta ctc ttg aga cac atc tct aga gag agc atc aaa ggc ttc act gct       240
Leu Leu Leu Arg His Ile Ser Arg Glu Ser Ile Lys Gly Phe Thr Ala
 65                  70                  75                  80

gac ctt aac aaa ggc gag aca tct ttc cac ctg aag aaa cca ttt gct       288
Asp Leu Asn Lys Gly Glu Thr Ser Phe His Leu Lys Lys Pro Phe Ala
                 85                  90                  95

caa gag gaa gac tca gcc atg tat tac tgt gct cta agt ggc aca gta       336
Gln Glu Glu Asp Ser Ala Met Tyr Tyr Cys Ala Leu Ser Gly Thr Val
            100                 105                 110

gct ggt ttt gca agg aag cag aac aca aac cct tta aat aca gga aat       384
Ala Gly Phe Ala Arg Lys Gln Asn Thr Asn Pro Leu Asn Thr Gly Asn
        115                 120                 125

att tct ttg caa act ctc tgt atg gcc aca gca ggg cat tct ttc tcc       432
Ile Ser Leu Gln Thr Leu Cys Met Ala Thr Ala Gly His Ser Phe Ser
    130                 135                 140

aga aat taa tattgag tttatctcgt agatattata tcatcactca tcagctagcc       488
Arg Asn  *
145

atacacccac ctcacaattt tgtccaaaaa attctcatca tttaccctgc ctaaattaaa     548

tttaaaaata gtaaacgtat tcatttcgtc tagcagcact ggacacacac cttcgaaata     608

aaaactacct tgcactgcac aaaaaacaaa aacaaaaaca cattgccggc cgcccccttta    668

ttcccctcag tcagggctac cctaccttcc acctcatccg ctcatt                    714


<210> 360
<211> 3154
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (278)..(1483)

<400> 360
tggtttcttg gaagaacgtg ctcagcgcgg tctcgtatga aggagttttc cgcctgcagc      60

aactgcttcg cctggtcggc cgcgcacccg ccggtctagc gaactggttg atcatgacct     120

ggtgccgcag ctcgtccatg ttcaccgaca tggcgcggcc gcgcggggcc cggcgtctcc     180

ggccggacgc agacgcgggg ctgcgctcgt agcggggccc cggatccccg agtggcggcc     240

ggagcctcga aaagagattc tcagcgctga ttttgag atg atg ggc ttg gga aac      295
                                         Met Met Gly Leu Gly Asn
                                          1               5

ggg cgt cgc agc atg aag tcg ccg ccc ctc gtg ctg gcc gcc ctg gtg       343
Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val Leu Ala Ala Leu Val
             10                  15                  20

gcc tgc atc atc gtc ttg ggc ttc aac tac tgg att gcg agc tcc cgg       391
Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp Ile Ala Ser Ser Arg
         25                  30                  35

agc gtg gac ctc cag aca cgg atc atg gag ctg gaa ggc agg gtc cgc       439
Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly Arg Val Arg
     40                  45                  50

agg gcg gct gca gag aga ggc gcc gtg gag ctg aag aag aac gag ttc       487
Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys Asn Glu Phe
 55                  60                  65                  70

cag gga gag ctg gag aag cag cgg gag cag ctt gac aaa atc cag tcc       535
Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser
                 75                  80                  85

agc cac aac ttc cag ctg gag agc gtc aac aag ctg tac cag gac gaa       583
Ser His Asn Phe Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu
             90                  95                 100

aag gcg gtt ttg gtg aat aac atc acc aca ggt gag agg ctc atc cga       631
Lys Ala Val Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg
        105                 110                 115

gtg ctg caa gac cag tta aag acc ctg cag agg aat tac ggc agg ctg       679
Val Leu Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu
    120                 125                 130

cag cag gat gtc ctc cag ttt cag aag aac cag acc aac ctg gag agg       727
Gln Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
135                 140                 145                 150

aag ttc tcc tac gac ctg agc cag tgc atc aat cag atg aag gag gtg       775
Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu Val
                155                 160                 165
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aag gaa cag tgt gag gag cga ata gaa gag gtc acc aaa aag ggg aat        823
Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys Gly Asn
            170                 175                 180

gaa gct gta gct tcc aga gac ctg agt gaa aac aac gac cag aga cag        871
Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp Gln Arg Gln
        185                 190                 195

cag ctc caa gcc ctc agt gag cct cag ccc agg ctg cag gca gca ggc        919
Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu Gln Ala Ala Gly
    200                 205                 210

ctg cca cac aca gag gtg cca caa ggg aag gga aac gtg ctt ggt aac        967
Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly Asn Val Leu Gly Asn
215                 220                 225                 230

agc aag tcc cag aca cca gcc ccc agt tcc gaa gtg gtt ttg gat tca       1015
Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser Glu Val Val Leu Asp Ser
                235                 240                 245

aag aga caa gtt gag aaa gag gaa acc aat gag atc cag gtg gtg aat       1063
Lys Arg Gln Val Glu Lys Glu Glu Thr Asn Glu Ile Gln Val Val Asn
            250                 255                 260

gag gag cct cag agg gac agg ctg ccg cag gag cca ggc cgg gag cag       1111
Glu Glu Pro Gln Arg Asp Arg Leu Pro Gln Glu Pro Gly Arg Glu Gln
        265                 270                 275

gtg gtg gaa gac aga cct gta ggt gga aga ggc ttc ggg gga gcc gga       1159
Val Val Glu Asp Arg Pro Val Gly Gly Arg Gly Phe Gly Gly Ala Gly
    280                 285                 290

gaa ctg ggc cag acc cca cag gtg cag gct gcc ctg tca gtg agc cag       1207
Glu Leu Gly Gln Thr Pro Gln Val Gln Ala Ala Leu Ser Val Ser Gln
295                 300                 305                 310

gaa aat cca gag atg gag ggc cct gag cga gac cag ctt gtc atc ccc       1255
Glu Asn Pro Glu Met Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro
                315                 320                 325

gac gga cag gag gag gag cag gaa gct gcc ggg gaa ggg aga aac cag       1303
Asp Gly Gln Glu Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln
            330                 335                 340

cag aaa ctg aga gga gaa gat gac tac aac atg gat gaa aat gaa gca       1351
Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala
        345                 350                 355

gaa tct gag aca gac aag caa gca gcc ctg gca ggg aat gac aga aac       1399
Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn
    360                 365                 370

ata gat gtt ttt aat gtt gaa gat cag aaa aga gac acc ata aat tta       1447
Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu
375                 380                 385                 390
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ctt gat cag cgt gaa aag cgg aat cat aca ctc tga attg aactggaatc     1497
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu  *
                395                 400

acatatttca caacagggcc gaagagatga ctataaaatg ttcatgaggg actgaatact   1557

gaaaactgtg aaatgtacta aataaaatgt acatctgaag atgattattg tgaaatttta   1617

gtatgcactt tgtgtaggaa aaaatggaat ggtcttttaa acagcttttg ggggggtact   1677

ttggaagtgt ctaataaggt gtcacaattt ttggtagtag gtatttcgtg agaagttcaa   1737

caccaaaact ggaacatagt tctccttcaa gtgttggcga cagcggggct tcctgattct   1797

ggaatataac tttgtgtaaa ttaacagcca cctatagaag agtccatctg ctgtgaagga   1857

gagacagaga actctgggtt ccgtcgtcct gtccacgtgc tgtaccaagt gctggtgcca   1917

gcctgttacc tgttctcact gaaaagtctg gctaatgctc ttgtgtagtc acttctgatt   1977

ctgacaatca atcaatcaat ggcctagagc actgactgtt aacacaaacg tcactagcaa   2037

agtagcaaca gctttaagtc taaatacaaa gctgttctgt gtgagaattt tttaaaaggc   2097

tacttgtata ataacccttg tcatttttaa tgtacaaaac gctattaagt ggcttagaat   2157

ttgaacattt gtggtcttta tttactttgc ttcgtgtgtg ggcaaagcaa catcttccct   2217

aaatatatat taccaagaaa agcaagaagc agattaggtt tttgacaaaa caaacaggcc   2277

aaaagggggc tgacctggag cagagcatgg tgagaggcaa ggcatgagag ggcaagtttg   2337

ttgtggacag atctgtgcct actttattac tggagtaaaa gaaaacaaag ttcattgatg   2397

tcgaaggata tatacagtgt tagaaattag gactgtttag aaaaacagga atacaatggt   2457

tgtttttatc atagtgtaca catttagctt gtggtaaatg actcacaaaa ctgattttaa   2517

aatcaagtta atgtgaattt tgaaaattac tacttaatcc taattcacaa taacaatggc   2577

attaaggttt gacttgagtt ggttcttagt attatttatg gtaaataggc tcttaccact   2637

tgcaaataac tggccacatc attaatgact gacttcccag taaggctctc taaggggtaa   2697

gtaggaggat ccacaggatt tgagatgcta aggccccaga gatcgtttga tccaaccctc   2757

ttattttcag aggggaaaat ggggcctaga agttacagag catctagctg gtgcgctggc   2817

acccctggcc tcacacagac tcccgagtag ctgggactac aggcacacag tcactgaagc   2877

aggccctgtt tgcaattcac gttgccacct ccaacttaaa cattcttcat atgtgatgtc   2937

cttagtcact aaggttaaac tttcccaccc agaaaaggca acttagataa aatcttagag   2997

tactttcata ctcttctaag tcctcttcca gcctcacttt gagtcctcct tggggttgat   3057

aggaattttc tcttgctttc tcaataaagt ctctattcat ctcatgttta atttgtacgc   3117
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atagaattgc tgagaaataa aatgttctgt tcaactt                              3154



     <210> 361
     <211> 566
     <212> DNA
     <213> Homo sapiens

     <220>
     <221> CDS
     <222> (129)..(329)

     <400> 361
tttcgtgtta ttcctaattt aaacaggcaa atcacttact ctactgcagt gtttgtcaac       60

cttgttttca ttatctcccc ctaaggagcc tttacaggca ttattttcct agtcctcccc      120

atgtcctc atg ata ttt gaa tta cac aga tat acc tta tat ctg ctt atg       170
         Met Ile Phe Glu Leu His Arg Tyr Thr Leu Tyr Leu Leu Met
           1               5                  10

tac tgt ata tac atc tta gtt tta tat att aat cat aag att ttt tca        218
Tyr Cys Ile Tyr Ile Leu Val Leu Tyr Ile Asn His Lys Ile Phe Ser
 15                  20                  25                  30

ccc ttc ctc ctc caa gaa caa att ttt acc ccc ttc aaa gca ata tgg        266
Pro Phe Leu Leu Gln Glu Gln Ile Phe Thr Pro Phe Lys Ala Ile Trp
                 35                  40                  45

ccc cac tgt tcc att gct tta agg gaa ata cca tgt aag cct cta tta        314
Pro His Cys Ser Ile Ala Leu Arg Glu Ile Pro Cys Lys Pro Leu Leu
             50                  55                  60

tct acc aag ctc tga gcaggctctt cacatagttt cattaactca tcaaaaccct        369
Ser Thr Lys Leu  *
         65

gcttcctgat ctctaatcct tttcctcatt ttggtaccaa caaacatgac cttcagtgga      429

gatatttgtt tagcaaaaga gattacctat ttttttctcc aaccagttgt tgatgccatg      489

aatttctatt aagaaaagcc tggatagttc tttcaaattt gccgaaacac aacttgacct      549

tttttgtgt gtgcgcc                                                       566



     <210> 362
     <211> 691
     <212> DNA
     <213> Homo sapiens

     <220>
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<222> (364)..(588)

<400> 362
atattatgca actttcagta ttagtactct cagcaagttg gactgttact acatcatagt      60

tattgttgct gtaaatattc tgtggtaggt aatacactga tactgtgttt ttgccaagaa     120

gtatagtttt tcatttatca gctgatttgt cactgaaagc atgtgcacca tacccataaa     180

tactggatga agtttttcag cccttactat gacccatatt tcttttgcac actgattgtc     240

tttctcctta agatttgcgg aacagctctc tgagctcgga cgtagttcac agcaacgtgg     300

ctaaaccaag aagttggaat cgttggtaaa tacaggaccc gctatggggt ctccctccag     360

aaa atg gtg aag aaa att gaa atc agc cag tac gcc aag tac att tgc       408
    Met Val Lys Lys Ile Glu Ile Ser Gln Tyr Ala Lys Tyr Ile Cys
    1               5                   10                  15

tct ttt ctg tgg caa aac caa gat gaa gag acg agc tgt ggg gat ctg       456
Ser Phe Leu Trp Gln Asn Gln Asp Glu Glu Thr Ser Cys Gly Asp Leu
                20                  25                  30

gtg ctg tgg ttt tgc atg aag aca gta aag gtg tct tca tcc agg aac       504
Val Leu Trp Phe Cys Met Lys Thr Val Lys Val Ser Ser Ser Arg Asn
            35                  40                  45

cac att gtc tgg acc tac aat acc act tca gct gtc acg gta aag tcc       552
His Ile Val Trp Thr Tyr Asn Thr Thr Ser Ala Val Thr Val Lys Ser
        50                  55                  60

acc atc aga aga ctg aag caa ttg aaa gac cag tag acgc tcctctactc       602
Thr Ile Arg Arg Leu Lys Gln Leu Lys Asp Gln  *
    65                  70                  75

tttgagacat cactagccta taataaatgg gttaatttat gtaaccaaaa aaattaaaaa     662

ggtttgtgga aaaactgaaa aaaaaaaaa                                       691
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